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Docket No.: 787CIP2B

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Jc840 U.S. PTO

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE
PATENT APPLICATION TRANSMITTAL UNDER 37 CFR 1.53

Jc836 U.S. PTO
09/620325
07/19/00

BOX PATENT APPLICATION
Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

Transmitted herewith for filing is the patent application of

Inventor(s): Y. Tom Tang, Ping Zhou, Chenghua Liu, Vinod Asundi, Jie Zhang, Feiyan Ren,
Rui-hong Chen, Qing A. Zhao, Aidong J. Xue, Yonghong Yang, Tom Wehrman,
Jian-Rui Wang, Yunqing Ma, Dunrui Wang, John Tillinghast, Radoje T.
Drmanac

Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. Type of application

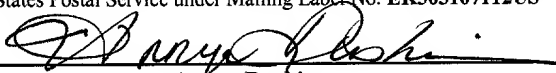
- ☒ This is a new application for a
- ☒ Utility patent.
- ☐ Design patent.
- ☒ This is a continuation-in-part application of prior application no. 09/560,875 filed April 27, 2000, Attorney Docket No. 787CIP, which is a continuation-in-part application of prior application no. 09/496,914 filed February 03, 2000, Attorney Docket No. 787.

2. Application Papers Enclosed

- 1 Title Page
- 138 Pages of Specification (excluding Claims, Abstract, Drawings & Sequence Listing)
- 4 Page(s) of Claims
- 1 Page(s) of Abstract
- 0 Sheet(s) of Drawings (Figs. X-X) ☐ Formal ☐ Informal
- 1357 Page(s) of Sequence Listing

CERTIFICATION UNDER 37 CFR 1.10

I hereby certify that this Patent Application Transmittal and the documents referred to as enclosed therewith are being deposited with the United States Postal Service on **July 19, 2000**, in an envelope addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231 utilizing the "Express Mail Post Office to Addressee" service of the United States Postal Service under Mailing Label No. **EK305107112US**


Anya Dushine

3. Oath or Declaration

- ☐ Enclosed
 - ☐ Executed by (check all applicable boxes)
 - ☐ Inventor(s)
 - ☐ Legal representative of inventors(s) (37 CFR 1.42 or 1.43)
 - ☐ Joint inventor or person showing a proprietary interest on behalf of inventor who refused to sign or cannot be reached
 - ☐ The petition required by 37 CFR 1.47 and the statement required by 37 CFR 1.47 are enclosed. See Item 5D below for fee.
- ☒ Unexecuted – the undersigned attorney or agent is authorized to file this application on behalf of the applicant(s). An executed declaration will follow.

4. Additional Papers Enclosed

- ☐ Preliminary Amendment
- ☐ Information Disclosure Statement
- ☐ Declaration of Biological Deposit
- ☒ Computer readable copy of sequence listing containing nucleotide and/or amino acid sequence
- ☒ Statement Under 37 CFR § 1.821
- ☒ Paper copy of sequence listing identical to computer copy (1357 pages)
- ☐ Microfiche computer program
- ☒ Verified statement claiming small entity status under 37 CFR 1.9 and 1.27
- ☐ Associate Power of Attorney
- ☐ Verified translation of a non-English patent application
- ☒ Return receipt postcard
- ☐ Other _____

5. Priority Applications Under 35 USC 119

Certified copies of applications from which priority under 35 USC 119 is claimed are listed below and

- ☐ are attached.
- ☐ will follow.

6. **Filing Fee Calculation (37 CFR 1.16)**

A. ☒ **Utility Application**

CLAIMS AS FILED – INCLUDING PRELIMINARY AMENDMENT (IF ANY)						
			SMALL ENTITY		OTHER THAN A SMALL ENTITY	
	NO. FILED	NO. EXTRA	RATE	FEE	RATE	FEE
BASIC FEE				\$345.00		\$690.00
TOTAL	28-20	= 8	X 9 =	\$72.00	X 18 =	\$0.00
INDEP.	3-3	= 0	X 39 =	\$0.00	X 78 =	\$0.00
<input checked="" type="checkbox"/> First Presentation of Multiple Dependent Claim			+ 130 =	\$130.00	+ 260 =	\$0.00
FILING FEE:				\$547.00	OR	\$0.00

B. ☐ **Design Application (\$155.00/\$310.00)** Filing Fee: \$ _____

C. ☐ **Plant Application (\$240.00/\$480.00)** Filing Fee: \$ _____

D. **Other fees**

☐ Recording Assignment [Fee -- \$40.00 per assignment] \$ _____

☐ Other \$ _____

TOTAL FEES \$ 547.00

7. Method of Payments of Fees

- ☐ Enclosed check
- ☒ Charge Deposit Account No. 501169. A duplicate copy of this transmittal is enclosed
- ☐ Not enclosed

8. Deposit Account and Refund Authorization

The Commissioner is hereby authorized to charge payment of any additional fees due or credit any overpayment to Deposit Account No. 501169. A duplicate copy of this transmittal is enclosed.

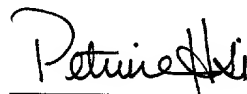
Please refund any overpayment to Hyseq, Inc. at the address below.

Please direct all future correspondence to Petrina S. Hsi at the address below.

Respectfully submitted,

Date: July 19, 2000

By:



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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s) or Patentee(s): Y. Tom Tang, Ping Zhou, Chenghua Liu, Vinod Asundi, Jie Zhang, Feiyan Ren, Rui-hong Chen, Qing A. Zhao, Aidong J. Xue, Yonghong Yang, Tom Wehrman, Jian-Rui Wang, Yunqing Ma, Dunrui Wang, John Tillinghast, Radoje T. Drmanac

Application No. or Patent No.: Not Yet Assigned

Filed or Issued: Herewith

For: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

**VERIFIED STATEMENT (DECLARATION) CLAIMING SMALL ENTITY STATUS
(37 CFR § 1.9(f) AND 1.27(c)) - SMALL BUSINESS CONCERN**

I hereby declare that I am

- ☐ The owner of the small business concern identified below:
- ☒ An official of the small business concern empowered to act on behalf of the concern identified below:

NAME OF CONCERN: HYSEQ, INC.
ADDRESS: 670 Almanor Avenue
Sunnyvale, CA 94085

I hereby declare that the above-identified small business concern qualifies as a small business concern as defined in 13 CFR § 121.12, and reproduced in 37 CFR § 1.9(d), for purposes of paying reduced fees under § 41(a) and (b) of Title 35, United States Code, in that the number of employees of the concern, including those of its affiliates, does not exceed 500 persons. For purposes of this statement, (1) the number of employees of the business concern is the average over the previous fiscal year of the concern of the persons employed on a full-time, part-time or temporary basis during each of the pay periods of the fiscal year, and (2) concerns are affiliates of each other when either, directly or indirectly, one concern controls or has the power to control the other, or a third party or parties controls or has the power to control both.

I hereby declare that rights under contract or law have been conveyed to, and remain with, the small business concern identified above with regard to the invention, entitled NOVEL NUCLEIC ACIDS AND POLYPEPTIDES by inventors, Y. Tom Tang, et al. described in

- ☒ The specification filed herewith.
- ☐ Application Serial No. [], filed [Date].
- ☐ Patent No. [], issued [Date].

If the rights held by the above identified small business concern are not exclusive, each individual, concern or organization having rights to the invention is listed below¹ and no rights to the invention are held by any person, other than the inventor, who could not qualify as a small business concern under 37 CFR § 1.9(c), or by any concern which would not qualify as a small business concern under 37 CFR § 1.9(d) or a nonprofit organization under 37 CFR § 1.9(e).

Full Name: _____

Address: _____

() Individual () Small Business Concern () Nonprofit Organization

I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small entity is no longer appropriate (37 CFR § 1.28(b)).

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under § 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

Name of person signing: Mark E. Gitter

Title of person
other than owner: Chief Financial Officer

Address of person signing: HYSEQ, INC.
670 Almanor Avenue
Sunnyvale, CA 94085

Signature: _____

Date: _____

7-18-00

¹NOTE: Separate verified statements are required from each named person, concern or organization having rights to the invention averring to their status as small entities. (37 CFR § 1.27)

Our Ref. No.: 787CIP2B

NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

Express Mail Label No.: EK305107112US

NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. CROSS REFERENCE TO RELATED APPLICATIONS

5 This application is a continuation-in-part application of U.S. Application Serial No. 09/560,875, filed April 27, 2000, which in turn is a continuation-in-part application of U.S. Application Serial No. 09/496,914, filed February 03, 2000, both of which are incorporated herein by reference in their entirety.

10 2. BACKGROUND OF THE INVENTION

2.1 TECHNICAL FIELD

15 The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

2.2 BACKGROUND

20 Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as
25 signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the

case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1 - 419 and are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanosine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO: 1 - 419 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO: 1 - 419. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO: 1 - 419 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1 - 419. The sequence information can be a segment of any one of SEQ ID NO: 1 - 419 that uniquely identifies or represents the sequence information of SEQ ID NO: 1 - 419.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-419 or novel segments or parts of the nucleic acids of the invention are used as primers in

expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-419 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as

5 expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in the SEQ ID NO: 1-419; a polynucleotide comprising any of the full length protein coding sequences of the SEQ ID NO: 1-419; and a polynucleotide comprising any of the nucleotide
10 sequences of the mature protein coding sequences of the SEQ ID NO: 1-419. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in the SEQ ID NO: 1-419; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the
15 Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

20 The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in the SEQ ID NO: 1-419; or (b)
25 polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The
30 polypeptides of the invention may be wholly or partially chemically synthesized but are

preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, e.g., *in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies,

are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a
5 therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

10 The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the
15 invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in
20 a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or
25 monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that
30 modulate (i.e., increase or decrease) the expression or activity of the polynucleotides

and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (*e.g.*, bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have the closest homology (set forth in Table 1). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

4. DETAILED DESCRIPTION OF THE INVENTION

4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived

The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of
5 nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating
10 sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides
15 or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide
20 linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment",
25 "portion," or "segment" or "probe" or "primer" are used interchangeable and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17
nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less
30 than about 200 nucleotides, more preferably less than about 100 nucleotides, more

preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOs:1-419.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NOs: 1-419. The sequence information can be a segment of any one of SEQ ID NOs: 1-419 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO: 1-419. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4^{20} possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosome. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used.

The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ($1 \div 4^{25}$) times the increased probability for mismatch at each nucleotide position (3×25). The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater

than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

5 The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

10 The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

15 The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

20 The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

25 The term "variant"(or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, *e g.*, recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino
30 acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be

selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

5 The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated
10 biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

 The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (*e.g.*, nucleic acid or polypeptide) present
15 with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

20 The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free
25 of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

 The term "recombinant expression vehicle or vector" refers to a plasmid or
30 phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence.

An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (*e.g.*, soluble proteins) or partially (*e.g.*, receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (*e.g.* Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134 -143) and factors released from damaged cells (*e.g.*

Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell.

5 Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

10 In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (i.e., the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, e.g., mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a

further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more than 5% (95% sequence identity). Substantially equivalent, *e.g.*, mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 90% sequence identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, and most preferably at least about 95% identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (*e.g.*, via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, *e.g.*, using the Jotun Hein method (Hein, J. (1990) *Methods Enzymol.* 183:626-645). Identity between sequences can also be determined by other methods known in the art, *e.g.* by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic

acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each,
5 unless the context dictates otherwise.

4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide
10 comprising the nucleotide sequences of the SEQ ID NO: 1 - 419; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO:1 - 419; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polynucleotides of any one of SEQ ID NO: 1 - 419. The polynucleotides of the present invention also include, but are not limited to, a
15 polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of the SEQ ID NO: 1 - 419; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above;
20 or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 1- 419. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable
25 immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The

polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known

5 methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to
10 any of the polynucleotides of the SEQ ID NO: 1 - 419 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of the SEQ ID NO: 1 - 419 or a portion thereof as a probe. Alternatively, the polynucleotides of the SEQ ID NO: 1 - 419 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate
15 genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide
20 identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, *e.g.*, at least about 65%, at least about 70%, at least about 75%, at least about 80%, more typically at least about
25 90%, and even more typically at least about 95%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of the SEQ ID NO: 1 - 419, or complements thereof, which
30 fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably

greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that are selective for (i.e. specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided in SEQ ID NO: 1 - 419, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NOs: 1 - 419 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor result for the nucleic acids of the present invention, including SEQ ID NOs: 1 - 419, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altschul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide

which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence

5 variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid

10 sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*,

15 hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as

20 intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed
25 protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on
30 either side of the site of being changed. In general, the techniques of site-directed

mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO: 1-419, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of the SEQ ID NOs: 1 - 419 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of the SEQ ID NOs: 1 - 419 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors

are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

5 The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are
10 exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

15 Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from
20 retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct
25 transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion
30 of translated protein into the periplasmic space or extracellular medium. Optionally,

the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

4.3 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated

fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more

salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be
5 disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains,
10 *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in
15 order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the
20 regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment
25 regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or

modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.4 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO: 1-419 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NOs: 1 - 419 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in the SEQ ID NOs: 1 - 419 or (b) polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO: 1-419 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO: 1-419 or the corresponding full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, typically at least about 95%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO: 1-419.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., *Bio/Technology* 10, 773-778 (1992) and in R. S. McDowell, et al., *J. Amer. Chem. Soc.* 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by

expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms,
5 part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which it is expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the
10 nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present
15 invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing
20 primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically
25 active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or
30 protein. As used herein, a cell is said to be altered to express a desired polypeptide or

protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, *e.g.*, Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*; Ausubel et al., *Current Protocols in Molecular Biology*. Polypeptide fragments that retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules

include but are not limited to, for e.g., small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO: 1-419.

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule.

Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological

activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion

proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak
5 (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be
10 employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted,
15 inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the
20 polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are
25 used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

4.4.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE 30 IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984);

- 5 Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-
10 Manning et al, ISMB-97, vol 4, pp. 202-209, herein incorporated by reference) and the Kyte-Doolittle hydrophobicity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).
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4.5 GENE THERAPY

- Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to
20 restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer
25 methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of
30 the present invention can also be accomplished with extrachromosomal substrates

(transient expression) or artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter

DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes

exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.6 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous

recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4.7 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

4.7.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding

interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

- 5 Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.
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4.7.2 NUTRITIONAL USES

- Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.
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4.7.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

- A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of
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therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco.

5 Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M.

Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte

10 Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J.

Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990;

Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I.

Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

15 Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell

stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in

Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons,

Toronto. 1994; and Measurement of mouse and human interleukin- γ , Schreiber, R. D.

In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8,

20 John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and

Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E.

In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12,

25 John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211,

1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad.

Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin

6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp.

6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Aced. Sci.

30 U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F.,

Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp.

5 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M.

10 Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

4.7.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotent or pluripotent state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells,

gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotent/pluripotent stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotent/pluripotent mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of

differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., *Differentiation*, 48: 173-182, (1991); Klug et al., *J. Clin. Invest.*, 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering eds.* Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one

of various cell sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

4.7.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone

marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic

5 lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al.,
10 Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc.,
15 New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay,
20 Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In
25 Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

4.7.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments.

The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation

of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

4.7.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses,

herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

5 Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease.

10 Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (*e.g.*, anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-
15 Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The
20 therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxicol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).
25

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited
30 by suppressing T cell responses or by inducing specific tolerance in T cells, or both.

Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent.

Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and

persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing

high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York,

1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate
5 activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived
10 cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include
15 murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as
20 a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

25 Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of
30 enhancing anti-viral immune responses would be to isolate infected cells from a patient,

transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J.

Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

5 Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in
10 Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan,
15 A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

20 Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of
Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine
25 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others,
30 proteins that prevent apoptosis after superantigen induction and proteins that regulate

lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad. Sci. USA 88:7548-7551, 1991.

4.7.8 ACTIVIN/INHIBIN ACTIVITY

A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986.

4.7.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for

movement and adhesion include, without limitation, those described in: Current
Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E.
M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience
(Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al.
5 J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et
al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994;
Johnston et al. J. of Immunol. 153:1762-1768, 1994.

4.7.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

10 A polypeptide of the invention may also be involved in hemostatis or
thrombolysis or thrombosis. A polynucleotide of the invention can encode a
polypeptide exhibiting such attributes. Compositions may be useful in treatment of
various coagulation disorders (including hereditary disorders, such as hemophilias) or
to enhance coagulation and other hemostatic events in treating wounds resulting from
15 trauma, surgery or other causes. A composition of the invention may also be useful for
dissolving or inhibiting formation of thromboses and for treatment and prevention of
conditions resulting therefrom (such as, for example, infarction of cardiac and central
nervous system vessels (e.g., stroke).

Therapeutic compositions of the invention can be used in the following:

20 Assay for hemostatic and thrombolytic activity include, without limitation, those
described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al.,
Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991);
Schaub, Prostaglandins 35:467-474, 1988.

4.7.11 CANCER DIAGNOSIS AND THERAPY

25 Polypeptides of the invention may be involved in cancer cell generation,
proliferation or metastasis. Detection of the presence or amount of polynucleotides or
polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or
more types of cancer. For example, the presence or increased expression of a
30 polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a

precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

5 Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced
10 tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and
15 polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain
20 cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Kaposi's sarcoma.

25 Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser
30 therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of

tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the

5 polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, 10 Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide 15 acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, 20 Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these 25 individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar 30 (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wiley-

Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

4.7.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA

84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor
5 for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands.

10 The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14 . Examples of
15 colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

4.7.13 DRUG SCREENING

20 This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host
25 cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being

tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (i.e., increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science* 282:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol.*, 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol*, 1(1):114-19 (1997); Dorner et al., *Bioorg Med Chem*, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the

“hit” to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

4.7.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s).

As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

5 The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion
10 of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications i.e. phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

15 **4.7.15 ANTI-INFLAMMATORY ACTIVITY**

 Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting
20 chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock,
25 sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and
30 hypersensitivity to an antigenic substance or material. Compositions of this invention

may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic myelogenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

4.7.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

4.7.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

(i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;

(ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;

(iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;

(iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;

(v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;

(vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;

(vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and

(viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or in vivo;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
- (iv) decreased symptoms of neuron dysfunction in vivo.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, *etc.*, depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, *e.g.*, weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

4.7.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

4.7.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration,

and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

5 Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, 10 the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, 15 traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide 20 sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of 25 the protein, e.g., by an antibody specific to the variant sequence.

4.7.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The 30 experimental model system is adjuvant induced arthritis in rats, and the protocol is

described by J. Holoshitz, et al., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

4.8 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

4.8.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the

invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01µg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1µg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

4.9 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF,

Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, e.g., treatment, healing, prevention or amelioration of the relevant medical

condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

4.9.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or

cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection.

Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

4.9.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present

invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For

transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art.

- 5 Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or
- 10 dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as
- 15 the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or
- 20 pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

- Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in
- 25 admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such

administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described

previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological

stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without

limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by
5 reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of
10 protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and
15 at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μ g to about 100 mg (preferably about 0.1 μ g to about 10 mg, more preferably about 0.1 μ g to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which
20 are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for
25 delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the
30 invention. Preferably for bone and/or cartilage formation, the composition would

include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent

useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby
5 providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming
10 growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical
15 composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other
20 clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays,
25 histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including,
30 without limitation, in the form of viral vectors or naked DNA). Cells may also be

cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

5 **4.9.3 EFFECTIVE DOSAGE**

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing
10 symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating
15 concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC_{50} as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately
20 determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard
pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for
25 determining the LD_{50} (the dose lethal to 50% of the population) and the ED_{50} (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD_{50} and ED_{50} . Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in
30 formulating a range of dosage for use in human. The dosage of such compounds lies

preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, *e.g.*, Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 µg/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

4.9.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration.

Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

5 4.10 ANTIBODIES

Another aspect of the invention is an antibody that specifically binds the polypeptide of the invention. Such antibodies include monoclonal and polyclonal antibodies, single chain antibodies, chimeric antibodies, bifunctional/bispecific antibodies, humanized antibodies, human antibodies, and complementary determining
10 region (CDR)-grafted antibodies, including compounds which include CDR and/or antigen-binding sequences, which specifically recognize a polypeptide of the invention. Preferred antibodies of the invention are human antibodies which are produced and identified according to methods described in WO93/11236, published June 20, 1993, which is incorporated herein by reference in its entirety. Antibody fragments,
15 including Fab, Fab', F(ab')₂, and F_v, are also provided by the invention. The term "specific for" indicates that the variable regions of the antibodies of the invention recognize and bind polypeptides of the invention exclusively (*i.e.*, able to distinguish the polypeptide of the invention from other similar polypeptides despite sequence identity, homology, or similarity found in the family of polypeptides), but may also
20 interact with other proteins (for example, *S. aureus* protein A or other antibodies in ELISA techniques) through interactions with sequences outside the variable region of the antibodies, and in particular, in the constant region of the molecule. Screening assays to determine binding specificity of an antibody of the invention are well known and routinely practiced in the art. For a comprehensive discussion of such assays, see
25 Harlow et al. (Eds), Antibodies A Laboratory Manual; Cold Spring Harbor Laboratory; Cold Spring Harbor, NY (1988), Chapter 6. Antibodies that recognize and bind fragments of the polypeptides of the invention are also contemplated, provided that the antibodies are first and foremost specific for, as defined above, full length polypeptides of the invention. As with antibodies that are specific for full length polypeptides of the
30 invention, antibodies of the invention that recognize fragments are those which can

distinguish polypeptides from the same family of polypeptides despite inherent sequence identity, homology, or similarity found in the family of proteins. Antibodies of the invention can be produced using any method well known and routinely practiced in the art.

5 Non-human antibodies may be humanized by any methods known in the art. In one method, the non-human CDRs are inserted into a human antibody or consensus antibody framework sequence. Further changes can then be introduced into the antibody framework to modulate affinity or immunogenicity.

10 Antibodies of the invention are useful for, for example, therapeutic purposes (by modulating activity of a polypeptide of the invention), diagnostic purposes to detect or quantitate a polypeptide of the invention, as well as purification of a polypeptide of the invention. Kits comprising an antibody of the invention for any of the purposes described herein are also comprehended. In general, a kit of the invention also includes a control antigen for which the antibody is immunospecific. The invention further
15 provides a hybridoma that produces an antibody according to the invention. Antibodies of the invention are useful for detection and/or purification of the polypeptides of the invention.

20 Polypeptides of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R. P. Merrifield, J. Amer. Chem. Soc. 85, 2149-2154 (1963); J. L.
25 Krstenansky, et al., FEBS Lett. 211, 10 (1987).

Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where
30 abnormal expression of the protein is involved. In the case of cancerous cells or

leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein. In general, techniques for preparing polyclonal and monoclonal antibodies as well as hybridomas capable of producing the desired antibody are well known in the art (Campbell, A.M., Monoclonal Antibodies Technology: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1984); St. Groth et al., J. Immunol. 35:1-21 (1990); Kohler and Milstein, Nature 256:495-497 (1975)), the trioma technique, the human B-cell hybridoma technique (Kozbor et al., Immunology Today 4:72 (1983); Cole et al., in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc. (1985), pp. 77-96).

Any animal (mouse, rabbit, *etc.*) which is known to produce antibodies can be immunized with a peptide or polypeptide of the invention. Methods for immunization are well known in the art. Such methods include subcutaneous or intraperitoneal injection of the polypeptide. One skilled in the art will recognize that the amount of the protein encoded by the ORF of the present invention used for immunization will vary based on the animal which is immunized, the antigenicity of the peptide and the site of injection. The protein that is used as an immunogen may be modified or administered in an adjuvant in order to increase the protein's antigenicity. Methods of increasing the antigenicity of a protein are well known in the art and include, but are not limited to, coupling the antigen with a heterologous protein (such as globulin or α -galactosidase) or through the inclusion of an adjuvant during immunization.

For monoclonal antibodies, spleen cells from the immunized animals are removed, fused with myeloma cells, such as SP2/0-Ag14 myeloma cells, and allowed to become monoclonal antibody producing hybridoma cells. Any one of a number of methods well known in the art can be used to identify the hybridoma cell which produces an antibody with the desired characteristics. These include screening the hybridomas with an ELISA assay, Western blot analysis, or radioimmunoassay (Lutz et al., Exp. Cell Research. 175:109-124 (1988)). Hybridomas secreting the desired antibodies are cloned and the class and subclass is determined using procedures known

in the art (Campbell, A.M., Monoclonal Antibody Technology: Laboratory
Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers,
Amsterdam, The Netherlands (1984)). Techniques described for the production of
single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce single chain
5 antibodies to proteins of the present invention.

For polyclonal antibodies, antibody-containing antiserum is isolated from the
immunized animal and is screened for the presence of antibodies with the desired
specificity using one of the above-described procedures. The present invention further
provides the above-described antibodies in delectably labeled form. Antibodies can be
10 delectably labeled through the use of radioisotopes, affinity labels (such as biotin,
avidin, etc.), enzymatic labels (such as horseradish peroxidase, alkaline phosphatase,
etc.) fluorescent labels (such as FITC or rhodamine, etc.), paramagnetic atoms, etc.
Procedures for accomplishing such labeling are well-known in the art, for example, see
(Sternberger, L.A. et al., J. Histochem. Cytochem. 18:315 (1970); Bayer, E.A. et al.,
15 Meth. Enzym. 62:308 (1979); Engval, E. et al., Immunol. 109:129 (1972); Goding,
J.W. J. Immunol. Meth. 13:215 (1976)).

The labeled antibodies of the present invention can be used for *in vitro*, *in vivo*,
and *in situ* assays to identify cells or tissues in which a fragment of the polypeptide of
interest is expressed. The antibodies may also be used directly in therapies or other
20 diagnostics. The present invention further provides the above-described antibodies
immobilized on a solid support. Examples of such solid supports include plastics such
as polycarbonate, complex carbohydrates such as agarose and Sepharose®, acrylic
resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies
to such solid supports are well known in the art (Weir, D.M. et al., "Handbook of
25 Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford,
England, Chapter 10 (1986); Jacoby, W.D. et al., Meth. Enzym. 34 Academic Press,
N.Y. (1974)). The immobilized antibodies of the present invention can be used for *in*
vitro, *in vivo*, and *in situ* assays as well as for immuno-affinity purification of the
proteins of the present invention.

4.11 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (*e.g.* text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NOs: 1 - 419 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any

of the nucleotide sequences of the SEQ ID NOs: 1 - 419 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting

search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

4.12 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991))

or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991);
Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca
Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA
transcription from DNA, while antisense RNA hybridization blocks translation of an
5 mRNA molecule into polypeptide. Both techniques have been demonstrated to be
effective in model systems. Information contained in the sequences of the present
invention is necessary for the design of an antisense or triple helix oligonucleotide.

4.13 DIAGNOSTIC ASSAYS AND KITS

10 The present invention further provides methods to identify the presence or
expression of one of the ORFs of the present invention, or homolog thereof, in a test
sample, using a nucleic acid probe or antibodies of the present invention, optionally
conjugated or otherwise associated with a suitable label.

15 In general, methods for detecting a polynucleotide of the invention can comprise
contacting a sample with a compound that binds to and forms a complex with the
polynucleotide for a period sufficient to form the complex, and detecting the complex,
so that if a complex is detected, a polynucleotide of the invention is detected in the
sample. Such methods can also comprise contacting a sample under stringent
hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the
20 invention under such conditions, and amplifying annealed polynucleotides, so that if a
polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

25 In general, methods for detecting a polypeptide of the invention can comprise
contacting a sample with a compound that binds to and forms a complex with the
polypeptide for a period sufficient to form the complex, and detecting the complex, so
that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of
the antibodies or one or more of the nucleic acid probes of the present invention and
assaying for binding of the nucleic acid probes or antibodies to components within the
test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly

5 available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention.

Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985).

10 The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

20 In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

25 In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are

not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4.14 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

4.15 SCREENING ASSAYS

Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in the SEQ ID NOs: 1 - 419, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
- (b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while

antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

5 Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

10 4.16 USE OF NUCLEIC ACIDS AS PROBES

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NOs: 1 - 419. Because the
15 corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from any of the nucleotide sequences SEQ ID NOs: 1 - 419 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188
20 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

25 Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively
30 labeled nucleotides. The nucleotide sequences may be used to construct hybridization

probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

4.17 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads
5 may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently
10 bound to the microwell surface termed CovaLink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups ($>NH$) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA
15 (Rasmussen *et al.*, (1991) Anal. Biochem. 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen *et al.*, (1991). In this technology, a phosphoramidate bond is employed (Chu *et al.*, (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred.
20 The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and
25 then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm₇), is then added to a final concentration of 10 mM 1-MeIm₇. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well)
30 standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm₇, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These

methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

4.18 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *Cvi*JI, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease *Cvi*JI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*Cvi*JI**), yield a quasi-random distribution of DNA fragments from the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *Cvi*JI** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *Cvi*JI** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed).

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.19 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may

represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12
5 cm membrane. Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm² and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid
10 molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other
15 embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are
20 within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

25 All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

5.0 EXAMPLES

5.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using
5 primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a
10 typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

15 5.2 EXAMPLE 2

Novel Nucleic Acids

The novel nucleic acids of the present invention of the invention were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public
20 databases. The nucleic acids were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from
25 the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the

assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 117, gb pri 117, UniGene version 117, Genepet release 117). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide and amino acid sequences, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS:1- 419.

Table 1 shows the various tissue sources of SEQ ID NO: 1-419.

The nearest neighbor results for SEQ ID NO: 1-419 were obtained by a BLASTP version 2.0a1 19MP-WashU search against Genpept release 118, using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1-419 from Genpept (and contains the translated amino acid sequences for which the nucleic acid sequence encodes). The nearest neighbor results for SEQ ID NO: 1-419 are shown in Table 2 below.

TABLE 1

TISSUE ORIGIN	RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
adult brain	GIBCO	AB3001	23 45 52 55 59 61 65-66 69 72 75-76 80 105 123 130 133-134 137 147 149 157-158 179 198 202 207 212-213 233 246 253-254 259 263 272-273 275 295 303 327 352 364 389 391-392 406
adult brain	GIBCO	ABD003	3 7 14 19 22-23 26 29 31-32 37 43-45 48 50-51 55 58-59 62 65 69-70 74 77 79-80 85-86 91 105 111 113 115-116 123 133 135 144-145 149-150 155 157-158 168 179 186 191 198 210-211 213 221 224 227-228 230-233 236-237 239 242-243 246 248 252 259 261 263-265 268-275 281-283 286 288 303 311 316-317 321 329 332 334 342-343 346 352 377 379 385 389 395-396 400
adult brain	Clontech	ABR001	7 29 32 44-45 52 69 77-78 80 110 191 222 233 236 257-258 262 271 297-298 341 343 368 385 389 393 401 407
adult brain	Clontech	ABR006	3 10-12 23 33 39 43 45 80-81 83-84 94 117 198 272 300 385 387-389 398 413-414 417
adult brain	Clontech	ABR008	1 3 5-7 12 15 18-23 25 28-30 32-35 37-43 47-48 51-52 54 58- 61 63 67-70 72-73 75-76 79 82- 86 92 94-99 101 105-106 109 111 113 120 128 131-132 134 137 139-147 154 156 159 165 168-171 173 176-181 184 187-188 191-194 197 200 202 204 210-211 215 218 220 224 230-233 238-239 243 247-248 252-259 262-263 265-266 268-269 272-273 275 281-286 294 296 298-301 303-305 308 310 312-314 317-318 321 325 327 342 346-352 354-355 361 364 368 370 377 381-383 385 387-388 391-393 398 400-403 406-408 410 414 416-417 419
adult brain	Clontech	ABR011	85
adult brain	BioChain	ABR012	344
adult brain	Invitrogen	ABR013	74 141-143 385
adult brain	Invitrogen	ABR014	43 48 417
adult brain	Invitrogen	ABR015	391-392 417
adult brain	Invitrogen	ABR016	23 45 48 54 337 395-396
adult brain	Invitrogen	ABT004	20 23 37 40 43 48 50 58 60 78 85-86 105 111 126 137 145 147 159 161 164 188 191 194 198 208 212 223 229 237 239 252-256 263 271-272 275 291 295 299 334 368

TABLE 1

			376 381 385 388-389 393 398 401 406 419
adipocytes	Stratagene	ADP001	10-11 20 23 37 43 50 52 54 60 69 86 102 115-116 119 123 127 145 156-158 166 179 181-182 234 238 243 253-254 259 261 268-272 281-282 284 290 294-295 314 346 382 399 414 418
adrenal gland	Clontech	ADR002	10-11 13 21 25-26 31 33 50-51 54-55 65 69 80 86 93 95 97 106 111 133 149 156 166 173 181-182 188 194 203 210-211 213 238 248 253-254 257-258 286 294 298 302 311 317 327 346 356 383 393 398 405 412 418
adult heart	GIBCO	AHR001	1 7 10-12 19-20 29 31-32 37 43- 45 47 50 52 54-55 59-65 72 74- 76 79-80 85 101-102 113-114 119-123 130-133 136-137 139 141-143 145 148-149 154-155 157-158 163 172 178-179 182 196-197 202 207 212-214 222 227-228 236-238 240 243 248 252-254 257-259 261-264 268-270 272-273 277-279 288-289 294-296 300 305 311 314 325 335-336 341 344 346 350 352 361 364 366 368 385 390 398 400-401 403-406 412 414 418
adult kidney	GIBCO	AKD001	1 3-4 7 10-12 14 19-20 22 25-27 29 31-32 37 44-48 50-52 54-55 58-62 65 67-69 74-77 79-80 89 91 101-103 111 113-114 119 121- 123 126 128 130 132-134 136-138 141-144 147-149 153 155 159 166 171 174 178-179 181-182 188 191-192 196 200-201 207 209-213 218-219 223-224 227-228 230-233 235-240 244-246 252-259 261-264 268-272 275 277-279 281-282 285-287 290 294-295 301 305 309 311 317-318 329-330 332 334 341-344 346 350 352 361 364 368 370 373-375 377 382-385 391-394 400-401 404-406 414 418
adult kidney	Invitrogen	AKT002	4 12 21 29 32 45 48 51 67-68 75-76 80 97 103 110 120-123 137-138 144 147 153 155 157-158 169-170 179 186 188-190 194 196 212 232-233 242 264 268-269 272 274-275 284 308 341 343 346 352 357 366 385 398 405-406 414 419
adult lung	GIBCO	ALG001	2 10-11 37 50 59 69-70 75-76 80 114 118 123 133 147 149 155 157-158 166 179 181 223 242 246 264 270-271 274 277-279 289 311

TABLE 1

			332 334 337 342 370 384 394
lymph node	Clontech	ALN001	43 54 60 69 71 108 113 123 134 152 155-156 181 212 222 232 270 274 281-282 294 322 337 350 366 368 380 400
young liver	GIBCO	ALV001	7 14 17 25 49 59-61 80 123 130- 131 134 145 149 153-154 166 169-171 173 179 181-182 196 200 212 231 233 261-262 272 275 286 295 344 361 364 368 373 405 408 414
adult liver	Invitrogen	ALV002	3 13 17 21 25 47-48 51 75-76 88 91 100 107 114 123 131 134 139 155 164 174 176 194 196 201 217 220 223-225 232 237 244-245 255-256 259 261 272 281-282 285-286 288 310 317 343 346 352 376 379 398 404 416
adult ovary	Invitrogen	AOV001	3-7 10-12 14 17 19-21 23 25 28- 29 31-32 37 43-45 47-48 50-51 54-55 58-61 65 67-70 72 74-82 87 91-92 98-101 103 111 113 115-116 118-120 123 128 131-133 137 139 141-145 147 149-153 155-158 160 164-167 169-173 178-179 181-182 186 188-191 194 200 204 207 209-214 218 220 222-223 227-228 231-233 235-240 242-243 246 248 251-256 259 261-262 264-265 268-279 284-288 290 294-295 298-301 303 305 307 309 311 317 321-323 325 327 332 334 337 341 344 346 350-352 354-355 366 370 374-375 377 382-385 391-397 400-403 405-406 408 412 414 418
adult placenta	Clontech	APL001	29 32 100 123 128 149 227-228 247 295 301 382
placenta	Invitrogen	APL002	20 23 43 48 110 139 232 238 253-258 261 271 352 398
adult spleen	GIBCO	ASP001	12 43 52 54-55 59-61 64 80 108 113 121-123 131 137 149 155 159 163 166 181 186 191 210-212 239 243 253-254 261 264 270 272 287 294-295 308 311 315 327 329 332 334-335 337 342 344-345 350 352 368 373 376 382 400-401
adult testis	GIBCO	ATS001	1 10-11 14 29 32 37 44 50 54-55 61 79-80 90 118-119 123 128 144-145 149 155 169-170 182 192 194 197 209 212 224 232 239-240 243 259 267-269 271 274-275 289 294-295 350 352 361 364 398 400-401 418
Genomic DNA from BAC 63I18	Research Genetics (CITB	BAC001	164

TABLE 1

	BAC Library)		
Genomic DNA from BAC 393I6	Research Genetics (CITB BAC Library)	BAC002	291
Genomic DNA from BAC 393I6	Research Genetics (CITB BAC Library)	BAC003	291
adult bladder	Invitrogen	BLD001	43 80 91 137 146 154 167 201 238-239 272 287 317 329 368 391-392
bone marrow	Clontech	BMD001	1-3 7 12 14 16 26 31 37 43-46 49 54 57 59-61 67-70 74-77 80 82 84 91 98-99 102 104 108 113 117-119 123 127-128 130 133 139 145 153 155 157-158 160 168-170 179 181 188 202 207-208 210-212 222 230 232 236 242 247 250 259 261 264-265 268-270 274 276-279 286 289 293-295 300 311 317 325 335 352 364 366 370 384 387 393 395-396 398 414
bone marrow	Clontech	BMD002	1-4 7 10-11 13 16 19 21 36 43- 44 48 52 54 58 60 98-99 108 110 117 123 137-138 173 179 181 230-232 242 253-254 262 268-269 272-273 281-283 292 294 314 316 347 370 383 387 393 398 405 408 414
bone marrow	Clontech	BMD007	419
adult colon	Invitrogen	CLN001	12 26 33 101 104 108 119 179 232 253-254 270 300 340 376 381 404 414
Mixture of 16 tissues-mRNAs*	Various Vendors*	CTL016	7 393 413
Mixture of 16 tissues-mRNAs*	Various Vendors*	CTL021	117 176
adult cervix	BioChain	CVX001	3 7 12 17 29 31-33 38 43 45 48 50 54-56 59 65 67-70 77 79-80 86 91 102-103 108 113 118 120- 122 125 129 133 141-144 149 153 155-158 165-166 175 179 181 194

* The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen), 4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia lymphoblastic mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

TABLE 1

			199-200 212-214 218 227-228 235-236 240 259 262 264 270 272 274 279 281-282 285-288 293 295 301 309-311 317-318 327 332 335 342-343 346 353 356 361 366 374-375 377 381 385 395-396 400 403 405 408 410 414 416
diaphragm	BioChain	DIA002	80 212
endothelial cells	Strategene	EDT001	1 3-4 7 10-12 14 16 20-21 24 28-29 32 38 43-44 47-52 54-55 58-61 74-77 86 91-92 97 103 113 115-116 123 128 130 139 141-147 149 152 155-158 160 166 169-170 172-173 179 181 186 189-191 207 210-212 214 218-219 223 231-233 236 238-239 246 253-259 261-262 264 268-273 276 279 281-282 284-288 294-295 298 301 303 305 312 314-315 335 341 343-346 349 351-352 361 365 368 370 373-375 377 380 382 393 398 401-403 405 414 418
Genomic clones from the short arm of chromosome 8	DNA from Genetic Research	EPM001	164 291
esophagus	BioChain	ESO002	20 123
fetal brain	Clontech	FBR001	82 95 152
fetal brain	Clontech	FBR004	33 81 134 150 198 304 400 407 414
fetal brain	Clontech	FBR006	3-6 12 16-20 23 37 40 43-44 48 51 54-55 59 63 69 75-76 85-86 91 93 103 105-106 109 111 113 119 129 134 141-143 156 159 165 173 177 179-181 188-191 198 202-203 210-211 230-232 238-239 253-259 262 266 268-270 272-273 275 283 287 293-294 298-300 304-306 314-315 319-322 325 330 344 368-369 383 388 393 405 407 414
fetal brain	Clontech	FBRS03	166 288 344 391-392
fetal brain	Invitrogen	FBT002	16 23 31 43 48 50 52 61 64 69 81 86 123 131 134 144 156 162 166 176 178-179 188-191 197 201 229 237-238 251 255-256 263 268-269 272-273 275 285 294-295 299 301 303 332 342 346 352 365 368 395-396 398 401-402 406
fetal heart	Invitrogen	FHR001	43 80 294
fetal kidney	Clontech	FKD001	7 45 67-69 123 133 155 157-158 166 169-170 181 196 202 207 216 218 237 246 259 261 264 270 273 277-278 294 332 387 398
fetal kidney	Clontech	FKD002	123 379
fetal kidney	Invitrogen	FKD007	81

TABLE 1

fetal lung	Clontech	FLG001	3 43 45 55 111 132-133 259 270 404
fetal lung	Invitrogen	FLG003	17 23 31 43 47 75-76 80-81 91 134 185 204-206 237 255-256 272 275 287 294-295 314 330-331 377 406
fetal lung	Clontech	FLG004	43 317
fetal liver- spleen	Soares	FLS001	1 3-8 10-14 16-17 20-23 25-29 31-32 37-38 43-45 47-48 50-60 62-63 65 67-70 74 77-79 81-82 86 88 91-93 98-99 101 105-106 110-119 121-123 127-128 130-131 133-134 136 139-143 146-148 153-156 160 163-164 166-170 172-173 175 178 181 186 189-190 196 204 207-208 212 225 227-228 230-246 249-250 252-254 257-259 261-264 268-275 277-279 281-282 285-287 290 294-295 299 301 307-309 316-318 325 327-328 332 334 337 339 341 344 346-352 364 366 368 370 372-379 382 385-386 391-393 398 401-402 404-406 410 412 414
normalized fetal liver- spleen	Soares	FLS002	1 3-4 7 10-14 16-17 20 22-23 25-26 31 37 43-45 47-48 50 54- 55 58-60 62 67-70 78 80 88-89 91-93 100-101 106 111-112 115- 117 119 123 126-128 130 132-133 136-137 140 144 148 153 157-158 165 168-170 173 175-177 179 181 186 189-190 192 194-196 199-200 202 204 209 213 217 224-225 227-228 230-242 246 248 251 253-254 259 261-262 264-265 268-269 272-273 279 281-282 285 288 290 292 294 296 299-300 307 311-312 318-320 322-328 332 334 337-338 341-343 346 348 350 361 364 366 368 370-372 376-380 382 384-387 391-392 394 398-399 402-403 406 412 414 419
fetal liver- spleen	Soares	FLS003	19 22-23 50 253-254 290 295 383 385 391-392 401 405
fetal liver	Invitrogen	FLV001	7 20 23 31 43 51 60-61 67-68 77 79 91 102 166 217-218 230 232 234 237 239 252-254 257-259 268-269 275 285 290 294-296 298 317-318 322 332 368 370 373 379 398 401 404
fetal liver	Clontech	FLV002	67-68 283
fetal liver	Clontech	FLV004	4 16 23 25 196 268-269 272 298 370 394
fetal muscle	Invitrogen	FMS001	23 52 55 58 106 110 134 154 166 177 179 189-190 193 198 203 207 229-230 233 253-254 259 290

TABLE 1

			294-295 307 317 352 368 383 390 404
fetal muscle	Invitrogen	FMS002	10-11 80 123 154 231 290 295 319-320
fetal skin	Invitrogen	FSK001	3-4 7 10-11 15 18 20-21 23 30- 31 33 35 43 50 52 54 62 64 77 80 86 89 109 115-116 121-122 126 130 132 144 148 153 166 171 181 185-186 188-190 194 205-207 218 224 226-228 230 234-235 237-239 242-243 253-254 257-259 263 268-269 272 275 285 288 290 294-295 299-300 317 326-327 329 333-334 342 352 358-360 362-368 377 381-383 391-393 398 401 405 418
fetal skin	Invitrogen	FSK002	3 16 49 54 123 138 169-170 196 207 210-211 235 246 383 393 401 408
fetal spleen	BioChain	FSP001	212
umbilical cord	BioChain	FUC001	12 16 21 23 28-29 32-33 41-43 46 48 51 54-55 59 74-76 78-79 98-99 123 125 133 146 148 150 153-154 159 164 166 181-182 188 198 200 207 212 218 222 224 227-228 231 236-237 248 253-254 259 261 268-270 272 277-278 285-288 290 294-295 311 316-317 327 343-344 346-347 352 366 368-370 373 377 379 382 391-392 399-400 402 412 414 418
fetal brain	GIBCO	HFB001	1 3 7 12 14 19-21 23 31 43-45 47 50 52 54-55 58-61 63 65 74- 76 80-81 86 91 94 102 105 111 115-116 118-119 121-123 128 132 137 139 141-146 149-150 153 155-159 169-170 173 179 186 188 194 198 201 207 209-211 213 218 229 232-233 236-237 246-247 253-259 261-263 265 268-275 277-279 281-282 284 286 289 293 295 299 301 309 311 314 329 332 341-342 346 349-350 364-365 368 377 379 384 388 398 400-402 405 407 414 418
macrophage	Invitrogen	HMP001	186 259 334 414
infant brain	Soares	IB2002	3 7 10-11 14-15 17 19-20 22-23 31 37 43-45 51 54-55 60-61 64- 65 69 73-74 77 80 85-86 89-90 93-94 102 105 109 114 123 128 131-132 137 144-145 147 150 152-153 155-159 164-166 169-170 173-174 178 180-181 183-184 186 188-191 193-194 198 210-211 218 224 227-228 230-233 236-237 239 242 246-247 251-259 261 263-264

TABLE 1

			267-269 271 273 275 280-283 285-286 288 293 295-296 300 303-304 306 314 316-317 329-330 342 346 348-351 361 364 373-375 377 383 385 388 393 398-401 407 418-419
infant brain	Soares	IB2003	3-4 7 10-12 31 37 39 43 45 48 51 69 74 80 91 111 123 131 133 137 144-145 159 169-171 173 178 189-190 198 212 232 236 238-239 246 251-254 257-258 263 268-269 271-272 283 299 303 332 373-375 377 388-389 399 404 407
infant brain	Soares	IBM002	25 43 70 89 137 186 242 257-258 286 393
infant brain	Soares	IBS001	3 15 37 137 191 231 238 271 299 317 385 393
lung fibroblast	Strategene	LFB001	1 21 45 47 61 63 86 102 113 119 130 141-143 157-158 181 188 231 234 268-270 272 279 284 295 341 344 398 405 414
lung tumor	Invitrogen	LGT002	1 3-4 12 14 20 29 31-32 37 43- 44 47-51 54-55 59-60 62 65 67- 68 75-76 88 91 101-102 107-108 110-111 113-114 119-120 123 127 132-133 139 144-145 148 159 171 173 177 185-186 189-190 192 197 205-207 209-214 220-221 223 230 232 237-238 242 248 253-256 259 261 263-264 268-273 276-280 284-285 287 292 294-296 301 314 317 322 332 341-342 344 346 352-353 361 370 376-377 383 386-387 391-393 398 400 402 405-406 414
lymphocytes	ATCC	LPC001	21 26 37 47-48 59 86 91 102 119 123 130 144 149 155 159 178 181 186 191 207 220 229 255-256 261 271 279 288 295 300 311 319-320 329 332 350 361 366 381 383 387 402 418
leukocyte	GIBCO	LUC001	2-3 7-8 10-14 17 20-21 24 37-38 43-44 46-50 52 54 56 58-61 70 74-76 81 86 91 97-99 101 106 109-110 117-120 123 125 128-131 133 141-143 145-147 149 155-159 165-166 169-170 173 178-179 181 186 189-193 200 202-203 207 209-214 218 227-228 230-233 236-237 239 242 246-248 253-254 257-259 261-275 277-279 281-282 285-286 293-295 300 307 310-311 314 316-318 322 325 330 332 337-342 344 349-350 352 361 364 366 368 370 374-377 381 383 391-393 400-402 408 414 418

TABLE 1

leukocyte	Clontech	LUC003	21 43 60-61 92 117-119 179 181 186 200 218 230-231 264 270 274 277-278 294 308 350 414
melanoma from cell line ATCC # CRL 1424	Clontech	MEL004	1 10-11 16 37 44 51 59 67-68 78 86 103 113-114 130 145 149 152 156 173 181 188 209-211 222 231-232 237 239 250 263-264 268-272 274 295 310 316-317 325 368 377 401 405 414
mammary gland	Invitrogen	MMG001	3 9 12 16 20 23 29 31-32 34 37 43-44 47 50-52 56 58 60-61 67- 69 75-76 79 84 86 91 98-102 108 110 114-117 119 123 126-127 129 132 134 137 147 149 152-153 156 164 168 171 173 178-181 187-190 193 196 204 209 212 214 218 223-224 229-230 232 234 237-239 243 248 252-261 263-264 266-269 271-273 275 285 287-288 290 294-296 298-299 303 310 316-317 327 329 332 341-342 344 346 349 354-356 366 368 370 381 383 385 391-392 394-396 398 402 404 406 416
induced neuron cells	Stratagene	NTD001	10-11 20-21 24 37 59 63 67-68 89 120 133 144 165 173 178-179 242 261 279 294 303 398 401 405 414
retinoid acid induced neuronal cells	Stratagene	NTR001	34 89 123 277-278 295 401
neuronal cells	Stratagene	NTU001	10-11 16 28 43 48 50 59 69 75- 76 123 128 156 179 229 232-233 261 268-269 287 295 311 385 393 418
pituitary gland	Clontech	PIT004	3 7 22-23 26 75-76 111 141-143 286
placenta	Clontech	PLA003	224
prostate	Clontech	PRT001	62 64 91 98-99 102 129 133 139 148-149 152 154-155 172 186 192 213 233 253-254 262 270 274 295 303 350 364 382 414 418
rectum	Invitrogen	REC001	3 33 43 50 69 74 91 95 108 132 134 169-170 181 194 208 230-231 234 242 253-258 261 263 266 270 285 288 298 308 317 336-337 394
salivary gland	Clontech	SAL001	12 26 44 47 49 51 54-55 59 79 91 108 111 123 132 134 212-213 229 237-238 250 253-254 295 311 352 381 383 390 394 401
saliva gland	Clontech	SALS03	37 261
skin fibroblast	ATCC	SFB001	166
skin fibroblast	ATCC	SFB002	341
small	Clontech	SIN001	12 22 24 31 37-38 41-43 46 49

TABLE 1

intestine			86 115-116 120 133 149 166 169-170 174 196 209 230-231 238 250 253-254 263 275 295 364 384 386-387 410 414
skeletal muscle	Clontech	SKM001	59 75-76 123 154 238 271 274 311 345 366 390
spinal cord	Clontech	SPC001	23 26 29 32 37 43 47 55 58-59 80 98-99 102 104 115-116 119-120 133-135 137 144 146 149 152 157-158 173 186 188 207 231 236 255-256 262 270 274 281-282 284 309 316 364 368 382 389 393-394 414
adult spleen	Clontech	SPLc01	14 52 80 110 207 261 368
stomach	Clontech	STO001	31 47 74 80 102 110 132 145 149 176 179 230 294 310 316 322 401 418
Mixture of 16 tissues-mRNAs*	Various Vendors*	SUP002	33 45 48 110 370 388 398 400-401 414
Mixture of 16 tissues-mRNAs*	Various Vendors*	SUP005	16 347 383
Mixture of 16 tissues-mRNAs*	Various Vendors*	SUP008	163 402
Mixture of 16 tissues-mRNAs*	Various Vendors*	SUP009	43 370
thalamus	Clontech	THA002	23 33 49 51 69 73 84-86 95 115-116 134 152 155 176 191 198 221 263 266 273 275 284 295-296 311 329 389
thymus	Clontech	THM001	3 7 14 16 21 27 37-38 44 47 60-61 69 72 84 101 149 157-158 166 173 181 186 200 207 209 218 227-228 232 236 249 259 262 273 295 337 368 374-376 381 393 419
thymus	Clontech	THMc02	3-4 7-8 12-13 16-17 21-22 31 36-38 44 49 51 60 63 75-76 86 89 91 98-99 103 106 111 113 118 123 128 130 134 139-140 155 157-158 160 166 171 175 177 181 191 200 203 210-211 213 215-219 230-232 235 239 248 250-251 253-259 262 264-265 270-272 276

* The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen), 4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia lymphoblastic mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

TABLE 1

			279 281-282 292 296 298 308 322 325 330 337 339-346 350 366 370 373 381 393 399 402 413-415
thyroid gland	Clontech	THR001	3 7 22 26 30-31 36 43 47 50-51 54-55 58-61 65 71 74-76 78-80 89 98-102 111 115-117 123 127- 128 130-133 139 141-145 149-150 154-155 166-167 171-174 181 186 189-190 194 200 207 209 212-213 222 230 233 237-239 243 248 250 257-258 261 268-272 276-279 284 286 293-295 311-312 317-322 327 335 339 341-344 349 352 368 377 383 393 395-396 400 403 405 412 414 418-419
trachea	Clontech	TRC001	1 62 75-76 115-116 149 151 153 230 236 261 264 284 294 341 344 364 377 391-392
uterus	Clontech	UTR001	33 43 48-49 52 55 60 74 80 83 86 89 111 123 134 139 157-158 175 181 229 268-270 287 294-295 325 414

TABLE 2

SEQ ID NO	CORRESPONDING SEQ ID NO. IN U.S.S.N. 09/560,875	ACCESSION NUMBER	DESCRIPTION	SMITH- WATERMAN SCORE	% IDENTITY
1	44	AL137294	Homo sapiens hypothetical protein	469	95
2	50	AJ271684	Homo sapiens myeloid DAP12-associating lectin	1013	100
3	93	AL133589	Homo sapiens hypothetical protein	2707	99
4	224	U51730	Murine leukemia virus reverse transcriptase	316	43
5	318	AB033027	Homo sapiens KIAA1201 protein	3847	100
6	318	AB033027	Homo sapiens KIAA1201 protein	3809	99
7	795	AF161432	Homo sapiens HSPC314	1059	93
8	857	AB029488	Homo sapiens C11orf21	758	99
9	924	AJ251024	Homo sapiens putative odorant binding protein ag	1239	100
10	944	AK001284	Homo sapiens unnamed protein product	2410	97
11	944	AK001284	Homo sapiens unnamed protein product	2410	97
12	967	AE003799	Drosophila melanogaster CG5323 gene product	288	40
13	1055	AF197927	Homo sapiens AF5q31 protein	3992	99
14	1091	D28500	Homo sapiens mitochondrial isoleucine tRNA synthetase	4286	98
15	1225	X97868	Homo sapiens arylsulphatase	3141	98
16	1257	AL162048	Homo sapiens hypothetical protein	1532	100
17	1289	AL137657	Homo sapiens hypothetical protein	586	100
18	1292	AL137662	Homo sapiens hypothetical protein	1339	99
19	1455	M15888	Bos taurus endozepine- related protein precursor	2425	85
20	1488	X66363	Homo sapiens serine/threonine protein kinase	2562	100
21	1666	AE003606	Drosophila melanogaster CG1078 gene product	412	30
22	1811	AF100772	Homo sapiens tenascin- M1	11535	99
23	1885	AF090934	Homo sapiens PRO0518	382	100
24	1911	AB021643	Homo sapiens	2761	99

TABLE 2

			gonadotropin inducible transcription repressor-3		
25	1935	Z83123	Caenorhabditis elegans T04A11.2	315	50
26	1971	AF070666	Homo sapiens Kruppel-associated box protein	466	97
27	1989	AK000137	Homo sapiens unnamed protein product	925	99
28	2041	A58331	Homo sapiens unnamed protein product	1126	61
29	2178	AF227906	Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 2 precursor	7820	99
30	2237	AF118566	Mus musculus hematopoietic zinc finger protein	1769	92
31	2279	AK000619	Homo sapiens unnamed protein product	810	100
32	2338	AF227906	Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 2 precursor	7820	99
33	2351	AF117946	Homo sapiens Link guanine nucleotide exchange factor II	2363	100
34	2405	AB032997	Homo sapiens KIAA1171 protein	2946	99
35	2531	AB032971	Homo sapiens KIAA1145 protein	2290	100
36	2584	AE003453	Drosophila melanogaster CG15670 gene product	352	37
37	2608	AF177388	Homo sapiens cancer-amplified transcriptional coactivator ASC-2	10748	99
38	2655	AJ002744	Homo sapiens UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 7	3469	96
39	2656	AF097366	Homo sapiens cone sodium-calcium potassium exchanger	3166	100
40	2866	AB032958	Homo sapiens KIAA1132 protein	9116	100
41	3015	AB018299	Homo sapiens KIAA0756 protein	4445	99
42	3015	AB018299	Homo sapiens KIAA0756 protein	4408	98
43	3043	X13916	Homo sapiens LDL-receptor related precursor (AA -19 to 4525)	4292	99
44	3986	AF151083	Homo sapiens HSPC249	444	98

TABLE 2

45	4647	AB017026	Mus musculus oxysterol-binding protein	2173	98
46	4659	D87077	Homo sapiens KIAA0240	5024	100
47	5032	AK001862	Homo sapiens unnamed protein product	954	100
48	5244	AB033010	Homo sapiens KIAA1184 protein	2024	100
49	5268	D86971	Homo sapiens no similarities to reported gene products	840	45
50	5281	AE001691	Thermotoga maritima conserved hypothetical protein	307	40
51	5282	AF174602	Homo sapiens F-box protein Fbx22	391	93
52	6147	Z50853	Homo sapiens CLPP	615	100
53	6178	M20153	Rattus norvegicus cytochrome c oxidase subunit VIc	81	55
54	6184	X03475	Rattus norvegicus ribosomal protein L35a (aa 1-110)	576	99
55	6187	AB029025	Homo sapiens KIAA1102 protein	4394	100
56	6190	U20239	Mus musculus fibrosin	288	76
57	6191	AF125101	Homo sapiens HSPC040 protein	70	100
58	6194	AB018333	Homo sapiens KIAA0790 protein	6546	100
59	6196	X54326	Homo sapiens glutaminyl-tRNA synthetase	7577	99
60	6201	X61585	Bos taurus polynucleotide adenylyltransferase	3715	97
61	6208	AB040921	Homo sapiens KIAA1488 protein	4418	99
62	6214	AC006370	Homo sapiens testis-specific basic protein Y 1	87	50
63	6217	AE003585	Drosophila melanogaster CG17652 gene product	400	40
64	6220	AJ245922	Homo sapiens alpha-tubulin 8	2370	100
65	6221	AB029001	Homo sapiens KIAA1078 protein	4418	100
66	6222	Z97653	Homo sapiens c380A1.2.1 (novel protein (isoform 1))	1567	100
67	6223	AJ404326	Homo sapiens SR+89	1871	99
68	6223	AJ404326	Homo sapiens SR+89	902	64
69	6226	AF134726	Homo sapiens G9A	5334	99
70	6227	AE003538	Drosophila melanogaster CG10191	358	44

TABLE 2

			gene product		
71	6229	M15530	Homo sapiens B-cell growth factor	89	40
72	6248	S67970	Homo sapiens ZNF75=KRAB zinc finger	951	76
73	6260	L28035	Mus musculus protein kinase C gamma	3768	98
74	6264	U16359	Rattus norvegicus nitric oxide synthase	91	58
75	6269	AK000566	Homo sapiens unnamed protein product	1053	100
76	6269	AK000566	Homo sapiens unnamed protein product	537	100
77	6275	X61118	Homo sapiens TTG-2a/RBTN-2a	876	100
78	6276	Z96932	Homo sapiens nuclear autoantigen fo 14 kDa	496	83
79	6280	AJ277291	Homo sapiens HELG protein	678	72
80	6287	X82157	Homo sapiens hevin	3525	99
81	6290	AC007192	Homo sapiens P85B_HUMAN; PTDINS-3-KINASE P85-BETA	3825	99
82	6293	AL021918	Homo sapiens b34I8.1 (Kruppel related Zinc Finger protein 184)	1713	51
83	6305	AF084464	Rattus norvegicus GTP-binding protein REM2	141	30
84	6308	AL049795	Homo sapiens dJ622L5.2 (novel protein)	1756	98
85	6309	D00189	Rattus norvegicus Na+,K+-ATPase alpha-subunit	4269	99
86	6312	U33460	Homo sapiens DNA-directed RNA polymerase I, largest subunit	8777	98
87	6314	D87076	Homo sapiens similar to human bromodomain protein BR140 (JC2069)	3067	100
88	6316	L43912	Macaca mulatta mannose-binding protein A	589	93
89	6336	AB018341	Homo sapiens KIAA0798 protein	1224	52
90	6341	U70976	Homo sapiens arrestin	2068	99
91	6343	U80931	Caenorhabditis elegans strong similarity to class-III of pyridoxal-phosphate-dependent aminotransferases	1049	46
92	6346	AE003435	Drosophila melanogaster CG3016 gene product	240	36
93	6357	AB037860	Homo sapiens KIAA1439	2670	99

TABLE 2

			protein		
94	6359	AL354615	Homo sapiens hypothetical protein	2418	100
95	6367	AE003789	Drosophila melanogaster CG15234 gene product	66	40
96	6383	AC006729	Caenorhabditis elegans Hypothetical protein Y24D9A.e	120	31
97	6385	AF070530	Homo sapiens unknown	2227	99
98	6396	AJ133352	Homo sapiens ZNF237 protein	2006	100
99	6396	AJ133352	Homo sapiens ZNF237 protein	1025	96
100	6403	AF170708	Homo sapiens T-box protein TBX3	3700	99
101	6405	AK002080	Homo sapiens unnamed protein product	1546	99
102	6414	L32977	Homo sapiens Rieske Fe-S protein	1239	93
103	6418	AL080125	Homo sapiens hypothetical protein	1652	56
104	6422	AJ271671	Homo sapiens IRT1 protein	432	36
105	6425	AB006631	Homo sapiens The human homolog of mouse Cux-2	6559	100
106	6436	AF067165	Homo sapiens zinc finger protein 3	977	64
107	6471	AF038169	Homo sapiens unknown	154	38
108	6474	X57817	Homo sapiens immunoglobulin lambda light chain	947	79
109	6482	U97002	Caenorhabditis elegans similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh), Score=57.4, E-value=1.7e-16, N=2; contains similarity to Pfam domain PF00702 (Hydrolase), Score=57.4, E-value=1e-13, N=1	583	37
110	6504	AL031282	Homo sapiens dJ283E3.6.1 (PUTATIVE novel protein similar to many (archae)bacterial, worm and yeast hypothetical proteins)	1041	99
111	6510	M93134	Friend murine leukemia virus pol protein	289	45
112	6515	AF055473	Homo sapiens GAGE-8	232	47
113	6529	X07383	Sus scrofa	60	38

TABLE 2

			preproendothelin (AA - 19 to 184)		
114	6535	S79410	Mus musculus nuclear localization signal binding protein	99	42
115	6536	AB020710	Homo sapiens KIAA0903 protein	4919	100
116	6536	AB020710	Homo sapiens KIAA0903 protein	3334	75
117	6541	AE003492	Drosophila melanogaster CG1998 gene product	799	47
118	6542	D38552	Homo sapiens The ha1539 protein is related to cyclophilin.	2995	100
119	6547	AF272981	Homo sapiens cytosolic aminopeptidase P	3305	100
120	6548	AJ224747	Homo sapiens C-terminal variant of hINADL including 2 amino acid exchanges and an insertion of 28 amino acids in frame.	7969	100
121	6552	AL080063	Homo sapiens hypothetical protein	1354	100
122	6552	AL080063	Homo sapiens hypothetical protein	998	98
123	6555	X63526	Homo sapiens homologue to elongation factor 1-gamma from A.salina	2273	99
124	6560	X15940	Homo sapiens ribosomal protein L31 (AA 1-125)	644	100
125	6566	M60832	Homo sapiens alpha-2 type VIII collagen	3581	99
126	6576	AF039697	Homo sapiens antigen NY-CO-31	1213	97
127	6584	AF156929	Sus scrofa inflammatory response protein 6	1588	83
128	6588	AF264717	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2	5610	99
129	6589	AF044578	Homo sapiens putative DNA polymerase; POL4P	2478	94
130	6590	X89750	Homo sapiens TGIF protein	1413	100
131	6597	M93107	Homo sapiens (R)-3-hydroxybutyrate dehydrogenase	1663	96
132	6600	AB018314	Homo sapiens KIAA0771 protein	4930	99
133	6602	AF151538	Homo sapiens deoxycytidyl transferase; Rev1p	4281	99

TABLE 2

134	6604	AB020716	Homo sapiens KIAA0909 protein	6344	99
135	6605	AJ243874	Homo sapiens oligophrenin-4	3682	100
136	6608	Z11737	Homo sapiens flavin-containing monooxygenase 4	2969	100
137	6610	AB002318	Homo sapiens KIAA0320	4639	99
138	6614	AJ245600	Homo sapiens hypothetical protein	2616	99
139	6623	AK001447	Homo sapiens unnamed protein product	1024	100
140	6629	AB006624	Homo sapiens KIAA0286	2246	99
141	6631	X90530	Homo sapiens ragB	1926	99
142	6631	X90530	Homo sapiens ragB	1405	99
143	6631	X90530	Homo sapiens ragB	1893	96
144	6632	AL022394	Homo sapiens dJ511B24.3 (KIAA0395 (probable Zinc Finger Homeobox protein))	4990	99
145	6633	Y11395	Homo sapiens seventransmembrane-domain protein	2168	100
146	6634	AJ010119	Homo sapiens Ribosomal protein kinase B (RSK-B)	4001	100
147	6635	AL080157	Homo sapiens hypothetical protein	2278	100
148	6639	X54131	Homo sapiens protein-tyrosine phosphatase	10465	99
149	6649	AK001972	Homo sapiens unnamed protein product	1665	100
150	6651	AC004142	Homo sapiens similar to murine leucine-rich repeat protein; possible role in neural development by protein-protein interactions; 93% similarity to D49802 (PID:g1369906)	3676	100
151	6655	AL117544	Homo sapiens hypothetical protein	1226	100
152	6658	AF203032	Homo sapiens neurofilament protein	5115	99
153	6667	AL034417	Homo sapiens bK215D11.2 (similar to rat gene 33)	2476	100
154	6672	X69090	Homo sapiens 190kD protein	7546	99
155	6682	AB032957	Homo sapiens KIAA1131 protein	5395	100
156	6683	AK000486	Homo sapiens unnamed protein product	801	100
157	6687	U39045	Rattus norvegicus cytoplasmic dynein	3241	97

TABLE 2

			intermediate chain 2B		
158	6687	AF063231	Mus musculus cytoplasmic dynein intermediate chain 2	3159	97
159	6688	AF202893	Mus musculus Kif21b	4336	95
160	6696	Y13115	Homo sapiens serine/threonine protein kinase	5071	99
161	6701	AB030207	Homo sapiens G gamma subunit	364	100
162	6707	AL133030	Homo sapiens hypothetical protein	6174	99
163	6712	AB037883	Homo sapiens Gb3/CD77 synthase	1916	99
164	6714	D90868	Escherichia coli similar to	1489	100
165	6720	X98834	Homo sapiens zinc finger protein Hsa12	5290	100
166	6721	D80007	Homo sapiens similar to hypothetical protein YM9959.11C of S.cerevisiae.	9568	100
167	6722	AF019926	Mus musculus protein kinase	1694	90
168	6736	M34513	Homo sapiens omega protein	317	91
169	6740	Y08612	Homo sapiens 88kDa nuclear pore complex protein	2313	99
170	6740	Y08612	Homo sapiens 88kDa nuclear pore complex protein	1561	99
171	6760	AB018310	Homo sapiens KIAA0767 protein	2968	100
172	6775	AF186249	Homo sapiens six transmembrane epithelial antigen of prostate	1790	100
173	6784	AB029012	Homo sapiens KIAA1089 protein	4933	100
174	6793	AB026893	Homo sapiens vascular cadherin-2	5962	100
175	6795	X74331	Homo sapiens DNA primase (p58 subunit)	1720	100
176	6796	AC002391	Arabidopsis thaliana hypothetical protein	72	30
177	6807	AC007228	Homo sapiens R31665_2	1488	48
178	6808	X14830	Homo sapiens acetylcholine receptor beta-subunit preprotein	2639	100
179	6810	U80446	Caenorhabditis elegans coded for by C. elegans cDNA yk172e6.3; coded for by C. elegans cDNA	420	40

TABLE 2

			yk158f7.3; coded for by C. elegans cDNA yk158f7.5; coded for by C. elegans cDNA yk172e6.5		
180	6815	AB002360	Homo sapiens KIAA0362	5766	99
181	6819	Z82215	Homo sapiens dJ6802.2 (myosin, heavy polypeptide 9, non- muscle)	9828	100
182	6821	AC004010	Homo sapiens similar to Leucine-rich transmembrane proteins; 44% similarity to U42767 (PID:g1736918)	2723	100
183	6827	AJ269537	Homo sapiens chondroitin-4- sulfotransferase	557	40
184	6829	X99688	Homo sapiens TYL	3326	99
185	6830	U90305	Homo sapiens iroquois- class homeodomain protein IRX-3	1022	99
186	6835	AF180473	Homo sapiens Not2p	2267	100
187	6848	AB029009	Homo sapiens KIAA1086 protein	4798	99
188	6849	AF023453	Homo sapiens actin- related protein 3-beta	2219	100
189	6851	AB020699	Homo sapiens KIAA0892 protein	3222	100
190	6851	AC003030	Homo sapiens R29828_1	2294	100
191	6863	AB020630	Homo sapiens KIAA0823 protein	2159	100
192	6869	AK001387	Homo sapiens unnamed protein product	1255	99
193	6874	D63484	Homo sapiens The KIAA0150 gene product is novel.	4940	99
194	6887	Y07595	Homo sapiens transcription factor TFIIH	2373	100
195	6890	AF143321	Homo sapiens unknown	918	95
196	6894	X83618	Homo sapiens hydroxymethylglutaryl- CoA synthase	2647	100
197	6899	AF134726	Homo sapiens NG37	4359	99
198	6900	AB035356	Homo sapiens neurexin I-alpha protein	6948	99
199	6903	Z68005	Caenorhabditis elegans F59F3.4	67	37
200	6910	AB018323	Homo sapiens KIAA0780 protein	5220	99
201	6913	AB043634	Homo sapiens PAR-6A	885	100
202	6918	AP000693	Homo sapiens partial CDS	4875	99
203	6923	AF002223	Homo sapiens	3490	100

TABLE 2

			myotubularin related 1		
204	6926	AC004893	Homo sapiens similar to NEDD-4 (KIA0093); similar to P46934 (PID:g1171682)	1611	100
205	6929	AB002355	Homo sapiens KIAA0357	10119	100
206	6929	AF257737	Homo sapiens ciliary dynein heavy chain 9	11126	99
207	6932	X65873	Homo sapiens kinesin heavy chain	4860	100
208	6941	AL080159	Homo sapiens hypothetical protein	1942	100
209	6951	AC004883	Homo sapiens similar to KIAA0766; similar to PID:g3882253	2782	99
210	6954	X71125	Homo sapiens glutaminyl-peptide cyclotransferase	1914	100
211	6954	X71125	Homo sapiens glutaminyl-peptide cyclotransferase	1456	97
212	6956	X54304	Homo sapiens myosin regulatory light chain	897	100
213	6957	AB007883	Homo sapiens KIAA0423	8621	99
214	6960	AK000432	Homo sapiens unnamed protein product	1622	100
215	6966	AF039563	Mus musculus retinoblastoma binding protein	792	94
216	6968	AL117352	Homo sapiens dJ876B10.2 (novel protein (ortholog of rat EXO84))	3713	99
217	6969	AF228603	Homo sapiens pleckstrin 2	1841	100
218	6970	AL117455	Homo sapiens hypothetical protein	4598	100
219	6971	AK002077	Homo sapiens unnamed protein product	989	100
220	6989	AF156271	Homo sapiens RING finger protein terf	476	40
221	6990	AC005551	Homo sapiens R26529_2, partial CDS	1020	100
222	6994	AL080129	Homo sapiens hypothetical protein	3789	99
223	6996	AE003603	Drosophila melanogaster CG1172 gene product	512	54
224	6997	AB002379	Homo sapiens KIAA0381	4437	99
225	7009	U03399	Homo sapiens T-complex protein 10A	846	77
226	7016	AB014091	Xenopus laevis alpha-1-antiprotease	850	42
227	7023	AB029040	Homo sapiens KIAA1117 protein	7032	99
228	7023	AL121716	Homo sapiens	6329	99

TABLE 2

			dJ202D23.2 (novel protein)		
229	7035	X92715	Homo sapiens KRAB /C2H2 zinc finger protein	3102	97
230	7038	X54637	Homo sapiens protein tyrosine kinase	5564	98
231	7039	AB007925	Homo sapiens KIAA0456 protein	5491	99
232	7040	AJ251245	Rattus norvegicus SECIS binding protein 2	3086	72
233	7041	AF113125	Homo sapiens E-1 enzyme	581	100
234	7044	M19529	Sus scrofa follistatin A	1906	98
235	7059	AB040902	Homo sapiens KIAA1469 protein	3403	100
236	7060	D87685	Homo sapiens similar to human transcription factor TFIIS (S34159).	8083	99
237	7063	AB029334	Halocynthia roretzi HrPET-1	638	35
238	7067	AK001603	Homo sapiens unnamed protein product	2079	99
239	7070	D86973	Homo sapiens similar to Yeast translation activator GCN1 (P1:A48126)	12033	99
240	7071	AL034452	Homo sapiens dJ682J15.1 (novel Collagen triple helix repeat containing protein)	1979	100
241	7079	AF088219	Homo sapiens lysozyme homolog	307	42
242	7085	AF007872	Homo sapiens torsinB	1277	98
243	7148	U94586	Homo sapiens NADH:ubiquinone oxidoreductase MLRQ subunit	277	66
244	7156	U28486	Mus musculus proline-rich acidic protein	313	48
245	7156	U28486	Mus musculus proline-rich acidic protein	297	47
246	7171	AF022770	Mus musculus peripheral benzodiazepine receptor associated protein; PBR associated protein; PAP7	2078	91
247	7241	AC004990	Homo sapiens supported by Genscan and several ESTs: C83049 (NID:g3062006),	2685	99

TABLE 2

			AA823760 (NID:g2893628), AA215791 (NID:g1815572), AI095488 (NID:g3434464), and AA969095 (NID:g3144275)		
248	7265	AB037756	Homo sapiens KIAA1335 protein	3590	99
249	7268	AF070447	Homo sapiens barrier- to-autointegration factor	290	90
250	7308	AB020719	Homo sapiens KIAA0912 protein	6488	100
251	7336	X79828	Mus musculus NK10	202	53
252	7347	AB004109	Cricetulus griseus phosphatidylserine synthase II	2262	92
253	7405	AB028972	Homo sapiens KIAA1049 protein	2866	99
254	7405	AB028972	Homo sapiens KIAA1049 protein	2754	97
255	7412	AF006264	Homo sapiens recombination and sister chromatid cohesion protein homolog	2850	100
256	7412	AF006264	Homo sapiens recombination and sister chromatid cohesion protein homolog	2530	100
257	7436	X82260	Homo sapiens RanGAP1	2929	100
258	7436	X82260	Homo sapiens RanGAP1	1843	97
259	7454	AF160909	Drosophila melanogaster BcDNA.LD03471	943	59
260	7476	AF225324	Centrocercus urophasianus gag polyprotein	94	33
261	7598	X74801	Homo sapiens gamma subunit of CCT chaperonin	2745	99
262	7619	AL031427	Homo sapiens dJ167A19.1 (novel protein)	1608	100
263	7644	AF258614	Canis familiaris vacuolar proton-ATPase subunit ATP6H	345	72
264	7648	X16396	Homo sapiens precursor polypeptide (AA -29 to 315)	1749	100
265	7659	AK000281	Homo sapiens unnamed protein product	1814	99
266	7661	AB011128	Homo sapiens KIAA0556	5761	99

TABLE 2

			protein		
267	7669	AL050284	Homo sapiens hypothetical protein	2857	100
268	7686	D26068	Homo sapiens KIAA0038	1208	100
269	7686	AF045555	Homo sapiens wbscr1 alternative spliced product	1318	100
270	7694	U22229	Felis catus ribosomal protein L41	128	100
271	7697	Y17169	Homo sapiens A6 related protein	1819	100
272	7733	Y12065	Homo sapiens hNop56	2956	99
273	7734	AF177758	Homo sapiens ubiquitin specific protease 16	2998	100
274	7744	AB020681	Homo sapiens KIAA0874 protein	3090	100
275	7751	AL050297	Homo sapiens hypothetical protein	1227	99
276	7756	AC007204	Homo sapiens BC273239_1	3398	99
277	7761	Z68747	Homo sapiens imogen 38	2024	99
278	7761	Z68747	Homo sapiens imogen 38	1958	97
279	7776	AK001467	Homo sapiens unnamed protein product	3416	99
280	7783	AF095687	Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x	409	100
281	7800	AF119664	Homo sapiens transcriptional regulator protein HCNGP	1574	100
282	7800	AF119664	Homo sapiens transcriptional regulator protein HCNGP	1150	89
283	7801	Y17849	Homo sapiens ganglioside-induced differentiation associated protein 1	1839	98
284	7811	X55740	Homo sapiens 5'-nucleotidase	3012	100
285	7817	AF039688	Homo sapiens antigen NY-CO-3	931	100
286	7821	AL050282	Homo sapiens hypothetical protein	2424	100
287	7822	AB007836	Homo sapiens Hic-5	2544	100
288	7841	AB002301	Homo sapiens KIAA0303	11166	100
289	7847	U32305	Caenorhabditis elegans B0336.11 gene product	233	26
290	7880	AF078844	Homo sapiens hqp0376 protein	416	81
291	7910	U28377	Escherichia coli ORF_f239; was ORF_f191 and ORF_f194 before	1198	100

TABLE 2

			splice		
292	7925	AL122047	Homo sapiens hypothetical protein	404	100
293	7936	AL080123	Homo sapiens hypothetical protein	3321	99
294	7945	U58682	Homo sapiens ribosomal protein S28	340	100
295	7948	X57432	Rattus rattus ribosomal protein S2	1520	98
296	7963	AB002348	Homo sapiens KIAA0350 protein	5186	99
297	7984	AC000098	Arabidopsis thaliana YUP8H12.9	37	46
298	7985	AF110645	Homo sapiens candidate tumor suppressor p33 ING1 homolog	843	69
299	8014	AB011168	Homo sapiens KIAA0596 protein	6279	99
300	8025	AJ237839	Homo sapiens hypothetical protein	11699	99
301	8029	AP001633	Oryza sativa ESTs AU083470 (E11568), C20136 (E11568) correspond to a region of the predicted gene.~Similar to Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence; unknown protein (AC003028)	424	43
302	8043	AL163201	Homo sapiens tensin, putative protein-tyrosine phosphatase, EC 3.1.3.48	74	35
303	8164	AC002550	Homo sapiens Unknown gene product	858	99
304	8175	U26592	Homo sapiens diabetes mellitus type I autoantigen	253	66
305	8250	X60155	Homo sapiens zinc finger 41	4349	100
306	8253	X53330	Platynereis dumerilii H4 protein (AA 1 - 103)	523	100
307	8255	AC003682	Homo sapiens R27945_2	2558	100
308	8258	X80473	Mus musculus rab19	596	56
309	8270	J02649	Rattus norvegicus unknown protein	201	95
310	8271	AC006014	Homo sapiens similar to RFP transforming protein; similar to P14373 (PID:g132517)	1331	99
311	8272	X92972	Homo sapiens protein phosphatase 6	1666	100
312	8279	L35269	Homo sapiens zinc	2803	99

TABLE 2

			finger protein		
313	8284	AC003682	Homo sapiens F18547_1	3184	96
314	8285	X79204	Homo sapiens ataxin-1	4195	99
315	8304	X17620	Homo sapiens Nm23 protein	965	99
316	8309	AB029004	Homo sapiens KIAA1081 protein	2362	100
317	8320	Z56281	Homo sapiens interferon regulatory factor 3	2331	100
318	8331	Z73906	Caenorhabditis elegans Similarity to B.subtilis YQJC protein (TR:G1303954)-cDNA EST EMBL:T01187 comes from this gene	470	70
319	8332	Z70200	Homo sapiens U5 snRNP-specific 200kD protein	8819	99
320	8332	Z70200	Homo sapiens U5 snRNP-specific 200kD protein	8589	97
321	8335	AF153450	Manduca sexta juvenile hormone esterase binding protein	225	32
322	8337	AF227198	Homo sapiens CDC2-related protein kinase 7	7231	99
323	8353	X99586	Homo sapiens SMT3C protein	441	87
324	8355	Y18198	Homo sapiens ONECUT-2 transcription factor (OC-2)	2592	100
325	8358	AK001550	Homo sapiens unnamed protein product	3654	99
326	8361	AF139471	Homo sapiens putative calcium-activated potassium channel regulatory subunit	1385	100
327	8369	AL110479	Caenorhabditis elegans predicted using Genefinder-cDNA EST yk524f8.5 comes from this gene-cDNA EST yk631e2.5 comes from this gene-cDNA EST EMBL:C08367 comes from this gene-cDNA EST yk524f8.3 comes from this gene	709	48
328	8385	AF007826	Homo sapiens bax epsilon	133	66
329	8397	AE003544	Drosophila melanogaster CG11712 gene product	514	47
330	8414	AE003536	Drosophila melanogaster CG17365	267	35

TABLE 2

			gene product		
331	8431	U83115	Homo sapiens non-lens beta gamma-crystallin like protein	8569	99
332	8433	AF203687	Homo sapiens prolactin regulatory element-binding protein	2181	100
333	8444	M27685	Mus musculus ultra-high sulphur keratin	650	59
334	8446	U04968	Cricetulus griseus nucleotide excision repair protein	3712	97
335	8460	AF188181	Homo sapiens G-protein gamma 12 subunit	356	100
336	8478	AF117587	Manduca sexta unknown	255	74
337	8490	X67699	Homo sapiens CDw52 antigen	297	100
338	8505	AF022789	Homo sapiens ubiquitin hydrolyzing enzyme I	1892	100
339	8523	AJ001006	Mus musculus EMeg32 protein	938	96
340	8530	U31332	Homo sapiens DP prostanoid receptor	1467	100
341	8533	AF019661	Mus musculus zeta proteasome chain; PSMA5	1214	100
342	8534	AF156557	Homo sapiens stomatin related protein	2036	100
343	8536	AK000438	Homo sapiens unnamed protein product	593	100
344	8537	AF161512	Homo sapiens HSPC163	738	100
345	8543	AL031115	Homo sapiens ZXDA, ZXDB (zinc finger X-linked protein)	4298	100
346	8546	L40410	Homo sapiens thyroid receptor interactor	806	100
347	8553	AC004542	Homo sapiens OXYSTEROL-BINDING PROTEIN-like; similar to P22059 (PID:g129308)	2533	99
348	8556	AB002298	Homo sapiens KIAA0300	8265	99
349	8561	AE003691	Drosophila melanogaster CG5276 gene product	875	53
350	8562	AK000051	Homo sapiens unnamed protein product	1613	100
351	8569	U10362	Homo sapiens GP36b glycoprotein	790	57
352	8587	AL133506	Unknown /prediction=(method:""genscan"", version:""1.0"", score:""109.13""); /prediction=(method:	825	48
353	8597	X61001	Gallus gallus lysozyme	422	42

TABLE 2

354	8610	AC003034	Homo sapiens Gene with similarity to rat kidney-specific (KS) gene	1190	100
355	8610	AC003034	Homo sapiens Gene with similarity to rat kidney-specific (KS) gene	937	95
356	8615	AJ242832	Homo sapiens calpain	3756	100
357	8622	S52624	Homo sapiens orf 5' of PAF receptor	185	100
358	8626	AF005081	Homo sapiens skin-specific protein	652	100
359	8628	Y16793	Homo sapiens keratin, type I	2232	100
360	8629	AF005080	Homo sapiens skin-specific protein	438	73
361	8630	AK001429	Homo sapiens unnamed protein product	682	99
362	8632	AF005080	Homo sapiens skin-specific protein	375	62
363	8634	Y16132	Homo sapiens CDT6	1874	100
364	8643	D64048	Rattus norvegicus phosphatidylinositol 3-kinase p45 subunit	2347	97
365	8644	X63422	Homo sapiens H(+)-transporting ATP synthase	209	100
366	8645	M73837	Homo sapiens modulator recognition factor 2	1284	100
367	8646	X52563	Bos taurus permability increasing protein	383	29
368	8657	X82385	Homo sapiens RNA polymerase II subunit	429	95
369	8661	AJ245586	Homo sapiens KRAB protein domain	396	98
370	8670	AF223466	Homo sapiens HT015 protein	1311	97
371	8692	AF250878	Salmonella typhi plasmid maintenance protein	50	40
372	8698	AF117383	Homo sapiens placental protein 13; PP13	746	100
373	8762	AK000192	Homo sapiens unnamed protein product	1446	99
374	8768	AK001715	Homo sapiens unnamed protein product	715	99
375	8768	AL163815	Arabidopsis thaliana putative protein	302	67
376	8799	AL031685	Homo sapiens dJ963K23.2 (novel protein)	343	48
377	8806	AB023191	Homo sapiens KIAA0974 protein	2953	100
378	8809	AL031778	Homo sapiens dJ34B21.1 (novel BZRP	920	100

TABLE 2

			(benzodiazapine receptor (peripheral) (MBR, PBR, PBKS, IBP, Isoquinoline-binding protein)) LIKE protein)		
379	8814	AL021939	Homo sapiens dJ352A20.2 (aldehyde dehydrogenase family protein)	1764	100
380	8822	AB037784	Homo sapiens KIAA1363 protein	1895	98
381	8833	Y08565	Homo sapiens UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase	3331	99
382	8835	AB037755	Homo sapiens KIAA1334 protein	1655	100
383	8877	AB037811	Homo sapiens KIAA1390 protein	1563	99
384	8886	AK000767	Homo sapiens unnamed protein product	2470	100
385	9003	AF178432	Homo sapiens SH3 protein	3302	100
386	9157	U60269	Homo sapiens putative envelope protein; orf similar to env of Type A and Type B retroviruses and to class II HERVs	893	95
387	9175	AF015454	Xenopus laevis ER1	1716	80
388	9205	U09355	Oryctolagus cuniculus protein phosphatase 2A1 B gamma subunit	2352	99
389	9260	X89480	Sus scrofa transmembrane protein	601	80
390	9295	AB027003	Mus musculus protein phosphatase	378	84
391	9307	AF112200	Homo sapiens NADH-oxidoreductase B18 subunit	739	100
392	9307	AF112200	Homo sapiens NADH-oxidoreductase B18 subunit	613	88
393	9312	AL133565	Homo sapiens hypothetical protein	6331	100
394	9347	AE003511	Drosophila melanogaster CG14194 gene product	825	48
395	9370	L27479	Homo sapiens X123	1237	99
396	9370	L27479	Homo sapiens X123	1206	97
397	9382	AF182066	Mus musculus Bv8 variant 3 precursor	293	51
398	9591	AJ001019	Homo sapiens ring finger protein	1292	99
399	9650	X68453	Sus scrofa tubulin-	1882	94

TABLE 2

			tyrosine ligase		
400	9655	AK001723	Homo sapiens unnamed protein product	624	56
401	9663	AF151069	Homo sapiens HSPC235	1694	96
402	9715	AF043695	Caenorhabditis elegans Similar to mitochondrial carrier protein	556	43
403	9755	AK000149	Homo sapiens unnamed protein product	2589	99
404	9766	AF130979	Homo sapiens SH3 domain-containing protein 6511	2249	99
405	9771	AL008635	Homo sapiens dJ510H16.2 (high-mobility group protein 2-like 1)	3026	99
406	9784	AL137593	Homo sapiens hypothetical protein	1124	100
407	9925	AF111179	Rattus norvegicus G-septin alpha	1739	98
408	9970	AF004161	Oryctolagus cuniculus peroxisomal Ca-dependent solute carrier	2371	95
409	9997	Z19585	Homo sapiens thrombospondin-4	4239	100
410	10008	AB033053	Homo sapiens KIAA1227 protein	1857	100
411	10010	AC005534	Homo sapiens supported by human ESTs AA412402 (NID:g2070990) NH44021 (NID:g1182549), mouse EST AA065933 (NID:g1562789), and genscan	756	100
412	10023	AF090326	Mus musculus AE-1 binding protein AEBP2	1540	97
413	10043	U39412	Homo sapiens alpha SNAP	879	81
414	10093	AC003007	Homo sapiens Unknown gene product (partial)	649	96
415	10172	U66372	Bos taurus ribosomal protein S29	230	73
416	10184	AB032910	Hylobates muelleri dopamine receptor D4	83	46
417	10205	AF225903	Homo sapiens D1 dopamine receptor interacting protein calcyon	1152	100
418	10246	AE003486	Drosophila melanogaster CG1749 gene product	1291	65
419	10298	X92666	Bos taurus cysteine string protein	1085	98

CLAIMS

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1 - 419, a mature protein coding portion of SEQ ID NO: 1 - 419, an active domain of SEQ ID NO:1 - 419, and complementary sequences thereof.

2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.

3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.

4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.

5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.

6. A vector comprising the polynucleotide of claim 1.

7. An expression vector comprising the polynucleotide of claim 1.

8. A host cell genetically engineered to comprise the polynucleotide of claim 1.

9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.

10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

- (a) a polypeptide encoded by any one of the polynucleotides of claim 1;
and
- (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1 - 419.

5

11. A composition comprising the polypeptide of claim 10 and a carrier.

12. An antibody directed against the polypeptide of claim 10.

10

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and

15

b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

20

a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;

b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and

25

c) detecting said product and thereby the polynucleotide of claim 1 in the sample.

15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

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16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and

b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-419, a mature protein coding portion of SEQ ID NO: 1-419, an active domain of SEQ ID NO: 1-419, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-419, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides from the Sequence Listing, the mature protein portion thereof, or the active domain thereof.

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21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

10

22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO: 1 - 419.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

15

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

20

26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

25

27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

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28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

ABSTRACT OF THE INVENTION

The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

5

DECLARATION FOR PATENT APPLICATION AND POWER OF ATTORNEY

As [a] below named inventor(s), I/we hereby declare that:

Y. Tom Tang, Ping Zhou, Chenghua Liu, Vinod Asundi, Jie Zhang, Feiyan Ren, Rui-hong Chen, Qing A. Zhao, Aidong J. Xue, Yonghong Yang, Tom Wehrman, Jian-Rui Wang, Yunqing Ma, Dunrui Wang, John Tillinghast, Radoje T. Drmanac

My/our residence, post office address and citizenship is/are as stated below next to my/our name(s).

I/we believe I/we am/are an/the original, first and sole/joint inventor of the subject matter which is claimed and for which a patent is sought on the invention entitled: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES, the specification of which

 X is attached hereto.

 was filed on [date] as Application Serial Number []
and was amended on [date].

I/We hereby state that I/we have reviewed and understand the contents of the above-identified specification, including the claims as amended by any amendment referred to above.

I/We acknowledge the duty to disclose information which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, Section 1.56(a).

I/We hereby claim foreign priority benefits under Title 35, United States Code, § 119 of any foreign application(s) for patent or inventor's certificate, listed below and so identified, and I/we have also identified below any foreign application for patent or inventor's certificate on this invention filed by me or my legal representatives or assigns and having a filing date before that of the application on which priority is claimed:

NUMBER	COUNTRY	DAY/MONTH/ YEAR FILED	PRIORITY CLAIMED - YES OR NO

I/We hereby claim the benefit under Title 35, United States Code, § 120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, § 112, I/we acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, § 1.56(a) which occurred between the filing date of the prior application and the national or PCT international filing date of this application.

SERIAL NUMBER	FILING DATE	STATUS
09/560,875	April 27, 2000	Pending
09/496,914	February 03, 2000	Pending

I/We hereby declare that all statements made herein of my/our own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under § 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

I/We hereby appoint the following attorneys and agents, with full power of substitution and revocation, to prosecute this application and to transact all business in the United States Patent and Trademark Office connected therewith and request that all correspondence and telephone calls with respect to this application be directed to Petrina S. Hsi, HYSEQ, INC., 670 Almanor Avenue, Sunnyvale, CA 94085, Telephone No. (408) 524-8100:

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Asundi, Vinod
Zhang, Jie
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Chen, Rui-hong
Zhao, Qing A.
Xue, Aidong J.
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Gly Gly His Leu Arg Met Ile Lys Arg Val Gln Asn Leu Leu Gly His		
77 82 87 92		
tat ctt atc cat ggc ttc cgg gta cgg cca gag cct aat gga gac ctt	337	
Tyr Leu Ile His Gly Phe Arg Val Arg Pro Glu Pro Asn Gly Asp Leu		
93 98 103 108		
gac ttg gag gcc atg gtg gct gtg ttt gga agc aag gga ctc cga gtt	385	
Asp Leu Glu Ala Met Val Ala Val Phe Gly Ser Lys Gly Leu Arg Val		
109 114 119 124		
gtg aaa att agc tgg gga cag ggc cac ttc tgg gag ctt tgg cgc tct	433	
Val Lys Ile Ser Trp Gly Gln Gly His Phe Trp Glu Leu Trp Arg Ser		
125 130 135 140		
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Gly Leu Trp Asn Met Ser Asp Trp Ile Trp Asp Ala Arg Trp Leu Glu		
141 146 151 156		
gga aat ata gcc ttg gcc ctg ggc cac aac tca gtg gtg cta tat gac	529	
Gly Asn Ile Ala Leu Ala Leu Gly His Asn Ser Val Val Leu Tyr Asp		
157 162 167 172		
cct gta gta ggg tgc atc ctg caa gag gtg ccc tgc aca gac agg tgc	577	
Pro Val Val Gly Cys Ile Leu Gln Glu Val Pro Cys Thr Asp Arg Cys		
173 178 183 188		
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Thr Leu Ser Ser Ala Cys Leu Ile Gly Asp Ala Trp Lys Glu Leu Thr		
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Gly His Val Gly Ile	Ile Phe Ser Met Ser	Tyr Leu Glu Ser Lys Gly		
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Leu Leu Ala Thr Ala	Ser Glu Asp Arg Ser	Val Arg Ile Trp Lys Val		
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Phe Gly His Ser Ala	Arg Val Trp Gln Val	Lys Leu Leu Glu Asn Tyr		
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Leu Ile Ser Ala Gly	Glu Asp Cys Val Cys	Leu Val Trp Ser His Glu		
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Gly Glu Ile Leu Gln	Ala Phe Arg Gly His	Gln Gly Arg Gly Ile Arg		
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gcc ata gct gcc cat	gag agg cag gcc tgg	gtg atc act ggg ggt gat		1057
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Asp Ser Gly Ile Arg	Leu Trp His Leu Val	Gly Arg Gly Tyr Arg Gly		
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Leu Lys Ala Val Thr	Leu Ala Gly Ser Trp	Arg Leu Leu Ala Val Thr		
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Asp Thr Gly Ala Leu	Tyr Leu Tyr Asp Val	Glu Val Lys Cys Trp Glu		
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Gln Leu Leu Glu Asp	Lys His Phe Gln Ser	Tyr Cys Leu Leu Glu Ala		
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Ala Pro Gly Pro Glu	Gly Phe Gly Leu Cys	Ala Met Ala Asn Gly Glu		
429	434	439	444	

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Gly Arg Val Lys Val Val Pro Ile Asn Thr Pro Thr Ala Ala Val Asp	
445 450 455 460	
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Gln Thr Leu Phe Pro Gly Lys Val His Ser Leu Ser Trp Ala Leu Arg	
461 466 471 476	
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Gly Tyr Glu Glu Leu Leu Leu Leu Ala Ser Gly Pro Gly Gly Val Val	
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Ala Cys Leu Glu Ile Ser Ala Ala Pro Ser Gly Lys Ala Ile Phe Val	
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Arg Arg Gly Ser Val Leu Leu Phe Pro Ser Gly Pro Gly Arg Asp Gly	
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Ala Tyr Tyr Gln Leu Phe Val Arg Asp Gly Gln Leu Gln Pro Val Leu	
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Arg Gln Lys Ser Cys Arg Gly Met Asn Trp Leu Ala Gly Leu Arg Ile	
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589 594 599 604	
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Val Val Trp Asn Pro Arg Ser His Glu Lys Leu His Ile Ile Asn Cys	
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Glu Tyr Gly Val Pro Ser Phe Met Gln Pro Asp Asp Leu Glu Pro Gly	
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Ser Glu Gly Pro Asp Leu Thr Asp Ile Val Ile Thr Cys Ser Glu Asp	
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Thr Thr Val Cys Val Leu Ala Leu Pro Thr Thr Thr Gly Ser Ala His	
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Cys His Val Met His Leu Ser Ser His Arg Leu Asp Glu Tyr Trp Asp	
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Tyr Met Ser Leu Ala Val Cys Glu Leu Asp Gln Pro Gly Leu Gly Pro	
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Ala	Phe	Trp	Asp	Leu	Thr	Thr	Met	Leu	Asp	His	Asp	Ser	Thr	Val	Leu		
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gag	cct	cca	gtg	gat	cct	ggg	ctt	ccc	tac	cgg	ctt	ggc	acc	ccc	tcc	2833	
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Leu	Thr	Leu	Gln	Ala	His	Ser	Cys	Gly	Ile	Asn	Ser	Leu	His	Thr	Leu		
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Pro	Thr	Arg	Glu	Gly	His	His	Leu	Val	Ala	Ser	Gly	Ser	Glu	Asp	Gly		
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Tyr	Ser	Val	Pro	Cys	Ala	His	Ala	Ala	His	Val	Thr	Gly	Leu	Lys	Ile		
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Leu	Ser	Pro	Ser	Ile	Met	Val	Ser	Ala	Ser	Ile	Asp	Gln	Arg	Leu	Thr		
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1037					1042					1047					1052		
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Phe	His	Val	Pro	Asp	Val	Ala	Asp	Met	Asp	Cys	Trp	Pro	Val	Ser	Pro		
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Glu	Phe	Gly	His	Arg	Cys	Ala	Leu	Gly	Gly	Gln	Gly	Leu	Glu	Val	Tyr		
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aac	tgg	tat	gac	tga	ggat	cctgc	ggt	ggct	ggc	gtg	ctggg	ca	tgggg	cctgc		3320	
Asn	Trp	Tyr	Asp	*													
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 Met Asn Cys Thr Leu Lys
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 Gly Phe Leu Pro Phe Glu Ile Met Tyr Gly Arg Ala Leu Pro Ile Leu
 39 44 49 54
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 Pro Lys Leu Arg Asp Ala Gln Leu Ala Lys Ile Ser Gln Thr Asn Leu
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Cys His Ser Phe Pro Pro Gly Asp Leu Leu Phe Val Lys Lys Phe Gln	
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Arg Glu Gly Leu Pro Pro Ala Trp Lys Arg Pro His Thr Val Ile Thr	
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Met Pro Thr Ala Leu Lys Val Asp Gly Ile Pro Ala Trp Ile His His	
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Arg Ala Gly Ser Gly Pro Leu Lys Leu His Leu Ser Trp Val Lys Pro	
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Leu Asp *	
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Phe Lys Leu Ser Cys Thr Ala Ser Asn Ser Asn Arg Ser Thr Pro Ala						
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Cys Ser Pro Ile Leu Arg Lys Arg Ser Arg Ser Pro Thr Pro Gln Asn						
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Lys Ser Pro Ser Thr Pro Glu Gln Gly Val Gln Arg Ser Cys Ser Ser						
52 57 62 67						
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Gln Ser Gly Arg Ser Gly Gly Lys Asn Ser Lys Lys Ser Gln Ser Trp						
68 73 78 83						
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Tyr Asn Val Leu Ser Pro Thr Tyr Lys Gln Arg Asn Glu Asp Phe Arg						
84 89 94 99						
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Lys Leu Phe Lys Gln Leu Pro Asp Thr Glu Arg Leu Ile Val Asp Tyr						
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Leu Leu Thr Val Arg Leu Lys Asp Ile Cys Ser Met Thr Lys Glu Lys						
148 153 158 163						
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Lys	His	Phe	Phe	Thr	Ser	Phe	Gly	Ala	Arg	Asp	Arg	Thr	Tyr	Met	Met	
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Cys Ser Pro Ile Leu Arg Lys Arg Ser Arg Ser Pro Thr Pro Gln Asn	
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Arg Pro Gly Arg Arg Ser Ala Val Pro Arg Trp Pro His Leu Ser Ser
13          18          23          28

caa agt ggc gtc gaa ccc cct gac agg tgg acg gga acc ccc ggc tgg      264
Gln Ser Gly Val Glu Pro Pro Asp Arg Trp Thr Gly Thr Pro Gly Trp
29          34          39          44

ccc tcc aga gac cag gag gcc cct ggc tca atg atg cca cct gca gct      312
Pro Ser Arg Asp Gln Glu Ala Pro Gly Ser Met Met Pro Pro Ala Ala
45          50          55          60

gcc caa ccc tcc gcc cat ggt gcc ctt gtt cca cct gcc acc gct cat      360
Ala Gln Pro Ser Ala His Gly Ala Leu Val Pro Pro Ala Thr Ala His
61          66          71          76

gaa cct gtg gat cac cca gct ctg cac tgg ctt gcc tgc tgc tgc tgt      408
Glu Pro Val Asp His Pro Ala Leu His Trp Leu Ala Cys Cys Cys Cys
77          82          87          92

ctc agt tta cct ggg cag ttg ccc ctg gct atc cgg ctg gga tgg gac      456
Leu Ser Leu Pro Gly Gln Leu Pro Leu Ala Ile Arg Leu Gly Trp Asp
93          98          103          108

ttg gac tta gaa gca ggc ccc tcc tct gga aag ctg tgt cct cgg gcc      504
Leu Asp Leu Glu Ala Gly Pro Ser Ser Gly Lys Leu Cys Pro Arg Ala
109          114          119          124

agg agg tgg cag cct cta cct tcc tga gacag ggaccctttt ctgtccatca      556
Arg Arg Trp Gln Pro Leu Pro Ser *
125          130

gaggacagct gtatgaagac acagagagaa ggcagccatc tgtaagccag gaagagagcc      616

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                                   Met Lys Thr Leu Phe Leu
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ggt gtc acg ctc ggc ctg gcc gct gcc ctg tcc ttc acc ctg gag gag      160
Gly Val Thr Leu Gly Leu Ala Ala Ala Leu Ser Phe Thr Leu Glu Glu
  7                      12                      17                      22

gag gat atc aca ggg acc tgg tac gtg aag gcc atg gtg gtc gat aag      208
Glu Asp Ile Thr Gly Thr Trp Tyr Val Lys Ala Met Val Val Asp Lys
  23                      28                      33                      38

gac ttt ccg gag gac agg agg ccc agg aag gtg tcc cca gtg aag gtg      256
Asp Phe Pro Glu Asp Arg Arg Pro Arg Lys Val Ser Pro Val Lys Val
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aca gcc ctg ggc ggt ggg aac ttg gaa gcc acg ttc acc ttc atg agg      304
Thr Ala Leu Gly Gly Gly Asn Leu Glu Ala Thr Phe Thr Phe Met Arg
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gag gat cgg tgc atc cag aag aaa atc ctg atg cgg aag acg gag gag      352
Glu Asp Arg Cys Ile Gln Lys Lys Ile Leu Met Arg Lys Thr Glu Glu
  71                      76                      81                      86

cct ggc aaa ttc agc gcc tat ggg ggc agg aag ctc ata tac ctg cag      400
Pro Gly Lys Phe Ser Ala Tyr Gly Gly Arg Lys Leu Ile Tyr Leu Gln
  87                      92                      97                      102

gag ctg ccc ggg acg gac gac tac gtc ttt tac tgc aaa gac cag cgc      448
Glu Leu Pro Gly Thr Asp Asp Tyr Val Phe Tyr Cys Lys Asp Gln Arg
  103                      108                      113                      118

cgt ggg ggc ctg cgc tac atg gga aag ctt gtg gca tct gct ccc tgc      496
Arg Gly Gly Leu Arg Tyr Met Gly Lys Leu Val Ala Ser Ala Pro Cys
  119                      124                      129                      134

agg gcc gtg ccg ctg tcc cca cgt cgg ctc acc tgg cca cct cac ctg      544
Arg Ala Val Pro Leu Ser Pro Arg Arg Leu Thr Trp Pro Pro His Leu
  135                      140                      145                      150

cag gta gga atc cta ata cca acc tgg agg ccc tgg aag aat tta aga      592
Gln Val Gly Ile Leu Ile Pro Thr Trp Arg Pro Trp Lys Asn Leu Arg
  151                      156                      161                      166

aat tgg tgc agc aca agg gac tct cgg agg agg aca ttt tca tgc ccc      640
Asn Trp Cys Ser Thr Arg Asp Ser Arg Arg Thr Phe Ser Cys Pro

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tgc aga cgg gaa gct	gcg ttc tcg aac act	agg cag ccc ccg ggt ctg		688
Cys Arg Arg Glu Ala	Ala Phe Ser Asn Thr	Arg Gln Pro Pro Gly Leu		
183	188	193	198	
cac ctc cag agc cca	ccc tac cac cag aca	cag agc ccg gac cac ctg		736
His Leu Gln Ser Pro	Pro Tyr His Gln Thr	Gln Ser Pro Asp His Leu		
199	204	209	214	
gac cta ccc tcc agc	cat gac cct tcc ctg	ctc cca ccc acc tga		781
Asp Leu Pro Ser Ser	His Asp Pro Ser Leu	Leu Pro Pro Thr *		
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Met Arg Gln Lys Arg Lys Gly Asp Leu Ser Pro	Ala Glu Leu Met Met	
1 5 10 15		
ctg act ata gga gat gtt att aaa caa ctg att	gaa gcc cac gag cag	153
Leu Thr Ile Gly Asp Val Ile Lys Gln Leu Ile	Glu Ala His Glu Gln	
17 22 27 32		
ggg aaa gac atc gat cta aat aag gtg aaa acc	aag aca gct gcc aaa	201
Gly Lys Asp Ile Asp Leu Asn Lys Val Lys Thr	Lys Thr Ala Ala Lys	
33 38 43 48		
tat ggc ctt tct gcc cag ccc cgc ctg gtg gat	atc att gct gcc gtc	249
Tyr Gly Leu Ser Ala Gln Pro Arg Leu Val Asp	Ile Ile Ala Ala Val	
49 54 59 64		
cct cct cag tat cgc aag gtc ttg atg ccc aag	tta aag gcg aaa ccc	297
Pro Pro Gln Tyr Arg Lys Val Leu Met Pro Lys	Leu Lys Ala Lys Pro	
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atc aga act gct agt ggg att gct gtc gtg gct	gtg atg tgc aaa ccc	345
Ile Arg Thr Ala Ser Gly Ile Ala Val Val Ala	Val Met Cys Lys Pro	
81 86 91 96		
cac aga tgt cca cac atc agt ttt aca gga aat	ata tgt gta tac tgc	393
His Arg Cys Pro His Ile Ser Phe Thr Gly Asn	Ile Cys Val Tyr Cys	
97 102 107 112		

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Pro Gly Gly Pro Asp Ser Asp Phe Glu Tyr Ser Thr Gln Ser Tyr Thr	
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Gly Tyr Glu Pro Thr Ser Met Arg Ala Ile Arg Ala Arg Tyr Asp Pro	
129 134 139 144	
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Phe Leu Gln Thr Arg His Arg Ile Glu Gln Leu Lys Gln Leu Gly His	
145 150 155 160	
agt gtg gat aaa gtg gag ttt att gtg atg ggt gga acg ttt atg gcc	585
Ser Val Asp Lys Val Glu Phe Ile Val Met Gly Gly Thr Phe Met Ala	
161 166 171 176	
ctt cca gaa gaa tac aga gat tat ttt att cga aat tta cat gat gcc	633
Leu Pro Glu Glu Tyr Arg Asp Tyr Phe Ile Arg Asn Leu His Asp Ala	
177 182 187 192	
tta tca gga cat act tcc aac aat att tac gag gca gtc aag tat tct	681
Leu Ser Gly His Thr Ser Asn Asn Ile Tyr Glu Ala Val Lys Tyr Ser	
193 198 203 208	
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Glu Arg Ser Leu Thr Lys Cys Ile Gly Ile Thr Ile Glu Thr Arg Pro	
209 214 219 224	
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Asp Tyr Cys Met Lys Arg His Leu Ser Asp Met Leu Thr Tyr Gly Cys	
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Thr Arg Leu Glu Ile Gly Val Gln Ser Val Tyr Glu Asp Val Ala Arg	
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Asp Thr Asn Arg Gly His Thr Val Lys Ala Val Cys Glu Ser Phe His	
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Leu Ala Lys Asp Ser Gly Phe Lys Val Val Ala His Met Met Pro Asp	
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Leu Pro Asn Val Gly Leu Glu Arg Asp Ile Glu Gln Phe Thr Glu Phe	
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Phe Glu Asn Pro Ala Phe Arg Pro Asp Gly Leu Lys Leu Tyr Pro Thr	
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Asp Lys Ser Tyr Ser Pro Ser Asp Leu Val Glu Leu Val Ala Arg Ile	
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Leu Ala Leu Val Pro Pro Trp Thr Arg Val Tyr Arg Val Gln Arg Asp	
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Ile Pro Met Pro Leu Val Ser Ser Gly Val Glu His Gly Asn Leu Arg	
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Pro Tyr Gln Val Glu Leu Val Arg Arg Asp Tyr Val Ala Asn Gly Gly	
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Trp Glu Thr Phe Leu Ser Tyr Glu Asp Pro Asp Gln Asp Ile Leu Ile	
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Val Val Pro Val Ser Ser Arg Asp Pro Thr Lys Phe Gln His Gln Gly	
481 486 491 496	
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Phe Gly Met Leu Leu Met Glu Glu Ala Glu Arg Ile Ala Arg Glu Glu	
497 502 507 512	
cat ggg tct ggg aaa atc gct gtg ata tca gga gtg gat gtc ctg ggg	1641
His Gly Ser Gly Lys Ile Ala Val Ile Ser Gly Val Asp Val Leu Gly	
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Gln Arg Gln Arg Gly Gly His His Arg Ser Cys Ser Leu *	
529 534 539	
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 Met Arg Gln Lys Arg Lys Gly Asp Leu Ser Pro Ala Glu Leu Met Met
 1 5 10 15
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 Leu Thr Ile Gly Asp Val Ile Lys Gln Leu Ile Glu Ala His Glu Gln
 17 22 27 32
 ggg aaa gac atc gat cta aat aag gtg aaa acc aag aca gct gcc aaa 201
 Gly Lys Asp Ile Asp Leu Asn Lys Val Lys Thr Lys Thr Ala Ala Lys
 33 38 43 48
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 Tyr Gly Leu Ser Ala Gln Pro Arg Leu Val Asp Ile Ile Ala Ala Val
 49 54 59 64
 cct cct cag tat cgc aag gtc ttg atg ccc aag tta aag gcg aaa ccc 297
 Pro Pro Gln Tyr Arg Lys Val Leu Met Pro Lys Leu Lys Ala Lys Pro
 65 70 75 80
 atc aga act gct agt ggg att gct gtc gtg gct gtg atg tgc aaa ccc 345
 Ile Arg Thr Ala Ser Gly Ile Ala Val Val Ala Val Met Cys Lys Pro
 81 86 91 96
 cac aga tgt cca cac atc agt ttt aca gga aat ata tgt gta tac tgc 393
 His Arg Cys Pro His Ile Ser Phe Thr Gly Asn Ile Cys Val Tyr Cys
 97 102 107 112
 cct ggt gga cct gat tct gat ttt gag tat tcc acc cag tct tac act 441
 Pro Gly Gly Pro Asp Ser Asp Phe Glu Tyr Ser Thr Gln Ser Tyr Thr
 113 118 123 128
 ggc tat gag cca acc tcc atg aga gct atc cgt gcc aga tat gac cct 489

Gly Tyr Glu Pro Thr Ser Met Arg Ala Ile Arg Ala Arg Tyr Asp Pro	
129 134 139 144	
ttc cta cag aca aga cac cga ata gaa cag tta aaa caa ctt ggt cat	537
Phe Leu Gln Thr Arg His Arg Ile Glu Gln Leu Lys Gln Leu Gly His	
145 150 155 160	
agt gtg gat aaa gtg gag ttt att gtg atg ggt gga acg ttt atg gcc	585
Ser Val Asp Lys Val Glu Phe Ile Val Met Gly Gly Thr Phe Met Ala	
161 166 171 176	
ctt cca gaa gaa tac aga gat tat ttt att cga aat tta cat gat gcc	633
Leu Pro Glu Glu Tyr Arg Asp Tyr Phe Ile Arg Asn Leu His Asp Ala	
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193 198 203 208	
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Glu Arg Ser Leu Thr Lys Cys Ile Gly Ile Thr Ile Glu Thr Arg Pro	
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Asp Thr Asn Arg Gly His Thr Val Lys Ala Val Cys Glu Ser Phe His	
257 262 267 272	
ctg gcc aaa gat tcc ggt ttt aaa gtg gtg gcc cat atg atg cct gac	921
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Leu Pro Asn Val Gly Leu Glu Arg Asp Ile Glu Gln Phe Thr Glu Phe	
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Asp Lys Ser Tyr Ser Pro Ser Asp Leu Val Glu Leu Val Ala Arg Ile	
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Leu Ala Leu Val Pro Pro Trp Thr Arg Val Tyr Arg Val Gln Arg Asp	

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Glu Leu Ala Leu Ala Arg Met Lys Asp Leu	Gly Ile Gln Cys Arg Asp			
385	390 395 400			
gtg aga acc aga gaa gtt gga atc caa gaa att	cat cac aaa gta cgg	1305		
Val Arg Thr Arg Glu Val Gly Ile Gln Glu	Ile His His Lys Val Arg			
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Pro Tyr Gln Val Glu Leu Val Arg Arg Asp	Tyr Val Ala Asn Gly Gly			
417	422 427 432			
tgg gaa aca ttc ttg tca tac gaa gac cca	gat caa gac att ttg att	1401		
Trp Glu Thr Phe Leu Ser Tyr Glu Asp Pro	Asp Gln Asp Ile Leu Ile			
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Gly Leu Leu Arg Leu Arg Lys Cys Ser Glu	Glu Thr Phe Arg Phe Glu			
449	454 459 464			
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465	470 475 480			
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Tyr Tyr Arg Lys Ile Gly Tyr Arg Leu Gln	Gly Pro Tyr Met Val Lys			
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Met Ala Glu Leu Gln Gln Leu Arg Val Gln Glu Ala Val
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Glu Ser Met Val Lys Ser Leu Glu Arg Glu Asn Ile Arg Lys Met Gln
14 19 24 29

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Gly Leu Met Phe Arg Cys Ser Ala Ser Cys Cys Glu Asp Ser Gln Ala
30 35 40 45

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Ser Met Lys Gln Val His Gln Cys Ile Glu Arg Cys His Val Pro Leu
46 51 56 61

gct caa gcc cag gct ttg gtc acc agt gag ctg gag aag ttc cag gac 301
Ala Gln Ala Gln Ala Leu Val Thr Ser Glu Leu Glu Lys Phe Gln Asp
62 67 72 77

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Arg Leu Ala Arg Cys Thr Met His Cys Asn Asp Lys Ala Lys Asp Ser
78 83 88 93

ata gat gct ggg agt aag gag ctt cag gtg aag cag cag ctg gac agt 397
Ile Asp Ala Gly Ser Lys Glu Leu Gln Val Lys Gln Gln Leu Asp Ser
94 99 104 109

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Cys Val Thr Lys Cys Val Asp Asp His Met His Leu Ile Pro Thr Met
110 115 120 125

acc aag aag atg aag gag gct ctc tta tca att gga aaa taa aagtatt 494
Thr Lys Lys Met Lys Glu Ala Leu Leu Ser Ile Gly Lys *
126 131 136

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Met Asn Arg Glu Asp Arg Asn Val Leu Arg Met Lys Glu Arg Glu Arg	
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Arg Asn Gln Glu Ile Gln Gln Gly Glu Asp Ala Phe Pro Pro Ser Ser	
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Phe Ile Gly Asp Arg Ser Ile Pro Lys Leu Val Ala Ile Pro Lys Pro	
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Gln Arg His Gly Gly Ser His Gln Ser Ser Lys Trp Thr Pro Val Gly	
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Pro Ala Pro Ser Thr Ser Gln Ser Gln Lys Arg Ser Ser Gly Leu Gln	
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Ser Gly His Ser Ser Gln Arg Thr Ser Ala Gly Ser Ser Ser Gly Thr	
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Ser His Ser Arg Ser His Gly Asn Asp His His Ser Lys Glu His Gln	
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Val Arg Pro Met Asp Gly Gln Glu Ser Met Glu Pro Lys Leu Ser Ser	
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Pro Ser Ser Lys Ala His Leu Thr Lys Leu Lys Ile Pro Ser Gln Pro	
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Lys Thr Ser Asn Gly His Gln Ser Lys Ser Met Leu Lys Asp Asp Leu	
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Lys Leu Ser Ser Ser Glu Asp Ser Asp Gly Glu Gln Asp Cys Asp Lys	
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Ser Asp Ser Glu Ala Asn Glu Pro Ser Gln Ser Ala Ser Pro Glu Pro				
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Glu Pro Pro Pro Thr Asn Lys Trp Gln Leu Asp Asn Trp Leu Asn Lys				
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Val Asn Pro His Lys Val Ser Pro Ala Ser Ser Val Asp Ser Asn Ile				
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Glu Ser Leu Pro Pro Ser Ser Gln Thr Pro Lys Tyr Pro Glu Ser Asn	
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Met Lys Leu Leu Gly Arg Gln Gln Pro Asp Thr Glu Leu
1 5 10

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Glu Ile Gln Gln Lys Cys Gly Phe Ser Glu Leu Tyr Ser Trp Gln Arg
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Asp Ile Ala Asn Arg Phe His Met Met Asn Gly Ser Lys Ile His Phe				
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Thr Phe Asp Gly Lys Tyr Glu Ala Lys Gln Leu Arg Thr Phe Tyr Gln				
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Ser Pro Ser Ser Arg Thr Ala Leu Ala Glu Ala Glu Leu Glu Tyr Asn				
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cct gag cat gtc agt cgt tca ata tat gta aaa ttt cct ctc tta aag				805
Pro Glu His Val Ser Arg Ser Ile Tyr Val Lys Phe Pro Leu Leu Lys				
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Pro Ser Pro Lys Leu Ala Ser Leu Ile Asp Gly Ser Ser Pro Val Ser				
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Ile Leu Val Trp Thr Thr Gln Pro Trp Thr Ile Pro Ala Asn Glu Ala				
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254	259	264	269	

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Asp Leu Glu Asn Gly Thr Cys Ser His Pro Leu Ile Pro Asp Lys Ala	
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Ala Pro Tyr Lys Thr Val Ile Val His Gly Phe Thr Leu Gly Glu Lys	
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Gly Glu Lys Met Ser Lys Ser Leu Gly Asn Val Ile His Pro Asp Val	
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Met Arg Pro Arg Arg Pro Leu Val Phe Met Ser Leu Val Cys
1 5 10

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Asn Ile Val Leu Ile Met Val Asp Asp Leu Gly Ile Gly Asp Leu Gly
31 36 41 46

tgc tac ggc aat gac acc atg agg acg cct cac atc gac cgc ctt gcc 251
Cys Tyr Gly Asn Asp Thr Met Arg Thr Pro His Ile Asp Arg Leu Ala
47 52 57 62

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Arg Glu Gly Val Arg Leu Thr Gln His Ile Ser Ala Ala Ser Leu Cys
63 68 73 78

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Ser Pro Ser Arg Ser Ala Phe Leu Thr Gly Arg Tyr Pro Ile Arg Ser
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Gly Met Val Ser Ser Gly Asn Arg Arg Val Ile Gln Asn Leu Ala Val
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Lys Gln Gly Tyr Ser Thr Gly Leu Ile Gly Lys Trp His Gln Gly Leu
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Asn Cys Asp Ser Arg Ser Asp Gln Cys His His Pro Tyr Asn Tyr Gly
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Pro Asp Pro Ser Arg Asn Thr Glu Leu Ala Phe Glu Ser Gln Leu Trp
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Ala Ile Ser Phe Leu Glu Arg His Ser Lys Glu Thr Phe Leu Leu Phe	
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Phe Ser Phe Leu His Val His Thr Pro Leu Pro Thr Thr Asp Asp Phe	
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act ggc acc agc aag cat ggc ttg tat ggg gat aat gtg gaa gag atg	1019
Thr Gly Thr Ser Lys His Gly Leu Tyr Gly Asp Asn Val Glu Glu Met	
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Gly Gly Ser Leu Pro Gln Asp Arg Val Ile Asp Gly Arg Asp Leu Met	
415 420 425 430	
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His	Tyr	Cys	Gly	Ser	Tyr	Leu	His	Ala	Val	Arg	Trp	Ile	Pro	Lys	Asp		
447					452					457					462		
gac	agt	ggg	tca	gtt	tgg	aag	gct	cac	tat	gtg	acc	ccg	gta	ttc	cag	1499	
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Pro	Pro	Ala	Ser	Gly	Gly	Cys	Tyr	Val	Thr	Ser	Leu	Cys	Arg	Cys	Phe		
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gga	gaa	cag	gtt	acc	tac	cac	aac	ccc	cct	ctg	ctc	ttc	gat	ctc	tcc	1595	
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Arg	Asp	Pro	Ser	Glu	Ser	Thr	Pro	Leu	Thr	Pro	Ala	Thr	Glu	Pro	Leu		
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tat	gat	ttt	gtg	att	aaa	aag	gtg	gcc	aac	gcc	ctg	aag	gaa	cac	cag	1691	
Tyr	Asp	Phe	Val	Ile	Lys	Lys	Val	Ala	Asn	Ala	Leu	Lys	Glu	His	Gln		
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gaa	acc	atc	gtg	cct	gtg	acc	tac	caa	ctc	tca	gaa	ctg	aat	cag	ggc	1739	
Glu	Thr	Ile	Val	Pro	Val	Thr	Tyr	Gln	Leu	Ser	Glu	Leu	Asn	Gln	Gly		
543					548					553					558		
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Arg	Thr	Trp	Leu	Lys	Pro	Cys	Cys	Gly	Val	Phe	Pro	Phe	Cys	Leu	Cys		
559					564					569					574		
gac	aag	gaa	gag	gaa	gtc	tct	cag	cct	cgg	ggg	cct	aac	gag	aag	aga	1835	
Asp	Lys	Glu	Glu	Glu	Val	Ser	Gln	Pro	Arg	Gly	Pro	Asn	Glu	Lys	Arg		
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Asp Asp Gln Leu Leu Gln Lys Leu Arg Ala Ser Arg Arg Arg Phe Gln	
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Arg Arg Met Gln Arg Leu Ile Glu Lys Tyr Asn Gln Pro Phe Glu Asp	
31 36 41 46	
acc ccg gtg gtg caa atg gcc acg ctg acc tac gag acg cca cag gga	194
Thr Pro Val Val Gln Met Ala Thr Leu Thr Tyr Glu Thr Pro Gln Gly	
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Leu Arg Ile Trp Gly Gly Arg Leu Ile Lys Glu Arg Asn Glu Gly Glu	
63 68 73 78	
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Ile Gln Asp Ser Ser Met Lys Pro Ala Asp Arg Thr Asp Gly Ser Val	
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caa gct gca gcc tgg ggt cct gag ctt ccc tcg cac cgc aca gtc ctg	338
Gln Ala Ala Ala Trp Gly Pro Glu Leu Pro Ser His Arg Thr Val Leu	
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gga gcc gat tca aaa agc ggt gag gtc gat gcc acg tca gac cag gaa	386
Gly Ala Asp Ser Lys Ser Gly Glu Val Asp Ala Thr Ser Asp Gln Glu	
111 116 121 126	
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Glu Ser Val Ala Trp Ala Leu Ala Pro Ala Val Pro Gln Ser Pro Leu	
127 132 137 142	
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Lys Asn Glu Leu Arg Arg Lys Tyr Leu Thr Gln Val Asp Ile Leu Leu	
143 148 153 158	
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Gln Gly Ala Glu Tyr Phe Glu Cys Ala Gly Asn Arg Ala Gly Arg Asp	
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Val Arg Val Thr Pro Leu Pro Ser Leu Ala Ser Pro Ala Val Pro Ala	
175 180 185 190	
ccc gga tac tgc agt cgt atc tcc aga aag agt cct ggt gac cca gcg	626
Pro Gly Tyr Cys Ser Arg Ile Ser Arg Lys Ser Pro Gly Asp Pro Ala	
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Thr Asp Met Ala Leu Val Pro Arg Asn Asp Ser Leu Ser Leu Gln Glu				
223	228	233	238	
acc agt agc agc agc ttc tta agc agc cag ccc ttt gaa gat gat gac				770
Thr Ser Ser Ser Ser Phe Leu Ser Ser Gln Pro Phe Glu Asp Asp Asp				
239	244	249	254	
att tgc aat gtg acc atc agt gac ctg tac gca ggg atg ctg cac tcc				818
Ile Cys Asn Val Thr Ile Ser Asp Leu Tyr Ala Gly Met Leu His Ser				
255	260	265	270	
atg agc cgg ctg ttg agc aca aag cca tca agc atc atc tcc acc aaa				866
Met Ser Arg Leu Leu Ser Thr Lys Pro Ser Ser Ile Ile Ser Thr Lys				
271	276	281	286	
acg ttc atc atg caa aac tgg aac tgc agg agg agg cac aga tat aag				914
Thr Phe Ile Met Gln Asn Trp Asn Cys Arg Arg Arg His Arg Tyr Lys				
287	292	297	302	
agc agg atg aac aaa aca tat tgc aaa gga gcc aga cgt tct cag agg				962
Ser Arg Met Asn Lys Thr Tyr Cys Lys Gly Ala Arg Arg Ser Gln Arg				
303	308	313	318	
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Ser Ser Lys Glu Asn Phe Ile Pro Cys Ser Glu Pro Val Lys Gly Thr				
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Gly Ala Leu Arg Asp Cys Lys Asn Val Leu Asp Val Ser Cys Arg Lys				
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Thr Gly Leu Lys Leu Glu Lys Ala Phe Leu Glu Val Asn Arg Pro Gln				
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Ile His Lys Leu Asp Pro Ser Trp Lys Glu Arg Lys Val Thr Pro Ser				
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Lys Tyr Ser Ser Leu Ile Tyr Phe Asp Ser Ser Ala Thr Tyr Asn Leu				
383	388	393	398	
gat gag gaa aat aga ttt agg aca tta aaa tgg tta att tct cct gta				1250
Asp Glu Glu Asn Arg Phe Arg Thr Leu Lys Trp Leu Ile Ser Pro Val				
399	404	409	414	
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Lys Ile Val Ser Arg Pro Thr Ile Arg Gln Gly His Gly Glu Asn Arg				
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Gln Arg Glu Ile Glu Ile Arg Phe Asp Gln Leu His Arg Glu Tyr Cys				
431	436	441	446	

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Glu Pro Gln Gly Ser Gly Arg Gln Gly Asn Ser Leu Gly Ala Ser Asp	
687 692 697 702	
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Gly Val Asp Asn Thr Val Arg Pro Gly Asp Gln Gly Ser Ser Ser Gln	
703 708 713 718	
 ccc aac tca gaa gag aga gga gag aac acg tct tac agg atg gaa gag	2210
Pro Asn Ser Glu Glu Arg Gly Glu Asn Thr Ser Tyr Arg Met Glu Glu	
719 724 729 734	
 aaa agt gat ttc atg cta gaa aaa ttg gaa act aaa agt gtg tag cta	2258
Lys Ser Asp Phe Met Leu Glu Lys Leu Glu Thr Lys Ser Val *	
735 740 745	
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tttgattctt gagactgtga ggacttggtt gacttctctg cccttaaagt aaatattagt	2378
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Met Leu Gln Tyr Arg Arg Asp Thr Ala Gly Trp Lys Ile Cys Arg Glu	
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Gly Asn Gly Val Ser Val Ser Trp Arg Pro Ser Val Glu Phe Pro Gly	
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Asn Leu Tyr Arg Gly Glu Gly Ile Val Tyr Gly Thr Leu Glu Glu Val	
49 54 59 64	

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Glu Asn Val Thr Gly Phe Glu Ile Ile Gln Ser Ile Thr Asp Thr Leu	
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tgt gta agc aga acc tcc act ccc tcc gct gcc atg aag ctc att tct	394
Cys Val Ser Arg Thr Ser Thr Pro Ser Ala Ala Met Lys Leu Ile Ser	
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Pro Arg Asp Phe Val Asp Leu Val Leu Val Lys Arg Tyr Glu Asp Gly	
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Thr Ile Ser Ser Asn Ala Thr His Val Glu His Pro Leu Cys Pro Pro	
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Lys Pro Gly Phe Val Arg Gly Phe Asn His Pro Cys Gly Cys Phe Cys	
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Glu Pro Leu Pro Gly Glu Pro Thr Lys Thr Asn Leu Val Thr Phe Phe	
161 166 171 176	
cat acc gac ctc agc ggt tac ctc cca cag aac gtg gtg gac tcc ttc	634
His Thr Asp Leu Ser Gly Tyr Leu Pro Gln Asn Val Val Asp Ser Phe	
177 182 187 192	
ttc ccc cgc agc atg acc cgg ttt tat gcc aac ctt cag aaa gca gtg	682
Phe Pro Arg Ser Met Thr Arg Phe Tyr Ala Asn Leu Gln Lys Ala Val	
193 198 203 208	
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Lys Gln Phe His Glu *	
209 214	
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atc ctg tct gcg ctc agc ttc ctg cac gcc tgc acc ccc cca atc atc      339
Ile Leu Ser Ala Leu Ser Phe Leu His Ala Cys Thr Pro Pro Ile Ile
  13          18          23          28

cac ggg aac ctg acc agc gac acc atc ttc att cag cac aac ggc ctc      387
His Gly Asn Leu Thr Ser Asp Thr Ile Phe Ile Gln His Asn Gly Leu
  29          34          39          44

atc aag atc ggc tcc gtg tgg cac cga atc ttc tcc aat gca ctt cca      435
Ile Lys Ile Gly Ser Val Trp His Arg Ile Phe Ser Asn Ala Leu Pro
  45          50          55          60

gat gat ctc cga agc ccc atc cgc gct gag cga gag gaa ctt cgg aac      483
Asp Asp Leu Arg Ser Pro Ile Arg Ala Glu Arg Glu Glu Leu Arg Asn
  61          66          71          76

ctg cac ttc ttc ccc cca gag tat gga gag gtg gcc gat ggg acc gct      531
Leu His Phe Phe Pro Pro Glu Tyr Gly Glu Val Ala Asp Gly Thr Ala
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gtg gac atc ttc tcc ttt ggg atg tgt gcg ctg gag atg gct gta ctg      579
Val Asp Ile Phe Ser Phe Gly Met Cys Ala Leu Glu Met Ala Val Leu
  93          98          103          108

gaa atc cag acc aat ggg gac acc cgg gtc aca gag gag gcc att gct      627
Glu Ile Gln Thr Asn Gly Asp Thr Arg Val Thr Glu Glu Ala Ile Ala
  109          114          119          124
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Cys Cys Leu Ala Arg Asp Pro Ala Arg Arg Pro Ser Ala His Ser Leu	
141 146 151 156	
ctc ttc cac cgc gtg ctc ttc gag gtg cac tcg ctg aag ctc ctg gca	771
Leu Phe His Arg Val Leu Phe Glu Val His Ser Leu Lys Leu Leu Ala	
157 162 167 172	
gcc cac tgC ttc atc cag cac cag tac ctc atg cct gag aat gtg gtg	819
Ala His Cys Phe Ile Gln His Gln Tyr Leu Met Pro Glu Asn Val Val	
173 178 183 188	
gag gag aag acc aag gcc atg gac ctg cac gcg gtc ttg gcg gag ctt	867
Glu Glu Lys Thr Lys Ala Met Asp Leu His Ala Val Leu Ala Glu Leu	
189 194 199 204	
ccc cgg ccc cgc agg ccc ccg ctg cag tgg cgg tac tcg gaa gtc tcc	915
Pro Arg Pro Arg Arg Pro Pro Leu Gln Trp Arg Tyr Ser Glu Val Ser	
205 210 215 220	
ttc atg gag ctg gac aaa ttc ctg gag gat gtc agg aat gga atc tac	963
Phe Met Glu Leu Asp Lys Phe Leu Glu Asp Val Arg Asn Gly Ile Tyr	
221 226 231 236	
cca ctg atg aac ttt gca gcc act cga ccc ctg ggg ctg ccc cgt gtg	1011
Pro Leu Met Asn Phe Ala Ala Thr Arg Pro Leu Gly Leu Pro Arg Val	
237 242 247 252	
ctg gcc cca ccc ccg gag gag gtc caa aag gcc aag acc ccg acg cca	1059
Leu Ala Pro Pro Pro Glu Glu Val Gln Lys Ala Lys Thr Pro Thr Pro	
253 258 263 268	
gag ccc ttt gac tct gag acc aga aag gtc atc cag atg cag tgc aac	1107
Glu Pro Phe Asp Ser Glu Thr Arg Lys Val Ile Gln Met Gln Cys Asn	
269 274 279 284	
ctg gag aga agc gag gac aag gcg cgc tgg cat ctc act ctg ctt ctg	1155
Leu Glu Arg Ser Glu Asp Lys Ala Arg Trp His Leu Thr Leu Leu Leu	
285 290 295 300	
gtg ctg gaa gac cgg ctg cac cgg cag ctg acc tac gac ctg ctc cca	1203
Val Leu Glu Asp Arg Leu His Arg Gln Leu Thr Tyr Asp Leu Leu Pro	
301 306 311 316	
acg gac agc gcc cag gac ctc gcc tcg gag ctc gtg cac tat ggc ttc	1251
Thr Asp Ser Ala Gln Asp Leu Ala Ser Glu Leu Val His Tyr Gly Phe	
317 322 327 332	
ctc cac gag cac gac cgg atg aag ctg gcc gcc ttc ctg gag agc acc	1299
Leu His Glu His Asp Arg Met Lys Leu Ala Ala Phe Leu Glu Ser Thr	
333 338 343 348	

ttc ctc aag tac cgt ggg acc cag gcc tga c ccggagcccc agccccaggg 1350
Phe Leu Lys Tyr Arg Gly Thr Gln Ala *
349 354

gaccatgccg ggggtgctgcc cgggcaggcc atgttgggga gactccagca ccgtggggct 1410

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c atg ttc cag ttt cat gca ggc tct tgg gaa agc tgg tgc tgc tgc 406
Met Phe Gln Phe His Ala Gly Ser Trp Glu Ser Trp Cys Cys Cys
1 5 10

tgc ctg att ccc gcc gac aga cct tgg gac cgg ggc caa cac tgg cag 454
Cys Leu Ile Pro Ala Asp Arg Pro Trp Asp Arg Gly Gln His Trp Gln
16 21 26 31

ctg gag atg gcg gac acg aga tcc gtg cac gag act agg ttt gag gcg 502
Leu Glu Met Ala Asp Thr Arg Ser Val His Glu Thr Arg Phe Glu Ala
32 37 42 47

gcc gtg aag gtg atc cag agt ttg ccg aag aat ggt tca ttc cag cca 550
Ala Val Lys Val Ile Gln Ser Leu Pro Lys Asn Gly Ser Phe Gln Pro
48 53 58 63

aca aat gaa atg atg ctt aaa ttt tat agc ttc tat aag cag gca act 598

Thr	Asn	Glu	Met	Met	Leu	Lys	Phe	Tyr	Ser	Phe	Tyr	Lys	Gln	Ala	Thr	
64					69					74					79	
gaa	gga	ccc	tgt	aaa	ctt	tca	agg	cct	gga	ttt	tgg	gat	cct	att	gga	646
Glu	Gly	Pro	Cys	Lys	Leu	Ser	Arg	Pro	Gly	Phe	Trp	Asp	Pro	Ile	Gly	
80					85					90					95	
aga	tat	aaa	tgg	gat	gct	tgg	agt	tca	ctg	ggg	gat	atg	acc	aaa	gag	694
Arg	Tyr	Lys	Trp	Asp	Ala	Trp	Ser	Ser	Leu	Gly	Asp	Met	Thr	Lys	Glu	
96					101					106					111	
gaa	gcc	atg	att	gca	tat	gtt	gaa	gaa	atg	aaa	aag	att	att	gaa	act	742
Glu	Ala	Met	Ile	Ala	Tyr	Val	Glu	Glu	Met	Lys	Lys	Ile	Ile	Glu	Thr	
112					117					122					127	
atg	cca	atg	act	gag	aaa	gtt	gaa	gaa	ttg	ctg	cgt	gtc	ata	ggg	cca	790
Met	Pro	Met	Thr	Glu	Lys	Val	Glu	Glu	Leu	Leu	Arg	Val	Ile	Gly	Pro	
128					133					138					143	
ttt	tat	gaa	att	gtc	gag	gac	aaa	aag	agt	ggc	agg	agt	tct	gat	ata	838
Phe	Tyr	Glu	Ile	Val	Glu	Asp	Lys	Lys	Ser	Gly	Arg	Ser	Ser	Asp	Ile	
144					149					154					159	
ccc	tca	gtc	cga	ctg	gag	aaa	atc	tct	aaa	tgt	tta	gaa	gat	ctt	ggg	886
Pro	Ser	Val	Arg	Leu	Glu	Lys	Ile	Ser	Lys	Cys	Leu	Glu	Asp	Leu	Gly	
160					165					170					175	
aat	gtt	ctc	act	tct	act	ccg	aac	gcc	aaa	acc	gtt	aat	ggg	aaa	gct	934
Asn	Val	Leu	Thr	Ser	Thr	Pro	Asn	Ala	Lys	Thr	Val	Asn	Gly	Lys	Ala	
176					181					186					191	
gaa	agc	agt	gac	agt	gga	gcc	gag	tct	gag	gaa	gaa	gag	gcc	caa	gaa	982
Glu	Ser	Ser	Asp	Ser	Gly	Ala	Glu	Ser	Glu	Glu	Glu	Glu	Ala	Gln	Glu	
192					197					202					207	
gaa	gtg	aaa	gga	gca	gac	caa	agt	gat	aat	gat	aag	aaa	atg	atg	aag	1030
Glu	Val	Lys	Gly	Ala	Asp	Gln	Ser	Asp	Asn	Asp	Lys	Lys	Met	Met	Lys	
208					213					218					223	
aag	tca	gca	gac	cat	aag	aat	ttg	gaa	gtc	att	gtc	act	aat	ggc	tat	1078
Lys	Ser	Ala	Asp	His	Lys	Asn	Leu	Glu	Val	Ile	Val	Thr	Asn	Gly	Tyr	
224					229					234					239	
gat	aaa	gat	ggc	ttt	gtt	cag	gat	ata	cag	aat	gac	att	cat	gcc	agt	1126
Asp	Lys	Asp	Gly	Phe	Val	Gln	Asp	Ile	Gln	Asn	Asp	Ile	His	Ala	Ser	
240					245					250					255	
tct	tcc	ctg	aat	ggc	aga	agc	act	gaa	gaa	gta	aag	ccc	att	gat	gaa	1174
Ser	Ser	Leu	Asn	Gly	Arg	Ser	Thr	Glu	Glu	Val	Lys	Pro	Ile	Asp	Glu	
256					261					266					271	
aac	ttg	ggg	caa	act	gga	aaa	tct	gct	gtt	tgc	att	cac	caa	gat	ata	1222
Asn	Leu	Gly	Gln	Thr	Gly	Lys	Ser	Ala	Val	Cys	Ile	His	Gln	Asp	Ile	
272					277					282					287	
aat	gat	gat	cat	gtt	gaa	gat	gtt	aca	gga	att	cag	cat	ttg	aca	agc	1270
Asn	Asp	Asp	His	Val	Glu	Asp	Val	Thr	Gly	Ile	Gln	His	Leu	Thr	Ser	

288	293	298	303	
gat tca gac agt gaa gtt tac tgt gat tct atg gaa caa ttt gga caa				1318
Asp Ser Asp Ser Glu Val Tyr Cys Asp Ser Met Glu Gln Phe Gly Gln				
304	309	314	319	
gaa gag tct tta gac agc ttt acg tcc aac aat gga cca ttt cag tat				1366
Glu Glu Ser Leu Asp Ser Phe Thr Ser Asn Asn Gly Pro Phe Gln Tyr				
320	325	330	335	
tac ttg ggt ggt cat tcc agt caa ccc atg gaa aat tct gga ttt cgt				1414
Tyr Leu Gly Gly His Ser Ser Gln Pro Met Glu Asn Ser Gly Phe Arg				
336	341	346	351	
gaa gat att caa gta cct cct gga aat ggc aac att ggg aat atg cag				1462
Glu Asp Ile Gln Val Pro Pro Gly Asn Gly Asn Ile Gly Asn Met Gln				
352	357	362	367	
gtg gtt gca gtt gaa gga aaa ggt gaa gtc aag cat gga gga gaa gat				1510
Val Val Ala Val Glu Gly Lys Gly Glu Val Lys His Gly Gly Glu Asp				
368	373	378	383	
ggc agg aat aac agc gga gca cca cac cgg gag aag cga ggc gga gaa				1558
Gly Arg Asn Asn Ser Gly Ala Pro His Arg Glu Lys Arg Gly Gly Glu				
384	389	394	399	
act gac gaa ttc tct aat gtt aga aga gga aga gga cat agg atg caa				1606
Thr Asp Glu Phe Ser Asn Val Arg Arg Gly Arg Gly His Arg Met Gln				
400	405	410	415	
cac ttg agc gaa gga acc aag ggc cgg cag gtg gga agt gga ggt gat				1654
His Leu Ser Glu Gly Thr Lys Gly Arg Gln Val Gly Ser Gly Gly Asp				
416	421	426	431	
ggg gag cgc tgg ggc tcc gac aga ggg tcc cga ggc agc ctc aat gag				1702
Gly Glu Arg Trp Gly Ser Asp Arg Gly Ser Arg Gly Ser Leu Asn Glu				
432	437	442	447	
cag atc gcc ctc gtg ctg atg aga ctg cag gag gac atg cag aat gtc				1750
Gln Ile Ala Leu Val Leu Met Arg Leu Gln Glu Asp Met Gln Asn Val				
448	453	458	463	
ctt cag aga ctg cag aaa ctg gaa acg ctg act gct ttg cag gca aaa				1798
Leu Gln Arg Leu Gln Lys Leu Glu Thr Leu Thr Ala Leu Gln Ala Lys				
464	469	474	479	
tca tca aca tca aca ttg cag act gct cct cag ccc acc tca cag aga				1846
Ser Ser Thr Ser Thr Leu Gln Thr Ala Pro Gln Pro Thr Ser Gln Arg				
480	485	490	495	
cca tct tgg tgg ccc ttc gag atg tct cct ggt gtg cta acg ttt gcc				1894
Pro Ser Trp Trp Pro Phe Glu Met Ser Pro Gly Val Leu Thr Phe Ala				
496	501	506	511	
atc ata tgg cct ttt att gca cag tgg ttg gtg tat tta tac tat caa				1942
Ile Ile Trp Pro Phe Ile Ala Gln Trp Leu Val Tyr Leu Tyr Tyr Gln				
512	517	522	527	

aga agg aga aga aaa ctg aac tga ggaaaatggt gttttcctca agaagactac 1996
 Arg Arg Arg Arg Lys Leu Asn *
 528 533

tggaactgga tgacctcaga atgaactgga ttgtggtggt cacaagaaaa tcttagtttg 2056

tgatgattac attgcttttt gttgtccagt agtttagttt gtgtacatat atacacatat 2116

atattttgca ctacacaaac gataacattt taaggactaa tattgctgat acttgaataa 2176

tcaatctcta ctagggtata agtagtatac acagatttac cctgcccttg aacttgaagg 2236

acattaaatt attaatgatc atttggtaac atgtttacct gattatcttc catagagtaa 2296

cataagctgc ttttcaaagg taccgttggtg ataatgagat caagtttata agttattcgt 2356

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cgccccaggc gccgcccgcg cgcccccgcg gctctgaggt tgctcgcgcg cccccgccga 180

tcgcc atg gat cgg atg aag aag atc aaa cgg cag ctg tca atg aca 227
 Met Asp Arg Met Lys Lys Ile Lys Arg Gln Leu Ser Met Thr
 1 5 10

ctc cga ggt ggc cga ggc ata gac aag acc aat ggt gcc cct gag cag 275
 Leu Arg Gly Gly Arg Gly Ile Asp Lys Thr Asn Gly Ala Pro Glu Gln
 15 20 25 30

ata ggc ctg gat gag agt ggt ggt ggt ggc ggc agt gac cct gga gag 323
 Ile Gly Leu Asp Glu Ser Gly Gly Gly Gly Gly Ser Asp Pro Gly Glu
 31 36 41 46

gcc ccc aca cgt gct gct cct ggg gaa ctt cgt tct gca cgg ggc cca 371
 Ala Pro Thr Arg Ala Ala Pro Gly Glu Leu Arg Ser Ala Arg Gly Pro
 47 52 57 62

ctc agc tct gca cca gag att gtg cac gag gac ttg aag atg ggg tct	419
Leu Ser Ser Ala Pro Glu Ile Val His Glu Asp Leu Lys Met Gly Ser	
63 68 73 78	
gat ggg gag agt gac cag gct tca gcc acg tcc tcg gat gag gtg cag	467
Asp Gly Glu Ser Asp Gln Ala Ser Ala Thr Ser Ser Asp Glu Val Gln	
79 84 89 94	
tct cca gtg aga gtg cgt atg cgc aac cat ccc cca cgc aag atc tcc	515
Ser Pro Val Arg Val Arg Met Arg Asn His Pro Pro Arg Lys Ile Ser	
95 100 105 110	
act gag gac atc aac aag cgc cta tca cta cca gct gac atc cgg ctg	563
Thr Glu Asp Ile Asn Lys Arg Leu Ser Leu Pro Ala Asp Ile Arg Leu	
111 116 121 126	
cct gag ggc tac ctg gag aag ctg acc ctc aat agc ccc atc ttt gac	611
Pro Glu Gly Tyr Leu Glu Lys Leu Thr Leu Asn Ser Pro Ile Phe Asp	
127 132 137 142	
aag ccc ctc agc cgc cgc ctc cgt cgt gtc agc cta tct gag att ggc	659
Lys Pro Leu Ser Arg Arg Leu Arg Arg Val Ser Leu Ser Glu Ile Gly	
143 148 153 158	
ttt ggg aaa ctg gag acc tac att aag ctg gac aaa ctg ggc gag ggt	707
Phe Gly Lys Leu Glu Thr Tyr Ile Lys Leu Asp Lys Leu Gly Glu Gly	
159 164 169 174	
acc tat gcc acc gtc tac aaa ggc aaa agc aag ctc aca gac aac ctt	755
Thr Tyr Ala Thr Val Tyr Lys Gly Lys Ser Lys Leu Thr Asp Asn Leu	
175 180 185 190	
gtg gca ctc aag gag atc aga ctg gaa cat gaa gag ggg gca ccc tgc	803
Val Ala Leu Lys Glu Ile Arg Leu Glu His Glu Glu Gly Ala Pro Cys	
191 196 201 206	
acc gcc atc cgg gaa gtg tcc ctg ctc aag gac ctc aaa cac gcc aac	851
Thr Ala Ile Arg Glu Val Ser Leu Leu Lys Asp Leu Lys His Ala Asn	
207 212 217 222	
atc gtt acg cta cat gac att atc cac acg gag aag tcc ctc acc ctt	899
Ile Val Thr Leu His Asp Ile Ile His Thr Glu Lys Ser Leu Thr Leu	
223 228 233 238	
gtc ttt gag tac ctg gac aag gac ctg aag cag tac ctg gat gac tgt	947
Val Phe Glu Tyr Leu Asp Lys Asp Leu Lys Gln Tyr Leu Asp Asp Cys	
239 244 249 254	
ggg aac atc atc aac atg cac aac gtg aaa ctg ttc ctg ttc cag ctg	995
Gly Asn Ile Ile Asn Met His Asn Val Lys Leu Phe Leu Phe Gln Leu	
255 260 265 270	
ctc cgt ggc ctg gcc tac tgc cac cgg cag aag gtg cta cac cga gat	1043
Leu Arg Gly Leu Ala Tyr Cys His Arg Gln Lys Val Leu His Arg Asp	
271 276 281 286	

ctc aag ccc cag aac ctg ctc atc aac gag agg gga gag ctc aag ctg Leu Lys Pro Gln Asn Leu Leu Ile Asn Glu Arg Gly Glu Leu Lys Leu 287 292 297 302	1091
gct gac ttt ggc ctg gcc cga gcc aag tca atc cca aca aag aca tac Ala Asp Phe Gly Leu Ala Arg Ala Lys Ser Ile Pro Thr Lys Thr Tyr 303 308 313 318	1139
tcc aat gag gtg gtg aca ctg tgg tac cgg ccc cct gac atc ctg ctt Ser Asn Glu Val Val Thr Leu Trp Tyr Arg Pro Pro Asp Ile Leu Leu 319 324 329 334	1187
ggg tcc acg gac tac tcc act cag att gac atg tgg ggt gtg ggc tgc Gly Ser Thr Asp Tyr Ser Thr Gln Ile Asp Met Trp Gly Val Gly Cys 335 340 345 350	1235
atc ttc tat gag atg gcc aca ggc cgt ccc ctc ttt ccg ggc tcc acg Ile Phe Tyr Glu Met Ala Thr Gly Arg Pro Leu Phe Pro Gly Ser Thr 351 356 361 366	1283
gtg gag gaa cag cta cac ttc atc ttc cgt atc tta gga acc cca act Val Glu Glu Gln Leu His Phe Ile Phe Arg Ile Leu Gly Thr Pro Thr 367 372 377 382	1331
gag gag acg tgg cca ggc atc ctg tcc aac gag gag ttc aag aca tac Glu Glu Thr Trp Pro Gly Ile Leu Ser Asn Glu Glu Phe Lys Thr Tyr 383 388 393 398	1379
aac tac ccc aag tac cga gcc gag gcc ctt ttg agc cac gca ccc cga Asn Tyr Pro Lys Tyr Arg Ala Glu Ala Leu Leu Ser His Ala Pro Arg 399 404 409 414	1427
ctt gat agc gac ggg gcc gac ctc ctc acc aag ctg ttg cag ttt gag Leu Asp Ser Asp Gly Ala Asp Leu Leu Thr Lys Leu Leu Gln Phe Glu 415 420 425 430	1475
ggg cga aat cgg atc tcc gca gag gat gcc atg aaa cat cca ttc ttc Gly Arg Asn Arg Ile Ser Ala Glu Asp Ala Met Lys His Pro Phe Phe 431 436 441 446	1523
ctc agt ctg ggg gag cgg atc cac aaa ctt cct gac act act tcc ata Leu Ser Leu Gly Glu Arg Ile His Lys Leu Pro Asp Thr Thr Ser Ile 447 452 457 462	1571
ttt gca cta aag gag att cag cta caa aag gag gcc agc ctt cgg tct Phe Ala Leu Lys Glu Ile Gln Leu Gln Lys Glu Ala Ser Leu Arg Ser 463 468 473 478	1619
tcg tcg atg cct gac tca ggc agg cca gct ttc cgc gtg gtg gac acc Ser Ser Met Pro Asp Ser Gly Arg Pro Ala Phe Arg Val Val Asp Thr 479 484 489 494	1667
gag ttc taa gccacag accgaggccc cagcaggcag cggttgagg gatgccacac Glu Phe * 495	1723
ccctcacagg gcagcccca actacatctt ccctgcttac tctctgcta cctgcctgag	1783

ccatgttcac ctgccactt gtcccctgct gcctgcccac acaccccacc attggcctgt 1843
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ttgatcgccg cgtttaagtt gcgctcgggg cggcc atg tcg gcc ggc gag gtc 173
Met Ser Ala Gly Glu Val
1
gag cgc cta gtg tcg gag ctg agc ggc ggg acc gga ggg gat gag gag 221
Glu Arg Leu Val Ser Glu Leu Ser Gly Gly Thr Gly Gly Asp Glu Glu
7 12 17 22
gaa gag tgg ctc tat ggc gat gaa aat gaa gtt gaa agg cca gaa gaa 269
Glu Glu Trp Leu Tyr Gly Asp Glu Asn Glu Val Glu Arg Pro Glu Glu
23 28 33 38
gaa aat gcc agt gct aat cct cca tct gga att gaa gat gaa act gct 317
Glu Asn Ala Ser Ala Asn Pro Pro Ser Gly Ile Glu Asp Glu Thr Ala
39 44 49 54
gaa aat ggt gta cca aaa ccg aaa gtg act gag acc gaa gat gat agt 365
Glu Asn Gly Val Pro Lys Pro Lys Val Thr Glu Thr Glu Asp Asp Ser
55 60 65 70

gat agt gac agc gat gat gat gaa gat gat gtt cat gtc act ata gga	413
Asp Ser Asp Ser Asp Asp Asp Glu Asp Asp Val His Val Thr Ile Gly	
71 76 81 86	
gac att aaa acg gga gca cca cag tat ggg agt tat ggt aca gca cct	461
Asp Ile Lys Thr Gly Ala Pro Gln Tyr Gly Ser Tyr Gly Thr Ala Pro	
87 92 97 102	
gta aat ctt aac atc aag aca ggg gga aga gtt tat gga act aca ggg	509
Val Asn Leu Asn Ile Lys Thr Gly Gly Arg Val Tyr Gly Thr Thr Gly	
103 108 113 118	
aca aaa gtc aaa gga gta gac ctt gat gca cct gga agc att aat gga	557
Thr Lys Val Lys Gly Val Asp Leu Asp Ala Pro Gly Ser Ile Asn Gly	
119 124 129 134	
gtt cca ctc tta gag gta gat ttg gat tct ttt gaa gat aaa cca tgg	605
Val Pro Leu Leu Glu Val Asp Leu Asp Ser Phe Glu Asp Lys Pro Trp	
135 140 145 150	
cgt aaa cct ggt gct gat ctt tct gat tat ttt aat tat ggg ttt aat	653
Arg Lys Pro Gly Ala Asp Leu Ser Asp Tyr Phe Asn Tyr Gly Phe Asn	
151 156 161 166	
gaa gat acc tgg aaa gct tac tgt gaa aaa caa aag agg ata cga atg	701
Glu Asp Thr Trp Lys Ala Tyr Cys Glu Lys Gln Lys Arg Ile Arg Met	
167 172 177 182	
gga ctt gaa gtt ata cca gta acc tct act aca aat aaa att acg gta	749
Gly Leu Glu Val Ile Pro Val Thr Ser Thr Thr Asn Lys Ile Thr Val	
183 188 193 198	
cag cag gga aga act gga aac tca gag aaa gaa act gcc ctt cca tct	797
Gln Gln Gly Arg Thr Gly Asn Ser Glu Lys Glu Thr Ala Leu Pro Ser	
199 204 209 214	
aca aaa gct gag ttt act tct cct cct tct ttg ttc aag act ggg ctt	845
Thr Lys Ala Glu Phe Thr Ser Pro Pro Ser Leu Phe Lys Thr Gly Leu	
215 220 225 230	
cca ccg agc aga aac agc act tct tct cag tct cag aca agt act gcc	893
Pro Pro Ser Arg Asn Ser Thr Ser Ser Gln Ser Gln Thr Ser Thr Ala	
231 236 241 246	
tcc aga aaa gcc aat tca agc gtt ggg aag tgg cag gat cga tat ggg	941
Ser Arg Lys Ala Asn Ser Ser Val Gly Lys Trp Gln Asp Arg Tyr Gly	
247 252 257 262	
agg gcc gaa tca cct gat cta agg aga tta cct ggg gca att gat gtt	989
Arg Ala Glu Ser Pro Asp Leu Arg Arg Leu Pro Gly Ala Ile Asp Val	
263 268 273 278	
atc ggt cag act ata act atc agc cga gta gaa ggc agg cga cgg gca	1037
Ile Gly Gln Thr Ile Thr Ile Ser Arg Val Glu Gly Arg Arg Arg Ala	
279 284 289 294	

aat gag aac agc aac ata cag gtc ctt tct gaa aga tct gct act gaa	1085
Asn Glu Asn Ser Asn Ile Gln Val Leu Ser Glu Arg Ser Ala Thr Glu	
295 300 305 310	
gta gac aac aat ttt agc aaa cca cct ccg ttt ttc cct cca gga gct	1133
Val Asp Asn Asn Phe Ser Lys Pro Pro Pro Phe Phe Pro Pro Gly Ala	
311 316 321 326	
cct ccc act cac ctt cca cct cct cca ttt ctt cca cct cct ccg act	1181
Pro Pro Thr His Leu Pro Pro Pro Pro Phe Leu Pro Pro Pro Pro Thr	
327 332 337 342	
gtc agc act gct cca cct ctg att cca cca ccg ggt att cca ata act	1229
Val Ser Thr Ala Pro Pro Leu Ile Pro Pro Pro Gly Ile Pro Ile Thr	
343 348 353 358	
gta cca cct cca ggt ttt cct cct cca cca ggc gct cca cct cca tct	1277
Val Pro Pro Pro Gly Phe Pro Pro Pro Pro Gly Ala Pro Pro Pro Ser	
359 364 369 374	
ctt ata cca aca ata gaa agt gga cat tcc tct ggt tat gat agt cgt	1325
Leu Ile Pro Thr Ile Glu Ser Gly His Ser Ser Gly Tyr Asp Ser Arg	
375 380 385 390	
tct gca cgt gca ttt cca tat ggc aat gtt gcc ttt ccc cat ctt cct	1373
Ser Ala Arg Ala Phe Pro Tyr Gly Asn Val Ala Phe Pro His Leu Pro	
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Glu Arg Glu Arg Glu Arg Asp His Ser Pro Thr Pro Ser Val Phe Asn	
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Ser Asp Glu Glu Arg Tyr Arg Tyr Arg Glu Tyr Ala Glu Arg Gly Tyr	
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Glu Arg His Arg Ala Ser Arg Glu Lys Glu Glu Arg His Arg Glu Arg	
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Arg His Arg Glu Lys Glu Glu Thr Arg His Lys Ser Ser Arg Ser Asn	
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Pro	Tyr	Gln	Pro	Leu	Pro	Lys	Val	Lys	His	Glu	Met	Asp	Leu	Ala	Tyr	
8					13					18					23	
acc	agt	tct	tct	gat	gag	agt	gaa	gat	gga	aga	aaa	cca	aga	cag	tca	507
Thr	Ser	Ser	Ser	Asp	Glu	Ser	Glu	Asp	Gly	Arg	Lys	Pro	Arg	Gln	Ser	
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tac	aac	tcc	agg	gag	acc	ctg	cac	gag	tat	aac	cag	gag	ctg	agg	atg	555
Tyr	Asn	Ser	Arg	Glu	Thr	Leu	His	Glu	Tyr	Asn	Gln	Glu	Leu	Arg	Met	
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Gln Glu Met Glu Phe Cys Glu Thr Ser His Thr Leu Cys Ser Gly Tyr	
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Gly Ser Asp Val Asp Thr Glu Thr Glu Gly Ala Ala Ser Pro Asp His	
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Ala Leu Arg Met Trp Ile Arg Gly Met Lys Ser Glu His Ser Ser Cys	
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Leu Ser Ser Arg Ala Asn Ser Ala Leu Ser Leu Thr Asp Thr Asp His	
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Cys Asp Met Glu Ala Gln Ala Gly Ser Thr Gln Asp Val Gln Ser Ser	
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Pro His Asn Gln Phe Thr Phe Arg Pro Leu Pro Pro Pro Pro Pro	
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Trp Val Leu Asn Ser Asn Ile Pro Leu Glu Thr Arg His Phe Leu Phe	
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Lys His Gly Ser Gly Ser Ser Ala Ile Phe Ser Ala Ala Ser Gln Asn	
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Tyr Pro Leu Thr Ser Asn Thr Val Tyr Ser Pro Pro Pro Arg Pro Leu	
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Pro Arg Ser Thr Phe Ser Arg Pro Ala Phe Thr Phe Asn Lys Pro Tyr	
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Arg Cys Cys Asn Trp Lys Cys Thr Ala Leu Ser Ala Thr Ala Ile Thr	
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Val Thr Leu Ala Leu Leu Leu Ala Tyr Val Ile Ala Val His Leu Phe	
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Ser Pro Ile Gly Gly Lys Val Ser Asp Lys Ser Glu Lys Lys Val Phe	
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Gln Lys Gly Arg Ala Ile Asp Thr Gly Glu Val Asp Ile Gly Ala Gln	
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Cys	Asn	Gly	Asn	Gly	Glu	Cys	Ile	Ser	Gly	His	Cys	His	Cys	Phe	Pro	
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cca	gga	tac	aaa	gga	gaa	ata	tgc	gag	gaa	gag	gac	tgc	cta	gac	cca	2283
Pro	Gly	Tyr	Lys	Gly	Glu	Ile	Cys	Glu	Glu	Glu	Asp	Cys	Leu	Asp	Pro	
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Thr	Met	Glu	Cys	Gly	Ser	His	Gly	Val	Cys	Ser	Arg	Gly	Ile	Cys	Gln	
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Cys	Glu	Glu	Gly	Trp	Val	Gly	Pro	Thr	Cys	Glu	Glu	Arg	Ser	Cys	His	
712					717					722					727	
tct	cat	tgt	act	gag	cat	ggc	caa	tgc	aaa	gat	gga	aaa	tgt	gag	tgt	2619
Ser	His	Cys	Thr	Glu	His	Gly	Gln	Cys	Lys	Asp	Gly	Lys	Cys	Glu	Cys	

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Ser Pro Gly Trp Glu Gly Asp His Cys Thr Ile Ala His Tyr Leu Asp				
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Ala Val Arg Asp Gly Cys Pro Gly Leu Cys Phe Gly Asn Gly Arg Cys				
760	765	770	775	
acc ctg gat caa aat ggt tgg cac tgt gtg tgt cag gtg ggt tgg agt				2763
Thr Leu Asp Gln Asn Gly Trp His Cys Val Cys Gln Val Gly Trp Ser				
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Gly Thr Gly Cys Asn Val Val Met Glu Met Leu Cys Gly Asp Asn Leu				
792	797	802	807	
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Asp Asn Asp Gly Asp Gly Leu Thr Asp Cys Val Asp Pro Asp Cys Cys				
808	813	818	823	
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Gln Gln Ser Asn Cys Tyr Ile Ser Pro Leu Cys Gln Gly Ser Pro Asp				
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cct ctt gac ctc att cag caa agc caa act ctc ttc tct cag cac act				2955
Pro Leu Asp Leu Ile Gln Gln Ser Gln Thr Leu Phe Ser Gln His Thr				
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Ser Arg Leu Phe Tyr Asp Arg Ile Lys Phe Leu Ile Gly Lys Asp Ser				
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act cat gtc att cct cct gag gtg tca ttt gac agc agg cgt gcc tgt				3051
Thr His Val Ile Pro Pro Glu Val Ser Phe Asp Ser Arg Arg Ala Cys				
872	877	882	887	
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Val Ile Arg Gly Gln Val Val Ala Ile Asp Gly Thr Pro Leu Val Gly				
888	893	898	903	
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Val Asn Val Ser Phe Leu His His Ser Asp Tyr Gly Phe Thr Ile Ser				
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Arg Gln Asp Gly Ser Phe Asp Leu Val Ala Ile Gly Gly Ile Ser Val				
920	925	930	935	
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Ile Leu Ile Phe Asp Arg Ser Pro Phe Leu Pro Glu Lys Arg Thr Leu				
936	941	946	951	
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Trp Leu Pro Trp Asn Gln Phe Ile Val Val Glu Lys Val Thr Met Gln				
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Arg Val Val Ser Asp Pro Pro Ser Cys Asp Ile Ser Asn Phe Ile Ser	
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Pro Asn Pro Ile Val Leu Pro Ser Pro Leu Thr Ser Phe Gly Gly Ser	
984 989 994 999	
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Cys Pro Glu Arg Gly Thr Ile Val Pro Glu Leu Gln Val Val Gln Glu	
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Glu Ile Pro Ile Pro Ser Ser Phe Val Arg Leu Ser Tyr Leu Ser Ser	
1016 1021 1026 1031	
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Arg Thr Pro Gly Tyr Lys Thr Leu Leu Arg Ile Leu Leu Thr His Ser	
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Thr Ile Pro Val Gly Met Ile Lys Val His Leu Thr Val Ala Val Glu	
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Thr Phe Ala Trp Asn Lys Thr Asp Ile Tyr Gly Gln Lys Val Trp Gly	
1080 1085 1090 1095	
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Phe Ile Ser Gln Gln Pro Pro Val Ile Ser Thr Ile Met Gly Asn Gly	
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His Gln Arg Ser Val Ala Cys Thr Asn Cys Asn Gly Pro Ala His Asn	
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1272 1277 1282 1287	
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Thr Asp Leu Ala Val Asn Pro Met Asp Asn Ser Leu Tyr Val Leu Asp	
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Lys	Val	Asn	Arg	Ile	Gln	Gln	Val	Thr	Thr	Asn	Gly	Glu	Ile	Tyr	Ile	
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Ser Ser Phe His Ser Asp Leu Glu Lys Leu Thr Lys Val Glu Leu Asp				
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Thr Ser Asn Arg Glu Asn Val Leu Met Ser Thr Asn Leu Thr Ala Thr				
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Ser Thr Ile Tyr Ile Leu Lys Gln Glu Asn Thr Gln Ser Thr Tyr Arg				
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Ile Gly Leu Ser Ser Glu Pro His Ile Leu Ala Gly Ala Val Asn Pro				
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Thr Leu Gly Lys Cys Asn Ile Ser Leu Pro Gly Glu His Asn Ala Asn				
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Leu Ile Glu Trp Arg Gln Arg Lys Glu Gln Asn Lys Gly Asn Val Ser				
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Gly Arg Ser Glu Met Arg Ala His Val Pro Gln Ala Pro Trp Ala Arg	
26 31 36 41	

caa gcg ccg cct gtt ctg ccc ctc tgg acc gtg gtg aat gac cat ccc	1275
Gln Ala Pro Pro Val Leu Pro Leu Trp Thr Val Val Asn Asp His Pro	
42 47 52 57	
cat gag aaa cct gtt tca aga ccc cag aat aca tag agac acacacatgg	1325
His Glu Lys Pro Val Ser Arg Pro Gln Asn Thr *	
58 63 68	
tacatagtct cctggtggga aacgacggac atggagttca tttttaaata ggtggctttg	1385
tctgtggcaa tataaaaata ttttggcctt tcaaggcaaa tacaaaagaa actaccatt	1445
aacatggctg agtgtctcag tcccaaacaa taaagaactt gaagaggttt agccggaaac	1505
tttgaagaca gaaaatctgc ccattatggt ttccagacat ttcgaggggg cgagcggagg	1565
tcattggagc ttgaagccca tttggaaggc tgggtccctcg gcctgcgttt tctccttggc	1625
cctttgaagg gccccccagc tcacagggca cttccatcct agtctgccga tttcgagctg	1685
gagaggggct ggggtccac attcgaggtc ctttcccacg taggcatcca ggtgatggct	1745
tccgccccaa ccaggaagga gacgagaggc ccgccaggaa gaagacttgg gtccgggatg	1805
gtgggcccc aagggcctc ttccgcagct tccatccga gttcttcagc cgaccagcc	1865
gggccacggc ccacgtgcct ttgtgagcgt gcttccacgg agtagagcga gtcaggaagc	1925
agtgggttga agaggaaatt ggaggtgagg aaggaagaca gcaagtgtag acaggccttt	1985
caagaagctt ggctgatgca aggagagccc gtggacaagg gctgcctgga gtgctgttgg	2045
agaataaata agacaagtaa gacaagcaag aggggtggga agggactgac ctgtcaaacc	2105
ttttcaacaa acatttgcct atcacctcct ctatgccaga tcctgcctga ggctcttttt	2165
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cccagggtccc cctcctgaga atttcccaaa gggatccttc cattcaggac atcataaggg	2405
tgatgacaga gtcagtcgac aaagactgac acccccttgg ggagggaaac actccagttt	2465
gctagcaggt gaacacaagc aaagacttat aggaaagtac tcatagagtc aaagtatgag	2525
catagcaaag gtcagggtct aatgccaat gccccctcac tagggcattg gtttaagtct	2585
ttaggtaaga gggacagctg gctggtcagt tccggtcctc ttcacctttt gccatcctgg	2645
tcctgggggt cagtgagtgg ctgctttgta tgttgggtgg atccaggaaa ccgtgctcct	2705
agtgcctcct tgaggtgtag atgggcagca gggcccttgg cagcagctca gcatggagag	2765
gaggtggtcc ttgaagacaa ggaggtggac ggatgatgtc atccctgagg agagaccgg	2825

gtgagggatc ctctcgtggg cgccccagct ctcttgagga gccgccgcca aggccagcga 2885
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 at 2947

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 <213> Homo sapiens

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 tttccaagag cagcagaaa atg aat aaa tcc ctg ggg cca gtg tca ttc aag 172
 Met Asn Lys Ser Leu Gly Pro Val Ser Phe Lys
 1 5
 gac gtg gct gtg gac ttc acc cag gag gaa tgg cag cag ctg gat cct 220
 Asp Val Ala Val Asp Phe Thr Gln Glu Glu Trp Gln Gln Leu Asp Pro
 12 17 22 27
 gag cag aag ata act tac agg gat gtg atg ctg gag aac tac agc aat 268
 Glu Gln Lys Ile Thr Tyr Arg Asp Val Met Leu Glu Asn Tyr Ser Asn
 28 33 38 43
 cta gtt tct gtg ggg tat cac att atc aaa ccg gat gtt atc agc aag 316
 Leu Val Ser Val Gly Tyr His Ile Ile Lys Pro Asp Val Ile Ser Lys
 44 49 54 59
 ttg gag caa gga gaa gag cca tgg ata gta gaa gga gaa ttc cta ctt 364
 Leu Glu Gln Gly Glu Glu Pro Trp Ile Val Glu Gly Glu Phe Leu Leu
 60 65 70 75
 cag agc tat cca gat gaa gtc tgg caa act gat gac cta ata gag aga 412
 Gln Ser Tyr Pro Asp Glu Val Trp Gln Thr Asp Asp Leu Ile Glu Arg
 76 81 86 91
 atc cag gaa gag gaa aat aaa cct tca agg caa act gtg ttc att gag 460
 Ile Gln Glu Glu Glu Asn Lys Pro Ser Arg Gln Thr Val Phe Ile Glu
 92 97 102 107
 acc ctg att gaa gag aga ggt aat gtt cct ggt aaa act ttt gat gta 508
 Thr Leu Ile Glu Glu Arg Gly Asn Val Pro Gly Lys Thr Phe Asp Val
 108 113 118 123
 gaa acg aac cct gtt cct tca aga aaa ata gcc tat aaa aat agc ctc 556

Glu Thr Asn Pro Val	Pro Ser Arg Lys Ile	Ala Tyr Lys Asn Ser Leu	
124	129	134	139
tgt gac tca tgt gaa aag tgt tta acg tct gtt tca gaa tat att agt			604
Cys Asp Ser Cys Glu Lys Cys Leu Thr Ser Val Ser Glu Tyr Ile Ser			
140	145	150	155
agt gat gga agc tat gca aga atg aaa gct gat gaa tgt agt gga tgt			652
Ser Asp Gly Ser Tyr Ala Arg Met Lys Ala Asp Glu Cys Ser Gly Cys			
156	161	166	171
ggg aaa tca ctc ctc cat att aag ctt gag aaa act cat cca gga gat			700
Gly Lys Ser Leu Leu His Ile Lys Leu Glu Lys Thr His Pro Gly Asp			
172	177	182	187
caa gct tat gaa ttt aat caa aat ggg gaa cct tat act cta aat gaa			748
Gln Ala Tyr Glu Phe Asn Gln Asn Gly Glu Pro Tyr Thr Leu Asn Glu			
188	193	198	203
gaa agt ctt tat cag aaa att cgt att ttg gag aaa cct ttt gaa tat			796
Glu Ser Leu Tyr Gln Lys Ile Arg Ile Leu Glu Lys Pro Phe Glu Tyr			
204	209	214	219
att gaa tgc cag aaa gcc ttc caa aag gac act gtt ttt gtt aat cac			844
Ile Glu Cys Gln Lys Ala Phe Gln Lys Asp Thr Val Phe Val Asn His			
220	225	230	235
atg gaa gaa aag ccc tat aag tgg aat gga tct gaa ata gcc ttt ctc			892
Met Glu Glu Lys Pro Tyr Lys Trp Asn Gly Ser Glu Ile Ala Phe Leu			
236	241	246	251
cag atg tcg gac ctc act gta cat cag aca tct cat atg gaa atg aag			940
Gln Met Ser Asp Leu Thr Val His Gln Thr Ser His Met Glu Met Lys			
252	257	262	267
ccc tat gaa tgc agt gaa tgt ggg aaa tcc ttc tgt aaa aag tca aaa			988
Pro Tyr Glu Cys Ser Glu Cys Gly Lys Ser Phe Cys Lys Lys Ser Lys			
268	273	278	283
ttt att ata cat cag agg act cac aca gga gag aaa cct tac gaa tgt			1036
Phe Ile Ile His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys			
284	289	294	299
aat cag tgt ggg aaa tcc ttc tgc cag aag gga acc ctt act gtg cat			1084
Asn Gln Cys Gly Lys Ser Phe Cys Gln Lys Gly Thr Leu Thr Val His			
300	305	310	315
cag aga aca cac aca ggg gag aag ccc tat gaa tgt aat gaa tgt ggg			1132
Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Asn Glu Cys Gly			
316	321	326	331
aag aac ttt tac cag aag tta cac ctc att cag cat cag aga act cac			1180
Lys Asn Phe Tyr Gln Lys Leu His Leu Ile Gln His Gln Arg Thr His			
332	337	342	347
tca gga gag aag ccc tat gaa tgt agt tat tgt gga aaa tcc ttt tgc			1228
Ser Gly Glu Lys Pro Tyr Glu Cys Ser Tyr Cys Gly Lys Ser Phe Cys			

348	353	358	363	
cag aag aca cac ctc	aca caa cat cag aga	aca cat tca gga gag aga		1276
Gln Lys Thr His Leu	Thr Gln His Gln Arg	Thr His Ser Gly Glu Arg		
364	369	374	379	
cct tat gtt tgt cat	gac tgt ggg aaa acc	ttc tcg cag aag tca gca		1324
Pro Tyr Val Cys His	Asp Cys Gly Lys Thr	Phe Ser Gln Lys Ser Ala		
380	385	390	395	
ctt aat gac cat cag	aaa att cac aca ggt	gtg aaa ctc tac aag tgt		1372
Leu Asn Asp His Gln	Lys Ile His Thr Gly	Val Lys Leu Tyr Lys Cys		
396	401	406	411	
agt gaa tgt ggg aaa	tgc ttc tgc cgc aag	tct act ctc acg acc cac		1420
Ser Glu Cys Gly Lys	Cys Phe Cys Arg Lys	Ser Thr Leu Thr Thr His		
412	417	422	427	
ctg agg acc cac aca	gga gag aaa ccg tat	gaa tgt aat gag tgt gga		1468
Leu Arg Thr His Thr	Gly Glu Lys Pro Tyr	Glu Cys Asn Glu Cys Gly		
428	433	438	443	
aaa gcc ttc tct cgg	atg tca tac ctc act	gta cat tat aga act cat		1516
Lys Ala Phe Ser Arg	Met Ser Tyr Leu Thr	Val His Tyr Arg Thr His		
444	449	454	459	
tca gga gag aaa ccc	tat gag tgt act gaa	tgt gga aaa aaa ttc tac		1564
Ser Gly Glu Lys Pro	Tyr Glu Cys Thr Glu	Cys Gly Lys Lys Phe Tyr		
460	465	470	475	
cac aaa tca gca ttc	aac agc cat cag aga	att cat agg aga ggc aat		1612
His Lys Ser Ala Phe	Asn Ser His Gln Arg	Ile His Arg Arg Gly Asn		
476	481	486	491	
atg aat gta ata gat	gtg gga agg ctt ctc	tga agtcagac ctcattttat		1663
Met Asn Val Ile Asp	Val Gly Arg Leu Leu	*		
492	497	502		
atcagagaac cctttcagta tagtgaatca gaaactcctg cctgaagtca aacaccttgt				1723
acatcagaga gttcacacag gttagtgtgg acatcccctt gtgtgttgga ctcataatct				1783
gaagactcac agaatggaaa ccatgattat aacaagacca catggtataa caatactaga				1843
ctatagacaa gtaaaaattt ataaatatta agaatgtata tacatgtcac catggattgg				1903
aactgttttg catatcaggg aatatcatagc caaggggaaa tctatcagta taaggaatgt				1963
ggaagacata atcctttgga aactgttaat actaaaagat atgtttctga tacaatagca				2023
aacttgaaaa aaaaaaaa				2041

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tcctccccc gctccagcct ctctcatctt gggaatctgc gtcagaagtc actcgagtc 120

ccgtcagccc agaagacgta aagcaggcta ccagcaattt tgagaacttg caaaaacagc 180

ttgcaaggaa a atg aag ctt cct att ttc ata gca gat gca ttc aca gca 230
Met Lys Leu Pro Ile Phe Ile Ala Asp Ala Phe Thr Ala
1 5 10

aga gca ttt cgt ggg aat cct gct gct gtt tgc ctc cta gaa aat gaa 278
Arg Ala Phe Arg Gly Asn Pro Ala Ala Val Cys Leu Leu Glu Asn Glu
14 19 24 29

ttg gat gaa gac atg cat cag aaa att gca agg gag atg aac ctc tct 326
Leu Asp Glu Asp Met His Gln Lys Ile Ala Arg Glu Met Asn Leu Ser
30 35 40 45

gaa act gct ttt atc cga aaa ctg cac ccg aca gac aac ttt gca caa 374
Glu Thr Ala Phe Ile Arg Lys Leu His Pro Thr Asp Asn Phe Ala Gln
46 51 56 61

agt tcc tgc ttt gga ctg aga tgg ttt aca cca gcg agt gag gtc cca 422
Ser Ser Cys Phe Gly Leu Arg Trp Phe Thr Pro Ala Ser Glu Val Pro
62 67 72 77

ctc tgt ggc cat gcc acc ctg gct tct gca gct gtg ctg ttt cac aaa 470
Leu Cys Gly His Ala Thr Leu Ala Ser Ala Ala Val Leu Phe His Lys
78 83 88 93

ata aaa aac atg aat agc acg ctc acg ttt gtc act ctg agt gga gaa 518
Ile Lys Asn Met Asn Ser Thr Leu Thr Phe Val Thr Leu Ser Gly Glu
94 99 104 109

cta agg gcc aga cga gca gag gac ggc atc gtc ctg gac ttg cct ctt 566
Leu Arg Ala Arg Arg Ala Glu Asp Gly Ile Val Leu Asp Leu Pro Leu
110 115 120 125

tat cca gcc cac ccc cag gac ttc cat gaa gta gag gac ttg ata aag 614
Tyr Pro Ala His Pro Gln Asp Phe His Glu Val Glu Asp Leu Ile Lys
126 131 136 141

act gcc ata ggc aac aca ctg gtc cag gac atc tgt tat tct cca gat 662
Thr Ala Ile Gly Asn Thr Leu Val Gln Asp Ile Cys Tyr Ser Pro Asp
142 147 152 157

acc caa aag ctc ctc gtc cgc ctc agt gac gtt tac aac agg tcg ttt 710
Thr Gln Lys Leu Leu Val Arg Leu Ser Asp Val Tyr Asn Arg Ser Phe
158 163 168 173

ctg gag aac ctg aaa gtg aac acg gag aat ctg ctg caa gtt gaa aac	758
Leu Glu Asn Leu Lys Val Asn Thr Glu Asn Leu Leu Gln Val Glu Asn	
174 179 184 189	
aca ggg aag gtg aaa ggg ctt att ctt acc ctt aaa gga gag cct ggt	806
Thr Gly Lys Val Lys Gly Leu Ile Leu Thr Leu Lys Gly Glu Pro Gly	
190 195 200 205	
ggg cag acc caa gca ttt gac ttt tac tca aga tat ttt gca ccg tgg	854
Gly Gln Thr Gln Ala Phe Asp Phe Tyr Ser Arg Tyr Phe Ala Pro Trp	
206 211 216 221	
gtt ggt gtg gct gaa gac cca gtg aca ggg tct gca cac gct gtt ctc	902
Val Gly Val Ala Glu Asp Pro Val Thr Gly Ser Ala His Ala Val Leu	
222 227 232 237	
agc agc tac tgg tcc cag cat ctg ggg aag aaa gaa atg cat gct ttt	950
Ser Ser Tyr Trp Ser Gln His Leu Gly Lys Lys Glu Met His Ala Phe	
238 243 248 253	
cag tgt tcc cac cga gga gga gag ctg gga att tcc ctt cgt cca gac	998
Gln Cys Ser His Arg Gly Gly Glu Leu Gly Ile Ser Leu Arg Pro Asp	
254 259 264 269	
gga agg gtt gac att aga gga ggt gca gct gtt gtt tta gag ggc aca	1046
Gly Arg Val Asp Ile Arg Gly Gly Ala Ala Val Val Leu Glu Gly Thr	
270 275 280 285	
ctg aca gcc tag agg tggttatgct gtgacgctgc tgtctctaac caccaagtat	1101
Leu Thr Ala *	
286	
tttctgctta aaaagaaatg taaggggctg ccttttagcaa atgtgcgtag tagtctactt	1161
aatcctcatg ttaaaaaatcg aaaaatgggc caggcgcagt ggctcatgcc tgtaatcgta	1221
gcactttgag aggccaaggt ggggtggatca cctgaggtca ggggttcgac accagcctgg	1281
ccaacatggt gaaacctcgt ctctataaaa aaaaa	1316

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 <212> DNA
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 <222> (172)..(456)

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cccatttcag cttcttagga ctctgcactt ccccagaagg aagaattaaa a atg aat	177
Met Asn	
1	
atg ttc aag gaa gca gtg acc ttc aag gac gtg gct gtg acc ttc acg	225
Met Phe Lys Glu Ala Val Thr Phe Lys Asp Val Ala Val Thr Phe Thr	
3 8 13 18	
gag gag gaa ttg ggg ctg ctg ggc cct gcc cag agg aag ctg tac cga	273
Glu Glu Glu Leu Gly Leu Leu Gly Pro Ala Gln Arg Lys Leu Tyr Arg	
19 24 29 34	
gat gtg atg gtg gag aac ttt agg aac ctg ctg tca gtg ggg cat cca	321
Asp Val Met Val Glu Asn Phe Arg Asn Leu Leu Ser Val Gly His Pro	
35 40 45 50	
ccc ttc aaa caa gat gta tca cct ata gaa aga aat gag cag ctt tgg	369
Pro Phe Lys Gln Asp Val Ser Pro Ile Glu Arg Asn Glu Gln Leu Trp	
51 56 61 66	
ata atg acg aca gca acc cga aga cag gga aat tta gat acc tta ctt	417
Ile Met Thr Thr Ala Thr Arg Arg Gln Gly Asn Leu Asp Thr Leu Leu	
67 72 77 82	
gta aaa gct ctt ttg ctc tat gac ctg gct caa act taa acttgattt	466
Val Lys Ala Leu Leu Leu Tyr Asp Leu Ala Gln Thr *	
83 88 93	
gaagttagaa gaaatgttgg aagtcattta tatatgaaga aatgttggaa ggactcatat	526
atgcatacat tccttgagtg actatgaatg actgccgggc agtaacttct gggctgtggg	586
tgtaaactgt gagcactaca aaatgttttt ccttattgat accatattat ggtaggaaag	646
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 <213> Homo sapiens

<220>
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 <222> (160)..(714)

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ccagcagctg ctgttgccac caccactagt tcaagcacc atg cag ttt acc tca	174
Met Gln Phe Thr Ser	
1	

ata tca aat tct ttg acc tcc act gct gct att ggg ctc tca ttt aca	222
Ile Ser Asn Ser Leu Thr Ser Thr Ala Ala Ile Gly Leu Ser Phe Thr	
6 11 16 21	
act tca acg act acc acc gcc act ttc acc acc aac act act acc aca	270
Thr Ser Thr Thr Thr Thr Ala Thr Phe Thr Thr Asn Thr Thr Thr Thr	
22 27 32 37	
atc acc agt ggc ttt act gtg aac caa aac caa ctg tta tca aga ggg	318
Ile Thr Ser Gly Phe Thr Val Asn Gln Asn Gln Leu Leu Ser Arg Gly	
38 43 48 53	
ttt gaa aac ctt gta cct tat act tca act gtt agt gta gta gca act	366
Phe Glu Asn Leu Val Pro Tyr Thr Ser Thr Val Ser Val Val Ala Thr	
54 59 64 69	
cct gtg atg aca tat ggt cat ctg gag ggt ctt ata aat gag tgg aac	414
Pro Val Met Thr Tyr Gly His Leu Glu Gly Leu Ile Asn Glu Trp Asn	
70 75 80 85	
ctt gag ctg gaa gat caa gag aag tac ttt ctt ctc cag gcc act cag	462
Leu Glu Leu Glu Asp Gln Glu Lys Tyr Phe Leu Leu Gln Ala Thr Gln	
86 91 96 101	
gtc aat gct tgg gac cat aca ttg att gag aat ggt gag atg att cgt	510
Val Asn Ala Trp Asp His Thr Leu Ile Glu Asn Gly Glu Met Ile Arg	
102 107 112 117	
att tta cat gga gaa gtg aac aaa gtg aaa ctg gat cag aaa aga ttg	558
Ile Leu His Gly Glu Val Asn Lys Val Lys Leu Asp Gln Lys Arg Leu	
118 123 128 133	
gaa caa gaa ttg gat ttt atc ctg tca cag cag cag gaa cta gaa ttt	606
Glu Gln Glu Leu Asp Phe Ile Leu Ser Gln Gln Gln Glu Leu Glu Phe	
134 139 144 149	
ctg ttg act tat tta gag gag tct acg cgc gac cag agt gga ctt cat	654
Leu Leu Thr Tyr Leu Glu Glu Ser Thr Arg Asp Gln Ser Gly Leu His	
150 155 160 165	
tat ctg cag gat gca gat gag gag cat gtg gag atc tcc acc aga tct	702
Tyr Leu Gln Asp Ala Asp Glu Glu His Val Glu Ile Ser Thr Arg Ser	
166 171 176 181	
gca gaa ttc tga atg cccatatgga ctccctgcag tggattgatc ggaattcagg	757
Ala Glu Phe *	
182	
catgctgcga aggaaggtag aagtggtaac acgggttttt cgaggattat cattcacgag	817
gggtcttttca catcatgttc atcactgttt tttagtgtat tgaccctttt ttcagcttgt	877
cgtttctgga ttattatcta ctaattcttt tgtttatttt	917

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gct cct gga atc agc tta gtc aat gaa gct acc ttt ggt tgt tca tgc	857
Ala Pro Gly Ile Ser Leu Val Asn Glu Ala Thr Phe Gly Cys Ser Cys	
118 123 128 133	
aca gat tgc ttc ttt caa aaa tgt tgt cct gct gaa gct gga gtt ctt	905
Thr Asp Cys Phe Phe Gln Lys Cys Cys Pro Ala Glu Ala Gly Val Leu	
134 139 144 149	
ttg gct tat aat aaa aac caa caa att aaa atc cca cct ggt act ccc	953
Leu Ala Tyr Asn Lys Asn Gln Gln Ile Lys Ile Pro Pro Gly Thr Pro	
150 155 160 165	
atc tat gaa tgc aac tca agg tgt cag tgt ggt cct gat tgt ccc aat	1001
Ile Tyr Glu Cys Asn Ser Arg Cys Gln Cys Gly Pro Asp Cys Pro Asn	
166 171 176 181	
agg att gta caa aaa ggc aca cag tat tcg ctt tgc atc ttt cga act	1049
Arg Ile Val Gln Lys Gly Thr Gln Tyr Ser Leu Cys Ile Phe Arg Thr	
182 187 192 197	
agc aat gga cgt ggc tgg ggt gta aag acc ctt gtg aag att aaa aga	1097
Ser Asn Gly Arg Gly Trp Gly Val Lys Thr Leu Val Lys Ile Lys Arg	
198 203 208 213	
atg agt ttt gtc atg gaa tat gtt gga gag gta atc aca agt gaa gaa	1145
Met Ser Phe Val Met Glu Tyr Val Gly Glu Val Ile Thr Ser Glu Glu	
214 219 224 229	
gct gaa aga cga gga cag ttc tat gac aac aag gga atc acg tat ctc	1193
Ala Glu Arg Arg Gly Gln Phe Tyr Asp Asn Lys Gly Ile Thr Tyr Leu	
230 235 240 245	
ttt gat ctg gac tat gag tct gat gaa ttc aca gtg gat gcg gct cga	1241
Phe Asp Leu Asp Tyr Glu Ser Asp Glu Phe Thr Val Asp Ala Ala Arg	
246 251 256 261	
tac ggc aat gtg tct cat ttt gtg aat cac agc tgt gac cca aat ctt	1289
Tyr Gly Asn Val Ser His Phe Val Asn His Ser Cys Asp Pro Asn Leu	
262 267 272 277	
cag gtg ttc aat gtt ttc att gat aac ctc gat act cgt ctt ccc cga	1337
Gln Val Phe Asn Val Phe Ile Asp Asn Leu Asp Thr Arg Leu Pro Arg	
278 283 288 293	
ata gca ttg ttt tcc aca aga acc ata aat gct gga gaa gag ctg act	1385
Ile Ala Leu Phe Ser Thr Arg Thr Ile Asn Ala Gly Glu Glu Leu Thr	
294 299 304 309	
ttt gat tat caa atg aaa ggt tct gga gat ata tct tca gat tct att	1433
Phe Asp Tyr Gln Met Lys Gly Ser Gly Asp Ile Ser Ser Asp Ser Ile	
310 315 320 325	
gac cac agc cca gcc aaa aag agg gtc aga aca gta tgt aaa tgt gga	1481
Asp His Ser Pro Ala Lys Lys Arg Val Arg Thr Val Cys Lys Cys Gly	
326 331 336 341	
gct gtg act tgc aga ggt tac ctc aac tga a ctttttcagg aaatagagct	1532

Ala Val Thr Cys Arg Gly Tyr Leu Asn *
342 347

gatgattata atattttttt cctaattgtta acatttttaa aaatacatat ttgggactct 1592

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<212> DNA
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<220>
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<400> 29

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Met
1

gcg cca gcg aaa gcc acg aac gtg gtg cgg ctg cta cta ggc tcc aca 166
Ala Pro Ala Lys Ala Thr Asn Val Val Arg Leu Leu Leu Gly Ser Thr
2 7 12 17

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Ser Val Thr Ala His Leu Ala Ala Lys Trp Pro Glu Thr Pro Leu Leu
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Gln Phe Leu Glu Thr Val Gln Glu Leu Ala Ile Tyr Lys Gln Thr Glu
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Lys Glu Asn Leu Pro Val Val Ile Leu Tyr Ala Glu Met Gly Thr Arg	
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 His Ala Arg Arg Val Lys Gly Ile Glu Ala Ala Lys Thr Arg Gly Arg
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Pro Thr Asn Gly Asp	Gly Val Ala Pro Arg	Pro Val Ser Met Glu Asn	
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Ala Leu Trp Leu Ser Gln Leu Gly Ser Gly Thr Val Ala Ala Ser Lys	
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Ser Val Thr Ala His Leu Ala Ala Lys Trp Pro Glu Thr Pro Leu Leu	
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Ser Asp Tyr Ser Tyr Tyr Asn Leu Ile Leu Lys Lys Ala Gly Gln Phe	
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Glu Tyr Lys Ala Leu Asp Asp Thr Gln Val Lys Thr Val Thr Asn Thr				
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258	263	268	273	
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Val Asp Met Asp Val Tyr Asp Ala Phe Ser Ile Leu Asp Met Leu Lys				
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Gly Ile His Ser Lys Tyr Asp Glu Glu Arg Lys Ala Gly Ala Ser Phe	
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Tyr Lys Met Thr Gly Leu Gly Pro Leu Pro Gln Ala Leu Tyr Asn Gly	
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Glu Pro Phe Lys His Glu Glu Met Asn Ile Lys Glu Leu Lys Met Ala	
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Lys Gln Asp Thr Ile Leu Thr His Asp Glu Leu *	
1506 1511 1516	
agaaggaagg cgaaagcatg acaggaaacc tgccgcctgc tggggaagtc tggagcccct	4740
gctgagacga tttggaagtc tcgttaagat cagtgcata ttctttaatt ttaaaaaatt	4800
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<400> 33

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gcagtggctg	cccagaacct	ttacacatgt	atgtgtgcgc	gtgtgcagag	catgacaagg	300		
caggtggctg	gggctccagc	ctggctaaag	agaacttgcc	cttaggggca	agagagggag	360		
gcactgcatt	tccagtttcg	ttctggaagt	gcccacctga	catctgtggt	gcccactgat	420		
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gaaatttctg	caggagctac	accagtactt	tgttcgggca	ggaggc	atg gag ggc	535		
					Met Glu Gly			
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cct gaa ggg	ctg ggc	cgg aag	caa gcc	tgt cta	gcc atg	ctt ctc	cat	583
Pro Glu Gly	Leu Gly	Arg Lys	Gln Ala	Cys Leu	Ala Met	Leu Leu	His	
4		9		14		19		
ttc ttg gac	acc tac	cag ggg	ctg ctt	caa gag	gaa gag	ggg gcc	ggc	631
Phe Leu Asp	Thr Tyr	Gln Gly	Leu Leu	Gln Glu	Glu Glu	Gly Ala	Gly	
20		25		30		35		
cac atc atc	aag gat	cta tac	ctg cta	att atg	aag gac	gag tcc	ctt	679
His Ile Ile	Lys Asp	Leu Tyr	Leu Leu	Ile Met	Lys Asp	Glu Ser	Leu	
36		41		46		51		
tac cag ggc	ctc cga	gag gac	act ctg	agg ctg	cac cag	ctg gtg	gag	727
Tyr Gln Gly	Leu Arg	Glu Asp	Thr Leu	Arg Leu	His Gln	Leu Val	Glu	
52		57		62		67		
acg gtg gaa	cta aag	att cca	gag gag	aac cag	cca ccc	agc aag	cag	775
Thr Val Glu	Leu Lys	Ile Pro	Glu Glu	Asn Gln	Pro Pro	Ser Lys	Gln	
68		73		78		83		
gtg aag cca	ctc ttc	cgc cac	ttc cgc	cgg ata	gac tcc	tgt ctg	cag	823
Val Lys Pro	Leu Phe	Arg His	Phe Arg	Arg Ile	Asp Ser	Cys Leu	Gln	
84		89		94		99		
acc cgg gtg	gcc ttc	cgg ggc	tct gat	gag atc	ttc tgc	cgt gta	tac	871
Thr Arg Val	Ala Phe	Arg Gly	Ser Asp	Glu Ile	Phe Cys	Arg Val	Tyr	
100		105		110		115		

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Met Pro Asp His Ser Tyr Val Thr Ile Arg Ser Arg Leu Ser Ala Ser	
116 121 126 131	
gtg cag gac att ctg ggc tct gtg acg gag aaa ctt caa tat tca gag	967
Val Gln Asp Ile Leu Gly Ser Val Thr Glu Lys Leu Gln Tyr Ser Glu	
132 137 142 147	
gag ccc gcg ggg cgt gag gat tcc ctc atc ctg gta gct gtg tcc tcc	1015
Glu Pro Ala Gly Arg Glu Asp Ser Leu Ile Leu Val Ala Val Ser Ser	
148 153 158 163	
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Ser Gly Glu Lys Val Leu Leu Gln Pro Thr Glu Asp Cys Val Phe Thr	
164 169 174 179	
gca ctg ggc atc aac agc cac ctg ttt gcc tgt act cgg gac agc tat	1111
Ala Leu Gly Ile Asn Ser His Leu Phe Ala Cys Thr Arg Asp Ser Tyr	
180 185 190 195	
gag gct ctg gtg ccc ctc ccc gag gag atc cag gtc tcc cct gga gac	1159
Glu Ala Leu Val Pro Leu Pro Glu Glu Ile Gln Val Ser Pro Gly Asp	
196 201 206 211	
aca gag atc cac cga gtg gag cct gag gac gtt gcc aac cac cta act	1207
Thr Glu Ile His Arg Val Glu Pro Glu Asp Val Ala Asn His Leu Thr	
212 217 222 227	
gcc ttc cac tgg gag ctg ttc cga tgt gtg cat gag ctg gag ttc gtg	1255
Ala Phe His Trp Glu Leu Phe Arg Cys Val His Glu Leu Glu Phe Val	
228 233 238 243	
gac tac gtg ttc cac ggg gag cgc ggc cgc cgg gag acg gcc aac ttg	1303
Asp Tyr Val Phe His Gly Glu Arg Gly Arg Arg Glu Thr Ala Asn Leu	
244 249 254 259	
gag ctg ctg ctg cag cgc tgc agc gag gtc acg cac tgg gtg gcc acc	1351
Glu Leu Leu Leu Gln Arg Cys Ser Glu Val Thr His Trp Val Ala Thr	
260 265 270 275	
gaa gtg ctg ctc tgc gag gcc ccg ggc aag cgc gcg cag ctg ctc aag	1399
Glu Val Leu Leu Cys Glu Ala Pro Gly Lys Arg Ala Gln Leu Leu Lys	
276 281 286 291	
aag ttc atc aag atc gcg gcc ctc tgc aag cag aac cag gac ctg ctg	1447
Lys Phe Ile Lys Ile Ala Ala Leu Cys Lys Gln Asn Gln Asp Leu Leu	
292 297 302 307	
tct ttc tac gcc gtg gtc atg ggg ctg gac aac gcc gct gtc agc cgc	1495
Ser Phe Tyr Ala Val Val Met Gly Leu Asp Asn Ala Ala Val Ser Arg	
308 313 318 323	
ctt cga ctc acc tgg gag aag ctg cca ggg aaa ttc aag aac ttg ttt	1543
Leu Arg Leu Thr Trp Glu Lys Leu Pro Gly Lys Phe Lys Asn Leu Phe	
324 329 334 339	
cgc aaa ttt gag aac ctg acg gac ccc tgc agg aac cac aaa agc tac	1591

Arg	Lys	Phe	Glu	Asn	Leu	Thr	Asp	Pro	Cys	Arg	Asn	His	Lys	Ser	Tyr	
340					345					350					355	
cga	gaa	gtg	atc	tcc	aaa	atg	aag	ccc	cct	gtg	att	ccc	ttc	gtg	cct	1639
Arg	Glu	Val	Ile	Ser	Lys	Met	Lys	Pro	Pro	Val	Ile	Pro	Phe	Val	Pro	
356					361					366					371	
ctg	atc	ctc	aaa	gac	ctg	act	ttc	ctg	cac	gaa	ggg	agt	aag	acc	ctt	1687
Leu	Ile	Leu	Lys	Asp	Leu	Thr	Phe	Leu	His	Glu	Gly	Ser	Lys	Thr	Leu	
372					377					382					387	
gta	gat	ggg	ttg	gtg	aac	atc	gag	aag	ctg	cat	tca	gtg	gcc	gaa	aaa	1735
Val	Asp	Gly	Leu	Val	Asn	Ile	Glu	Lys	Leu	His	Ser	Val	Ala	Glu	Lys	
388					393					398					403	
gtg	agg	aca	atc	cgc	aaa	tac	cgg	agc	cgg	ccc	ctt	tgc	ctg	gac	atg	1783
Val	Arg	Thr	Ile	Arg	Lys	Tyr	Arg	Ser	Arg	Pro	Leu	Cys	Leu	Asp	Met	
404					409					414					419	
gag	gca	tcc	ccc	aat	cac	ctg	cag	acc	aag	gcc	tat	gtg	cgc	cag	ttt	1831
Glu	Ala	Ser	Pro	Asn	His	Leu	Gln	Thr	Lys	Ala	Tyr	Val	Arg	Gln	Phe	
420					425					430					435	
cag	gtc	atc	gac	aac	cag	aac	ctc	ctc	ttc	gag	ctc	tcc	tac	aag	ctg	1879
Gln	Val	Ile	Asp	Asn	Gln	Asn	Leu	Leu	Phe	Glu	Leu	Ser	Tyr	Lys	Leu	
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gag	gca	aac	agt	cag	tga											1897
Glu	Ala	Asn	Ser	Gln	*											
452					457											

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acaaaggggg	ctggaggatt	tagccactct	gtcctcccct	tccggcagtc	cagggcctcc											180
tcccgagcac	agcggcgct	atg gac tct	cca gga tac	aac tgc ttc	gtg gac											232

Met Asp Ser Pro Gly Tyr Asn Cys Phe Val Asp
1 5

aaa gac aag atg gac gct gcc atc cag gac ctg ggg ccc aag gag ctg	280
Lys Asp Lys Met Asp Ala Ala Ile Gln Asp Leu Gly Pro Lys Glu Leu	
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agc tgc act gaa ctg cag gaa ctg aag cag ctg gcg cgc cag ggc tac	328
Ser Cys Thr Glu Leu Gln Glu Leu Lys Gln Leu Ala Arg Gln Gly Tyr	
28 33 38 43	
tgg gcc caa agc cac gcc ctg cgg gga aag gtg tac cag cgc ctg atc	376
Trp Ala Gln Ser His Ala Leu Arg Gly Lys Val Tyr Gln Arg Leu Ile	
44 49 54 59	
cgg gac att ccc tgc cgc acg gtc acg cct gac gcc agc gtg tac agc	424
Arg Asp Ile Pro Cys Arg Thr Val Thr Pro Asp Ala Ser Val Tyr Ser	
60 65 70 75	
gac atc gtg ggc aag atc gtg ggc aag cac agc agc agc tgc ctg ccg	472
Asp Ile Val Gly Lys Ile Val Gly Lys His Ser Ser Ser Cys Leu Pro	
76 81 86 91	
ctg ccc gag ttc gtg gac aac acg cag gtg ccc agc tac tgc ctg aat	520
Leu Pro Glu Phe Val Asp Asn Thr Gln Val Pro Ser Tyr Cys Leu Asn	
92 97 102 107	
gca cgc ggc gag ggg gcc gtg cgc aag atc ctc ctg tgc ctg gcc aac	568
Ala Arg Gly Glu Gly Ala Val Arg Lys Ile Leu Leu Cys Leu Ala Asn	
108 113 118 123	
cag ttc ccc gac atc tcc ttc tgc ccc gcc ctg ccg gcc gtg gtg gcc	616
Gln Phe Pro Asp Ile Ser Phe Cys Pro Ala Leu Pro Ala Val Val Ala	
124 129 134 139	
ctg ctg ctg cac tac agc atc gac gag gcc gag tgc ttc gag aag gcc	664
Leu Leu Leu His Tyr Ser Ile Asp Glu Ala Glu Cys Phe Glu Lys Ala	
140 145 150 155	
tgc cgc atc ctg gcc tgc aat gac ccc ggc agg agg ctg atc gac cag	712
Cys Arg Ile Leu Ala Cys Asn Asp Pro Gly Arg Arg Leu Ile Asp Gln	
156 161 166 171	
agc ttc ctg gcc ttt gag tgc tcc tgc atg acg ttt ggg gac ctg gtg	760
Ser Phe Leu Ala Phe Glu Ser Ser Cys Met Thr Phe Gly Asp Leu Val	
172 177 182 187	
aac aag tac tgc cag gcg gcc cac aag ctg atg gtg gcc gtg tgc gag	808
Asn Lys Tyr Cys Gln Ala Ala His Lys Leu Met Val Ala Val Ser Glu	
188 193 198 203	
gat gtc ctg cag gtc tat gcg gac tgg cag cgc tgg ctg ttt ggg gag	856
Asp Val Leu Gln Val Tyr Ala Asp Trp Gln Arg Trp Leu Phe Gly Glu	
204 209 214 219	
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Leu Pro Leu Cys Tyr Phe Ala Arg Val Phe Asp Val Phe Leu Val Glu	

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Gly Tyr Lys Val Leu	Tyr Arg Val Ala Leu	Ala Ile Leu Lys Phe	Phe				
236	241	246	251				
cat aag gtg agg gcc	ggg cag ccg ctg gag	tcg gac agc gtg aag	cag	1000			
His Lys Val Arg Ala	Gly Gln Pro Leu Glu	Ser Asp Ser Val Lys	Gln				
252	257	262	267				
gac atc cgc acg ttc	gtc aga gac atc gcg	aag acg gtg tcc cct	gag	1048			
Asp Ile Arg Thr Phe	Val Arg Asp Ile Ala	Lys Thr Val Ser Pro	Glu				
268	273	278	283				
aag ctg ctg gag aaa	gcg ttc gcc atc cgc	ctc ttg tcc cgc aag	gag	1096			
Lys Leu Leu Glu Lys	Ala Phe Ala Ile Arg	Leu Leu Ser Arg Lys	Glu				
284	289	294	299				
atc cag ctc ctg cag	atg gcc aat gag aaa	gcc ctg aag cag aag	ggc	1144			
Ile Gln Leu Leu Gln	Met Ala Asn Glu Lys	Ala Leu Lys Gln Lys	Gly				
300	305	310	315				
atc acc gtg aag cag	aag agt gtg tca ctt	tct aaa agg cag ttt	gta	1192			
Ile Thr Val Lys Gln	Lys Ser Val Ser Leu	Ser Lys Arg Gln Phe	Val				
316	321	326	331				
cac ttg gcc gtc cat	gca gag aac ttc cgc	tcg gag atc gtc agc	gtg	1240			
His Leu Ala Val His	Ala Glu Asn Phe Arg	Ser Glu Ile Val Ser	Val				
332	337	342	347				
agg gag atg aga gac	atc tgg tcc tgg gtc	ccc gag cgc ttt gcc	ctg	1288			
Arg Glu Met Arg Asp	Ile Trp Ser Trp Val	Pro Glu Arg Phe Ala	Leu				
348	353	358	363				
tgc cag ccc ctt ctg	ctg ttc tcc tcc ctg	cag cac ggg tac agc	ctg	1336			
Cys Gln Pro Leu Leu	Leu Phe Ser Ser Leu	Gln His Gly Tyr Ser	Leu				
364	369	374	379				
gcc agg ttc tac ttc	cag tgt gaa gga cat	gag cct acc ctc ttg	ctc	1384			
Ala Arg Phe Tyr Phe	Gln Cys Glu Gly His	Glu Pro Thr Leu Leu	Leu				
380	385	390	395				
atc aag acc acg cag	aag gag gtg tgt ggt	gct tac ctg tcc aca	gac	1432			
Ile Lys Thr Thr Gln	Lys Glu Val Cys Gly	Ala Tyr Leu Ser Thr	Asp				
396	401	406	411				
tgg agt gag aga aat	aag ttt gga ggc aaa	ctg ggc ttc ttt ggg	acc	1480			
Trp Ser Glu Arg Asn	Lys Phe Gly Gly Lys	Leu Gly Phe Phe Gly	Thr				
412	417	422	427				
gga gaa tgc ttt gtg	ttt agg ctg cag cct	gag gtg cag cgc tac	gag	1528			
Gly Glu Cys Phe Val	Phe Arg Leu Gln Pro	Glu Val Gln Arg Tyr	Glu				
428	433	438	443				
tgg gtg gtg atc aag	cac ccc gag ctg acc	aag ccc cca ccc ttg	atg	1576			
Trp Val Val Ile Lys	His Pro Glu Leu Thr	Lys Pro Pro Pro Leu	Met				
444	449	454	459				

gct gcc gag ccc acc gcc cca ctc agc cac tcc gcc tcc tca gac ccc	1624
Ala Ala Glu Pro Thr Ala Pro Leu Ser His Ser Ala Ser Ser Asp Pro	
460 465 470 475	
gct gac cgc ctc tcg ccc ttc ctg gcc gct cgc cac ttc aac ctg ccc	1672
Ala Asp Arg Leu Ser Pro Phe Leu Ala Ala Arg His Phe Asn Leu Pro	
476 481 486 491	
tcc aag acc gag tcc atg ttc atg gcg ggg ggc agc gac tgc ctc atc	1720
Ser Lys Thr Glu Ser Met Phe Met Ala Gly Gly Ser Asp Cys Leu Ile	
492 497 502 507	
gtc ggg gga gga ggc ggc cag gcg ctc tac atc gat ggg gac ctg aac	1768
Val Gly Gly Gly Gly Gly Gly Gln Ala Leu Tyr Ile Asp Gly Asp Leu Asn	
508 513 518 523	
cgg ggc cgc aca agc cac tgc gac acc ttc aac aac cag ccc ctc tgc	1816
Arg Gly Arg Thr Ser His Cys Asp Thr Phe Asn Asn Gln Pro Leu Cys	
524 529 534 539	
tcc gag aac ttc ctc att gct gcc gtg aag gcc tgg ggc ttc cag gac	1864
Ser Glu Asn Phe Leu Ile Ala Ala Val Lys Ala Trp Gly Phe Gln Asp	
540 545 550 555	
cct gac acc cag tga cggcctgtgc cacggtgact gagccgtggt ggggcggtgg	1919
Pro Asp Thr Gln *	
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Met Pro Gly Ser Asp Thr Ala Leu Thr Val	
1 5	
gac cgg acc tac tcg gac ccc ggc cgg cac cac cgc tgc aag agc cgg	159
Asp Arg Thr Tyr Ser Asp Pro Gly Arg His His Arg Cys Lys Ser Arg	
11 16 21 26	
gta gaa cgt cat gac atg aat acc tta agc ctg ccc ctg aac ata cgc	207

Val	Glu	Arg	His	Asp	Met	Asn	Thr	Leu	Ser	Leu	Pro	Leu	Asn	Ile	Arg	
27					32					37					42	
cga	ggg	ggg	tca	gac	acc	aac	ctc	aac	ttt	gat	gtc	ccg	gat	ggc	atc	255
Arg	Gly	Gly	Ser	Asp	Thr	Asn	Leu	Asn	Phe	Asp	Val	Pro	Asp	Gly	Ile	
43					48					53					58	
ctg	gac	ttc	cac	aag	gtc	aaa	ctc	act	gca	gac	agc	ctg	aag	caa	aaa	303
Leu	Asp	Phe	His	Lys	Val	Lys	Leu	Thr	Ala	Asp	Ser	Leu	Lys	Gln	Lys	
59					64					69					74	
att	cta	aag	gta	aca	gag	cag	ata	aaa	att	gag	caa	aca	tcg	cgc	gat	351
Ile	Leu	Lys	Val	Thr	Glu	Gln	Ile	Lys	Ile	Glu	Gln	Thr	Ser	Arg	Asp	
75					80					85					90	
ggg	aat	gtt	gcg	gag	tat	ctg	aaa	cta	gtg	aac	aac	gcg	gac	aag	cag	399
Gly	Asn	Val	Ala	Glu	Tyr	Leu	Lys	Leu	Val	Asn	Asn	Ala	Asp	Lys	Gln	
91					96					101					106	
cag	gcg	gga	cgt	atc	aag	caa	gtc	ttt	gag	aag	aag	aat	cag	aaa	tca	447
Gln	Ala	Gly	Arg	Ile	Lys	Gln	Val	Phe	Glu	Lys	Lys	Asn	Gln	Lys	Ser	
107					112					117					122	
gct	cac	tcc	atc	gcc	cag	ctg	cag	aag	aag	tta	gag	cag	tat	cat	cga	495
Ala	His	Ser	Ile	Ala	Gln	Leu	Gln	Lys	Lys	Leu	Glu	Gln	Tyr	His	Arg	
123					128					133					138	
aag	ctc	aga	gag	atc	gag	cag	aat	gga	gcc	tct	agg	agc	tca	aag	gac	543
Lys	Leu	Arg	Glu	Ile	Glu	Gln	Asn	Gly	Ala	Ser	Arg	Ser	Ser	Lys	Asp	
139					144					149					154	
att	tcc	aaa	gac	cac	ctg	aag	gat	ata	cat	cgc	tct	ttg	aaa	gat	gcc	591
Ile	Ser	Lys	Asp	His	Leu	Lys	Asp	Ile	His	Arg	Ser	Leu	Lys	Asp	Ala	
155					160					165					170	
cac	gtg	aaa	tct	cga	act	gcc	ccc	cat	tgc	atg	gag	agc	agc	aaa	tcg	639
His	Val	Lys	Ser	Arg	Thr	Ala	Pro	His	Cys	Met	Glu	Ser	Ser	Lys	Ser	
171					176					181					186	
ggc	atg	cca	ggg	gtc	tca	ctt	act	cca	cct	gtg	ttc	gtt	ttc	aat	aag	687
Gly	Met	Pro	Gly	Val	Ser	Leu	Thr	Pro	Pro	Val	Phe	Val	Phe	Asn	Lys	
187					192					197					202	
tcc	aga	gag	ttt	gcc	aac	ctg	atc	cgg	aat	aag	ttt	ggc	agc	gcc	gac	735
Ser	Arg	Glu	Phe	Ala	Asn	Leu	Ile	Arg	Asn	Lys	Phe	Gly	Ser	Ala	Asp	
203					208					213					218	
aac	att	gct	cac	ttg	aaa	aat	tcc	tta	gag	gag	ttt	agg	cca	gag	gcg	783
Asn	Ile	Ala	His	Leu	Lys	Asn	Ser	Leu	Glu	Glu	Phe	Arg	Pro	Glu	Ala	
219					224					229					234	
agt	gcc	agg	gcc	tac	ggg	ggc	agc	gct	acc	atc	gtg	aac	aaa	ccc	aag	831
Ser	Ala	Arg	Ala	Tyr	Gly	Gly	Ser	Ala	Thr	Ile	Val	Asn	Lys	Pro	Lys	
235					240					245					250	
tat	ggc	agt	gat	gat	gaa	tgt	tcg	agt	ggc	acg	tca	ggc	tcg	gcc	gac	879
Tyr	Gly	Ser	Asp	Asp	Glu	Cys	Ser	Ser	Gly	Thr	Ser	Gly	Ser	Ala	Asp	

251	256	261	266	
agt aac gga aac cag tct ttt ggg gct ggt gga gcc agc aca ctg gac				927
Ser Asn Gly Asn Gln Ser Phe Gly Ala Gly Gly Ala Ser Thr Leu Asp				
267	272	277	282	
agc cag ggc aag ctg gcc gtg atc ctg gag gaa ctg agg gag atc aag				975
Ser Gln Gly Lys Leu Ala Val Ile Leu Glu Glu Leu Arg Glu Ile Lys				
283	288	293	298	
gat acc caa gct cag ctg gct gag gac atc gag gca ctg aag gtg cag				1023
Asp Thr Gln Ala Gln Leu Ala Glu Asp Ile Glu Ala Leu Lys Val Gln				
299	304	309	314	
ttt aag aga gaa tat ggt ttt att tct cag acc ctg caa gag gaa aga				1071
Phe Lys Arg Glu Tyr Gly Phe Ile Ser Gln Thr Leu Gln Glu Glu Arg				
315	320	325	330	
tac agg tat gag cga ctg gag gac cag ctg cat gac ctg acg gac ctg				1119
Tyr Arg Tyr Glu Arg Leu Glu Asp Gln Leu His Asp Leu Thr Asp Leu				
331	336	341	346	
cat cag cat gag aca gcc aac ctg aag cag gag ctg gcc agc att gag				1167
His Gln His Glu Thr Ala Asn Leu Lys Gln Glu Leu Ala Ser Ile Glu				
347	352	357	362	
gag aag gtg gcc tac cag gcc tac gag cgc tct cgg gac atc cag gaa				1215
Glu Lys Val Ala Tyr Gln Ala Tyr Glu Arg Ser Arg Asp Ile Gln Glu				
363	368	373	378	
gcc ttg gaa tcc tgc cag act cgc att tct aag ctg gag ctg cac cag				1263
Ala Leu Glu Ser Cys Gln Thr Arg Ile Ser Lys Leu Glu Leu His Gln				
379	384	389	394	
caa gag cag caa gct ctg cag aca gac acc gtg aat gct aaa gtt ctg				1311
Gln Glu Gln Gln Ala Leu Gln Thr Asp Thr Val Asn Ala Lys Val Leu				
395	400	405	410	
ctg ggg agg tgc atc aac gtg atc ctg gcc ttc atg act gtc atc tta				1359
Leu Gly Arg Cys Ile Asn Val Ile Leu Ala Phe Met Thr Val Ile Leu				
411	416	421	426	
gtg tgt gtg tcc acc atc gcg aag ttc gtc tca ccc atg atg aag agt				1407
Val Cys Val Ser Thr Ile Ala Lys Phe Val Ser Pro Met Met Lys Ser				
427	432	437	442	
cgc tgc cac att ctt ggc acc ttc ttt gcc gtg act ctt ctt gct ata				1455
Arg Cys His Ile Leu Gly Thr Phe Phe Ala Val Thr Leu Leu Ala Ile				
443	448	453	458	
ttt tgt aaa aac tgg gac cat atc ctg tgt gcc ata gaa agg atg ata				1503
Phe Cys Lys Asn Trp Asp His Ile Leu Cys Ala Ile Glu Arg Met Ile				
459	464	469	474	
ata cca aga tga agc cactgggtcc tgccttcaag ttctttcaag tttttatttt				1558
Ile Pro Arg *				
475				

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Met Thr Ala Ala Ala Ala Ser Asn Trp Gly Leu Ile Thr Asn
1 5 10
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Ile Val Asn Ser Ile Val Gly Val Ser Val Leu Thr Met Pro Phe Cys
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Phe Lys Gln Cys Gly Ile Val Leu Gly Ala Leu Leu Leu Val Phe Cys
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tca tgg atg acg cac cag tcg tgc atg ttc ttg gtg aag tcg gcc agc 552
Ser Trp Met Thr His Gln Ser Cys Met Phe Leu Val Lys Ser Ala Ser
47 52 57 62
ctg agc aag cgg agg acc tac gcc ggc ctg gca ttc cac gcc tac ggg 600
Leu Ser Lys Arg Arg Thr Tyr Ala Gly Leu Ala Phe His Ala Tyr Gly
63 68 73 78
aag gca ggc aag atg ctg gtg gag acc agc atg atc ggg ctg atg ctg 648
Lys Ala Gly Lys Met Leu Val Glu Thr Ser Met Ile Gly Leu Met Leu
79 84 89 94

ggc acc tgc atc gcc ttc tac gtc gtg atc ggc gac ttg ggg tcc aac	696
Gly Thr Cys Ile Ala Phe Tyr Val Val Ile Gly Asp Leu Gly Ser Asn	
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Phe Phe Ala Arg Leu Phe Gly Phe Gln Val Gly Gly Thr Phe Arg Met	
111 116 121 126	
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Phe Leu Leu Phe Ala Val Ser Leu Cys Ile Val Leu Pro Leu Ser Leu	
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Gln Arg Asn Met Met Ala Ser Ile Gln Ser Phe Ser Ala Met Ala Leu	
143 148 153 158	
ctc ttc tac acc gtg ttt atg ttc gtg atc gtg ctc tcc cct ctc aag	888
Leu Phe Tyr Thr Val Phe Met Phe Val Ile Val Leu Ser Pro Leu Lys	
159 164 169 174	
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His Gly Leu Phe Ser Gly Gln Trp Leu Arg Arg Val Ser Tyr Val Arg	
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Trp Glu Gly Val Phe Arg Cys Ile Pro Ile Phe Gly His Val Leu Arg	
191 196 201 206	
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tctttggact tagaagatga cctggataaa tgataaaaat taagaaagag attttgaagt	180
tttcttattg tcctcttggc atatgcttct ggaataatat tcacc atg gtt ttg	234
	Met Val Leu

1

gat gac ctt cca aac tta gaa gac atc tat act tcc ttg tgt tca tca	282
Asp Asp Leu Pro Asn Leu Glu Asp Ile Tyr Thr Ser Leu Cys Ser Ser	
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Thr Met Glu Asp Ser Glu Met Asp Phe Asp Ser Gly Leu Glu Asp Asp	
20 25 30 35	
gac aca aaa agt gat agt att ttg gag gat tcc aca att ttt gtg gcc	378
Asp Thr Lys Ser Asp Ser Ile Leu Glu Asp Ser Thr Ile Phe Val Ala	
36 41 46 51	
ttc aaa gga aat ata gat gat aaa gac ttc aaa tgg aaa tta gat gca	426
Phe Lys Gly Asn Ile Asp Asp Lys Asp Phe Lys Trp Lys Leu Asp Ala	
52 57 62 67	
ata ttg aaa aac gtg ccc aat ttg tta cac atg gag tcc agc aag cta	474
Ile Leu Lys Asn Val Pro Asn Leu Leu His Met Glu Ser Ser Lys Leu	
68 73 78 83	
aaa gta cag aag gtg gag ccc tgg aac agc gtg cgt gtg aca ttc aac	522
Lys Val Gln Lys Val Glu Pro Trp Asn Ser Val Arg Val Thr Phe Asn	
84 89 94 99	
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Ile Pro Arg Glu Ala Ala Glu Arg Leu Arg Ile Leu Ala Gln Ser Asn	
100 105 110 115	
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Asn Gln Gln Leu Arg Asp Leu Gly Ile Leu Ser Val Gln Ile Glu Gly	
116 121 126 131	
gaa ggt gct att aac ctg gct ttg gct cag aac cga agc caa gat gtg	666
Glu Gly Ala Ile Asn Leu Ala Leu Ala Gln Asn Arg Ser Gln Asp Val	
132 137 142 147	
aga atg aat gga ccc atg gga gct gga aat tca gtt agg atg gag gcg	714
Arg Met Asn Gly Pro Met Gly Ala Gly Asn Ser Val Arg Met Glu Ala	
148 153 158 163	
gga ttt cct atg gca agt ggt cca gga ata ata agg atg aac aac cct	762
Gly Phe Pro Met Ala Ser Gly Pro Gly Ile Ile Arg Met Asn Asn Pro	
164 169 174 179	
gcc act gtt atg ata ccc ccg ggt gga aat gtg tca tct tcc atg atg	810
Ala Thr Val Met Ile Pro Pro Gly Gly Asn Val Ser Ser Ser Met Met	
180 185 190 195	
gca cca ggc ccc aat cca gag ctg cag ccc agg act cct cgc cct gct	858
Ala Pro Gly Pro Asn Pro Glu Leu Gln Pro Arg Thr Pro Arg Pro Ala	
196 201 206 211	
tct cag tca gat gca atg gat cca ctc ctc tct ggg ctc cat ata cag	906
Ser Gln Ser Asp Ala Met Asp Pro Leu Leu Ser Gly Leu His Ile Gln	
212 217 222 227	

cag caa agt cat ccc tca gga tct tta gct ccc cca cat cac cca atg	954
Gln Gln Ser His Pro Ser Gly Ser Leu Ala Pro Pro His His Pro Met	
228 233 238 243	
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Gln Pro Val Ser Val Asn Arg Gln Met Asn Pro Ala Asn Phe Pro Gln	
244 249 254 259	
ctg cag cag cag cag caa caa caa caa cag cag cag cag cag cag cag	1050
Leu Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln	
260 265 270 275	
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Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Leu Gln Ala Arg Pro Pro	
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Gln Gln His Gln Gln Gln Gln Pro Gln Gly Ile Arg Pro Gln Phe Thr	
292 297 302 307	
gcc cca act cag gtg cct gtt cct cca ggc tgg aac cag ctg cct tct	1194
Ala Pro Thr Gln Val Pro Val Pro Pro Gly Trp Asn Gln Leu Pro Ser	
308 313 318 323	
gga gcc ctt caa cct cct cca gcc cag ggt tct ctg ggc aca atg act	1242
Gly Ala Leu Gln Pro Pro Pro Ala Gln Gly Ser Leu Gly Thr Met Thr	
324 329 334 339	
gca aac caa ggg tgg aag aag gct ccc ttg ccc ggc cca atg caa cag	1290
Ala Asn Gln Gly Trp Lys Lys Ala Pro Leu Pro Gly Pro Met Gln Gln	
340 345 350 355	
caa ctc cag gca aga cca tcc tta gcc acg gta cag acg cct tcc cac	1338
Gln Leu Gln Ala Arg Pro Ser Leu Ala Thr Val Gln Thr Pro Ser His	
356 361 366 371	
cct ccc cct cca tat ccc ttt ggc agc cag caa gcc tca caa gcc cac	1386
Pro Pro Pro Pro Tyr Pro Phe Gly Ser Gln Gln Ala Ser Gln Ala His	
372 377 382 387	
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Thr Asn Phe Pro Gln Met Ser Asn Pro Gly Gln Phe Thr Ala Pro Gln	
388 393 398 403	
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Met Lys Ser Leu Gln Gly Gly Pro Ser Arg Val Pro Thr Pro Leu Gln	
404 409 414 419	
cag ccc cac ctc acc aac aag tct cct gcc tcc tca ccc tcc tcc ttc	1530
Gln Pro His Leu Thr Asn Lys Ser Pro Ala Ser Ser Pro Ser Ser Phe	
420 425 430 435	
cag cag gga tcc cct gca tcc tcc cca acg gtt aac caa act cag cag	1578
Gln Gln Gly Ser Pro Ala Ser Ser Pro Thr Val Asn Gln Thr Gln Gln	
436 441 446 451	
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Gln Met Gly Pro Arg Pro Pro Gln Asn Asn Pro Leu Pro Gln Gly Phe	
452 457 462 467	
cag cag cct gtc agc tct ccg ggt cgg aat cct atg gtt caa cag gga	1674
Gln Gln Pro Val Ser Ser Pro Gly Arg Asn Pro Met Val Gln Gln Gly	
468 473 478 483	
aat gtg cca cct aac ttc atg gtg atg cag cag caa cca cca aac cag	1722
Asn Val Pro Pro Asn Phe Met Val Met Gln Gln Gln Pro Pro Asn Gln	
484 489 494 499	
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Gly Pro Gln Ser Leu His Pro Gly Leu Gly Gly Met Pro Lys Arg Leu	
500 505 510 515	
cca cct ggc ttc tca gca gga cag gcc aat ccg aac ttt atg caa ggt	1818
Pro Pro Gly Phe Ser Ala Gly Gln Ala Asn Pro Asn Phe Met Gln Gly	
516 521 526 531	
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Gln Val Pro Ser Thr Thr Ala Thr Thr Pro Gly Asn Ser Gly Ala Pro	
532 537 542 547	
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Gln Leu Gln Ala Asn Gln Asn Val Gln His Ala Gly Gly Gln Gly Ala	
548 553 558 563	
ggg cct cct caa aac cag atg cag gtg tcc cac ggg ccg cca aat atg	1962
Gly Pro Pro Gln Asn Gln Met Gln Val Ser His Gly Pro Pro Asn Met	
564 569 574 579	
atg cag ccc agc ctc atg gga att cat ggc aac atg aac aat cag cag	2010
Met Gln Pro Ser Leu Met Gly Ile His Gly Asn Met Asn Asn Gln Gln	
580 585 590 595	
gct ggt act tct ggg gtt cct caa gtg aac ctc agc aac atg caa ggc	2058
Ala Gly Thr Ser Gly Val Pro Gln Val Asn Leu Ser Asn Met Gln Gly	
596 601 606 611	
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Gln Pro Gln Gln Gly Pro Pro Ser Gln Leu Met Gly Met His Gln Gln	
612 617 622 627	
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Ile Val Pro Ser Gln Gly Gln Met Val Gln Gln Gln Gly Thr Leu Asn	
628 633 638 643	
cct cag aac cct atg atc ctt tca agg gcc cag ctt atg cca cag ggc	2202
Pro Gln Asn Pro Met Ile Leu Ser Arg Ala Gln Leu Met Pro Gln Gly	
644 649 654 659	
cag atg atg gtg aac ccc ccg agc caa aat ctt ggg ccc tcg ccc caa	2250
Gln Met Met Val Asn Pro Pro Ser Gln Asn Leu Gly Pro Ser Pro Gln	
660 665 670 675	
agg atg acc cca ccc aag cag atg ctt tcc cag cag ggc cca caa atg	2298
Arg Met Thr Pro Pro Lys Gln Met Leu Ser Gln Gln Gly Pro Gln Met	

676	681	686	691	
atg gcg cca cat aac cag atg atg ggg cct cag ggg cag gtt ttg ctc				2346
Met Ala Pro His Asn Gln Met Met Gly Pro Gln Gly Gln Val Leu Leu				
692	697	702	707	
caa cag aac cca atg ata gag cag att atg acc aat caa atg cag ggg				2394
Gln Gln Asn Pro Met Ile Glu Gln Ile Met Thr Asn Gln Met Gln Gly				
708	713	718	723	
aat aag cag cag ttt aac act cag aac cag tcc aat gtc atg ccg gga				2442
Asn Lys Gln Gln Phe Asn Thr Gln Asn Gln Ser Asn Val Met Pro Gly				
724	729	734	739	
cca gcc cag ata atg agg gga cca act cca aac atg caa gga aat atg				2490
Pro Ala Gln Ile Met Arg Gly Pro Thr Pro Asn Met Gln Gly Asn Met				
740	745	750	755	
gtg cag ttt acg gga cag atg tca gga cag atg ctg ccc cag caa ggg				2538
Val Gln Phe Thr Gly Gln Met Ser Gly Gln Met Leu Pro Gln Gln Gly				
756	761	766	771	
cct gtg aac aac agt cca tct cag gtt atg ggc att cag gga cag gtc				2586
Pro Val Asn Asn Ser Pro Ser Gln Val Met Gly Ile Gln Gly Gln Val				
772	777	782	787	
ctg cgg cca cca ggg ccc agc cca cac atg gcc cag cag cat ggt gat				2634
Leu Arg Pro Pro Gly Pro Ser Pro His Met Ala Gln Gln His Gly Asp				
788	793	798	803	
cct gct act aca gca aat aac gat gtc agt tta tct cag atg atg cct				2682
Pro Ala Thr Thr Ala Asn Asn Asp Val Ser Leu Ser Gln Met Met Pro				
804	809	814	819	
gat gtt agc att caa caa acc aac atg gtc ccc cct cat gtg cag gcc				2730
Asp Val Ser Ile Gln Gln Thr Asn Met Val Pro Pro His Val Gln Ala				
820	825	830	835	
atg cag gga aac agt gcc tcg gga aac cac ttc tca ggc cat ggg atg				2778
Met Gln Gly Asn Ser Ala Ser Gly Asn His Phe Ser Gly His Gly Met				
836	841	846	851	
tct ttc aat gca cct ttc agt gga gct ccc aat gga aat cag atg tcc				2826
Ser Phe Asn Ala Pro Phe Ser Gly Ala Pro Asn Gly Asn Gln Met Ser				
852	857	862	867	
tgt ggt caa aat cca ggc ttc cca gtc aat aag gat gtc acg cta acg				2874
Cys Gly Gln Asn Pro Gly Phe Pro Val Asn Lys Asp Val Thr Leu Thr				
868	873	878	883	
agc cca ttg ttg gtc aac tta ttg cag agt gac ata tct gca ggc cat				2922
Ser Pro Leu Leu Val Asn Leu Leu Gln Ser Asp Ile Ser Ala Gly His				
884	889	894	899	
ttt ggg gta aac aat aag caa aat aat acc aac gca aat aaa ccg aag				2970
Phe Gly Val Asn Asn Lys Gln Asn Asn Thr Asn Ala Asn Lys Pro Lys				
900	905	910	915	

aag aag aaa ccc cct cgg aag aag aaa aat agt cag caa gat cta aac	3018
Lys Lys Lys Pro Pro Arg Lys Lys Lys Asn Ser Gln Gln Asp Leu Asn	
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acc cca gat act cgc cca gct ggt ctg gaa gag gct gat cag cca ccg	3066
Thr Pro Asp Thr Arg Pro Ala Gly Leu Glu Glu Ala Asp Gln Pro Pro	
932 937 942 947	
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Leu Pro Gly Glu Gln Gly Ile Ser Leu Asp Asn Ser Gly Pro Lys Leu	
948 953 958 963	
cca gaa ttt tca aac cgg cca cca ggt tat cct tct caa cca gtt gaa	3162
Pro Glu Phe Ser Asn Arg Pro Pro Gly Tyr Pro Ser Gln Pro Val Glu	
964 969 974 979	
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Gln Arg Pro Leu Gln Gln Met Pro Pro Gln Leu Met Gln His Val Ala	
980 985 990 995	
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Pro Pro Pro Gln Pro Pro Gln Gln Gln Pro Gln Pro Gln Leu Pro Gln	
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Gln Gln Gln Pro Pro Pro Pro Ser Gln Pro Gln Ser Gln Gln Gln Gln	
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Gln Gln Gln Gln Gln Met Met Met Met Leu Met Met Gln Gln Asp Pro	
1028 1033 1038 1043	
aaa tca gtt agg ctt cca gtc tct caa aat gtc cat cct cca agg ggc	3402
Lys Ser Val Arg Leu Pro Val Ser Gln Asn Val His Pro Pro Arg Gly	
1044 1049 1054 1059	
ccc ctg aac ccc gac tcc cag aga atg ccc atg caa cag agt ggc agt	3450
Pro Leu Asn Pro Asp Ser Gln Arg Met Pro Met Gln Gln Ser Gly Ser	
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Val Pro Val Met Val Ser Leu Gln Gly Pro Ala Ser Val Pro Pro Ser	
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Pro Asp Lys Gln Arg Met Pro Met Pro Val Asn Thr Pro Leu Gly Ser	
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1124 1129 1134 1139	

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Ala Pro Ser Val Pro Gly Gly Pro Asn Asn Met Pro Ser His Val Val	
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Ser Leu Pro Ser Ser His Gly His His Phe Pro Asn Val Ala Ala Pro	
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Tyr Tyr Pro Gln Thr Pro Asn Asn Arg Pro Pro Ser Thr Glu Pro Ser	
1220 1225 1230 1235	
gaa atc agt ctg tca cca gaa aga ctc aat gcc tcc ata gca gga ctc	3978
Glu Ile Ser Leu Ser Pro Glu Arg Leu Asn Ala Ser Ile Ala Gly Leu	
1236 1241 1246 1251	
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Phe Pro Pro Gln Ile Asn Ile Pro Leu Pro Pro Arg Pro Asn Leu Asn	
1252 1257 1262 1267	
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Arg Gly Phe Asp Gln Gln Gly Leu Asn Pro Thr Ile Leu Lys Ala Ile	
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Gly Gln Ala Pro Ser Asn Leu Thr Met Asn Pro Ser Asn Phe Ala Thr	
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cca caa act cac aaa tta gat tct gtg gta gtg aat tct gga aag cag	4170
Pro Gln Thr His Lys Leu Asp Ser Val Val Asn Ser Gly Lys Gln	
1300 1305 1310 1315	
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Ser Asn Ser Gly Ala Thr Lys Arg Ala Ser Pro Ser Asn Ser Arg Arg	
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Ser Ser Pro Gly Ser Ser Arg Lys Thr Thr Pro Ser Pro Gly Arg Gln	
1332 1337 1342 1347	
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Asn Ser Lys Ala Pro Lys Leu Thr Leu Ala Ser Gln Thr Asn Ala Ala	
1348 1353 1358 1363	
cta ttg cag aat gtg gag ttg ccg aga aat gta ttg gtc agt ccc act	4362

Leu	Leu	Gln	Asn	Val	Glu	Leu	Pro	Arg	Asn	Val	Leu	Val	Ser	Pro	Thr		
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Pro	Leu	Ala	Asn	Pro	Pro	Val	Pro	Gly	Ser	Phe	Pro	Asn	Asn	Ser	Gly		
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Leu	Asn	Pro	Gln	Asn	Ser	Thr	Val	Ser	Val	Ala	Ala	Val	Gly	Gly	Val		
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Gln	Asn	Ser	Gln	Ser	Arg	Lys	Glu	Gln	Val	Asn	Ile	Glu	Leu	Lys	Ala		
1428					1433					1438					1443		
gtc	cct	gcc	caa	gaa	gtt	aaa	atg	gtt	gtc	cct	gaa	gat	cag	tcc	aaa	4602	
Val	Pro	Ala	Gln	Glu	Val	Lys	Met	Val	Val	Pro	Glu	Asp	Gln	Ser	Lys		
1444					1449					1454					1459		
aag	gat	ggg	cag	cct	tcg	gat	cct	aac	aaa	ctt	ccc	agt	gtc	gaa	gag	4650	
Lys	Asp	Gly	Gln	Pro	Ser	Asp	Pro	Asn	Lys	Leu	Pro	Ser	Val	Glu	Glu		
1460					1465					1470					1475		
aac	aaa	aat	ttg	gtg	tct	cct	gct	atg	agg	gaa	gca	cca	aca	tcg	tta	4698	
Asn	Lys	Asn	Leu	Val	Ser	Pro	Ala	Met	Arg	Glu	Ala	Pro	Thr	Ser	Leu		
1476					1481					1486					1491		
agt	caa	ctt	ctt	gac	aac	tct	gga	gct	ccc	aat	gtg	aca	att	aaa	ccc	4746	
Ser	Gln	Leu	Leu	Asp	Asn	Ser	Gly	Ala	Pro	Asn	Val	Thr	Ile	Lys	Pro		
1492					1497					1502					1507		
cct	ggg	ctt	aca	gat	ctg	gaa	gta	aca	cct	cca	gta	gtt	tct	ggg	gag	4794	
Pro	Gly	Leu	Thr	Asp	Leu	Glu	Val	Thr	Pro	Pro	Val	Val	Ser	Gly	Glu		
1508					1513					1518					1523		
gac	ctc	aaa	aaa	gca	tct	gtc	att	ccc	aca	ctg	cag	gat	ctg	tct	tct	4842	
Asp	Leu	Lys	Lys	Ala	Ser	Val	Ile	Pro	Thr	Leu	Gln	Asp	Leu	Ser	Ser		
1524					1529					1534					1539		
tct	aaa	gaa	cct	tct	aat	tcc	cta	aac	tta	cct	cac	agt	aat	gag	ctg	4890	
Ser	Lys	Glu	Pro	Ser	Asn	Ser	Leu	Asn	Leu	Pro	His	Ser	Asn	Glu	Leu		
1540					1545					1550					1555		
tgt	tca	tcc	ctt	gtg	cat	ccc	gaa	ttg	agt	gag	gtc	agt	tct	aac	gtt	4938	
Cys	Ser	Ser	Leu	Val	His	Pro	Glu	Leu	Ser	Glu	Val	Ser	Ser	Ser	Val		
1556					1561					1566					1571		
gca	cca	agc	atc	cct	cca	gta	atg	tca	aga	cct	gtt	agc	tct	tcc	tcc	4986	
Ala	Pro	Ser	Ile	Pro	Pro	Val	Met	Ser	Arg	Pro	Val	Ser	Ser	Ser	Ser		
1572					1577					1582					1587		
att	tcc	act	ccc	ttg	ccc	cca	aat	caa	ata	act	gta	ttt	gtc	act	tcc	5034	
Ile	Ser	Thr	Pro	Leu	Pro	Pro	Asn	Gln	Ile	Thr	Val	Phe	Val	Thr	Ser		

1588	1593	1598	1603	
aat ccc atc aca act tca gct aac aca tca gca gct ttg cca act cac				5082
Asn Pro Ile Thr Thr Ser Ala Asn Thr Ser Ala Ala Leu Pro Thr His				
1604	1609	1614	1619	
ttg cag tct gca ttg atg tca aca gtt gtc aca atg ccc aat gcg ggt				5130
Leu Gln Ser Ala Leu Met Ser Thr Val Val Thr Met Pro Asn Ala Gly				
1620	1625	1630	1635	
agc aag gtt atg gtt tct gag gga cag tca gct gct cag tct aat gcc				5178
Ser Lys Val Met Val Ser Glu Gly Gln Ser Ala Ala Gln Ser Asn Ala				
1636	1641	1646	1651	
cgg cct cag ttc att aca cct gtc ttt atc aat tca tcc tca ata att				5226
Arg Pro Gln Phe Ile Thr Pro Val Phe Ile Asn Ser Ser Ser Ile Ile				
1652	1657	1662	1667	
cag gtt atg aaa gga tca cag cca agc aca att cct gca gcc cca ctg				5274
Gln Val Met Lys Gly Ser Gln Pro Ser Thr Ile Pro Ala Ala Pro Leu				
1668	1673	1678	1683	
aca acc aac tct ggc ctg atg cct ccc tct gtt gca gtt gtt ggc cct				5322
Thr Thr Asn Ser Gly Leu Met Pro Pro Ser Val Ala Val Val Gly Pro				
1684	1689	1694	1699	
tta cac ata cct cag aac ata aaa ttt tct tct gct cct gta ccg cct				5370
Leu His Ile Pro Gln Asn Ile Lys Phe Ser Ser Ala Pro Val Pro Pro				
1700	1705	1710	1715	
aat gcc ctc tcc agt agt cct gct cca aac atc cag aca ggt cga cct				5418
Asn Ala Leu Ser Ser Ser Pro Ala Pro Asn Ile Gln Thr Gly Arg Pro				
1716	1721	1726	1731	
ttg gtc ctt agc tca cga gcc acc cct gtt cag ctt cct tcc cct cct				5466
Leu Val Leu Ser Ser Arg Ala Thr Pro Val Gln Leu Pro Ser Pro Pro				
1732	1737	1742	1747	
tgt acg tct tct cca gtt gtc cct tct cat ccc cct gtg cag caa gtg				5514
Cys Thr Ser Ser Pro Val Val Pro Ser His Pro Pro Val Gln Gln Val				
1748	1753	1758	1763	
aaa gaa ttg aat cca gat gag gct agc cct cag gtg aac acc tca gca				5562
Lys Glu Leu Asn Pro Asp Glu Ala Ser Pro Gln Val Asn Thr Ser Ala				
1764	1769	1774	1779	
gat cag aac act ctt ccc tct tca cag tca acc aca atg gtt tct ccc				5610
Asp Gln Asn Thr Leu Pro Ser Ser Gln Ser Thr Thr Met Val Ser Pro				
1780	1785	1790	1795	
ctt ttg acc aat agt cca ggg tcc tct ggc aac cgg cga agc cca gtc				5658
Leu Leu Thr Asn Ser Pro Gly Ser Ser Gly Asn Arg Arg Ser Pro Val				
1796	1801	1806	1811	
tcg tct agt aag ggc aaa gga aaa gtg gac aaa att ggc caa att ttg				5706
Ser Ser Ser Lys Gly Lys Gly Lys Val Asp Lys Ile Gly Gln Ile Leu				
1812	1817	1822	1827	

ttg acc aag gca tgt aag aaa gtt aca ggc tct ctt gag aaa ggg gaa	5754
Leu Thr Lys Ala Cys Lys Lys Val Thr Gly Ser Leu Glu Lys Gly Glu	
1828 1833 1838 1843	
gaa caa tat ggt gca gat gga gag act gaa ggc caa ggg cta gac acc	5802
Glu Gln Tyr Gly Ala Asp Gly Glu Thr Glu Gly Gln Gly Leu Asp Thr	
1844 1849 1854 1859	
aca gct ccg ggg ctc atg gga aca gag cag tta tcc aca gag ctg gac	5850
Thr Ala Pro Gly Leu Met Gly Thr Glu Gln Leu Ser Thr Glu Leu Asp	
1860 1865 1870 1875	
agt aaa acc cca acg ccc cca gca ccc act ctg cta aaa atg acc tct	5898
Ser Lys Thr Pro Thr Pro Pro Ala Pro Thr Leu Leu Lys Met Thr Ser	
1876 1881 1886 1891	
agc cct gtg ggc ccg ggc act gcc tca gca gga ccc agc tta cct ggc	5946
Ser Pro Val Gly Pro Gly Thr Ala Ser Ala Gly Pro Ser Leu Pro Gly	
1892 1897 1902 1907	
ggt gct ctc ccc acc agt gta cgc tcg ata gta acc act ctg gta ccc	5994
Gly Ala Leu Pro Thr Ser Val Arg Ser Ile Val Thr Thr Leu Val Pro	
1908 1913 1918 1923	
tcc gag ctc atc tcc gcc gta ccg acc aca aaa agc aat cat ggt ggc	6042
Ser Glu Leu Ile Ser Ala Val Pro Thr Thr Lys Ser Asn His Gly Gly	
1924 1929 1934 1939	
ata gca tct gag tca ctt gcg ggt ggc cta gtg gag gag aag gtg gga	6090
Ile Ala Ser Glu Ser Leu Ala Gly Gly Leu Val Glu Glu Lys Val Gly	
1940 1945 1950 1955	
tcc cat cca gaa ctt cta ccc agc ata gcc ccg tcg cag aat tta gtc	6138
Ser His Pro Glu Leu Leu Pro Ser Ile Ala Pro Ser Gln Asn Leu Val	
1956 1961 1966 1971	
tca aag gaa act tca acc aca gca ctg cag gcc tct gtt gcc aga cca	6186
Ser Lys Glu Thr Ser Thr Thr Ala Leu Gln Ala Ser Val Ala Arg Pro	
1972 1977 1982 1987	
gag ctg gag gta aat gct gcc ata gtc tct gga caa agc agt gag ccc	6234
Glu Leu Glu Val Asn Ala Ala Ile Val Ser Gly Gln Ser Ser Glu Pro	
1988 1993 1998 2003	
aaa gag ata gtt gaa aag tcc aaa atc cca ggc cga aga aac tcc cga	6282
Lys Glu Ile Val Glu Lys Ser Lys Ile Pro Gly Arg Arg Asn Ser Arg	
2004 2009 2014 2019	
act gaa gag cca act gtg gcc tct gaa agt gtg gaa aat gga cat cgt	6330
Thr Glu Glu Pro Thr Val Ala Ser Glu Ser Val Glu Asn Gly His Arg	
2020 2025 2030 2035	
aaa cga tct tct cga cct gct tca gcc tcc agc tct act aaa gac ata	6378
Lys Arg Ser Ser Arg Pro Ala Ser Ala Ser Ser Ser Thr Lys Asp Ile	
2036 2041 2046 2051	

acc agt gcg gtg caa tcc aag cga aga aaa tcc aag taa acaagcagga 6427
 Thr Ser Ala Val Gln Ser Lys Arg Arg Lys Ser Lys *
 2052 2057 2062

ctgcgacttg atacttgga atgtgtgtga cttttacaaa gagcaatttt gagctgtgac 6487

ttttttaaat caatttctgt acagttagta attttaataa tgtggccctt ttcctagtcc 6547

ctgcaacctg tttcataaag tgcaatgggg aaagcaggac tgttgagccc ttttggtgtt 6607

gcgagttgaa gttcaagggt tctaaaatgt tgtcttgtat tgaaaggagc taatgccatt 6667

ataaatgtta ctagttttca catttcctaa gcagcctaga gtacaggggtg agcattttta 6727

gatctcctaa tgatattgtg ccgtggaagt actgtgtgtg aatagcagta gtgggggcaa 6787

aagcaatctt ctcatttga aatgttgtta ataattttat tatatagtgt tttggatgta 6847

tttgtttag aaatggacca gtgaataaag agaatctaag gatttgtaca atgtgaaata 6907

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tgtgagtctc tcgccgccgg aggaag atg agg ctg aag att gga ttc atc tta 113
 Met Arg Leu Lys Ile Gly Phe Ile Leu
 1 5

cgc agt ttg ctg gtg gtg gga agc ttc ctg ggg cta gtg gtc ctc tgg 161
 Arg Ser Leu Leu Val Val Gly Ser Phe Leu Gly Leu Val Val Leu Trp
 10 15 20 25

tct tcc ctg acc ccg cgg ccg gac gac cca agc ccg ctg agc agg atg 209
 Ser Ser Leu Thr Pro Arg Pro Asp Asp Pro Ser Pro Leu Ser Arg Met
 26 31 36 41

agg gaa gac aga gat gtc aat gac ccc atg ccc aac cga ggc ggc aat 257
 Arg Glu Asp Arg Asp Val Asn Asp Pro Met Pro Asn Arg Gly Gly Asn
 42 47 52 57

gga cta gct cct ggg gag gac aga ttc aaa cct gtg gta cca tgg cct 305
 Gly Leu Ala Pro Gly Glu Asp Arg Phe Lys Pro Val Val Pro Trp Pro

58	63	68	73	
cat gtt gaa gga gta gaa gtg gac tta gag tct att aga aga ata aac				353
His Val Glu Gly Val Glu Val Asp Leu Glu Ser Ile Arg Arg Ile Asn				
74	79	84	89	
aag gcc aaa aat gaa caa gag cac cat gct gga gga gat tcc cag aaa				401
Lys Ala Lys Asn Glu Gln Glu His His Ala Gly Gly Asp Ser Gln Lys				
90	95	100	105	
gat atc atg cag agg cag tat ctc aca ttt aag cct cag aca ttc acc				449
Asp Ile Met Gln Arg Gln Tyr Leu Thr Phe Lys Pro Gln Thr Phe Thr				
106	111	116	121	
tac cat gat cct gtg ctt cgc cca ggg atc ctc ggt aac ttt gaa ccc				497
Tyr His Asp Pro Val Leu Arg Pro Gly Ile Leu Gly Asn Phe Glu Pro				
122	127	132	137	
aaa gaa cct gag cct cct gga gtg gtt ggt ggc cct ggg aga gaa agc				545
Lys Glu Pro Glu Pro Pro Gly Val Val Gly Gly Pro Gly Arg Glu Ser				
138	143	148	153	
caa gcc att ggt ttt ggg gcc cag aat tta aac aag caa ttc aag cca				593
Gln Ala Ile Gly Phe Gly Ala Gln Asn Leu Asn Lys Gln Phe Lys Pro				
154	159	164	169	
gca ttt aaa gag ttt ggg ttt aac atg gtg gca agt gac atg ttc tca				641
Ala Phe Lys Glu Phe Gly Phe Asn Met Val Ala Ser Asp Met Phe Ser				
170	175	180	185	
ctg gac cgc aac gtc aat gac tta cgc caa gaa gaa tgc aag tat tgg				689
Leu Asp Arg Asn Val Asn Asp Leu Arg Gln Glu Glu Cys Lys Tyr Trp				
186	191	196	201	
cat tat gat gaa aac ttg ctc act tcg agc gtt gtc att gtc ttc cat				737
His Tyr Asp Glu Asn Leu Leu Thr Ser Ser Val Val Ile Val Phe His				
202	207	212	217	
aat gaa gga tgg tca acc ctc atg aga aca gtc cac agt gta att aaa				785
Asn Glu Gly Trp Ser Thr Leu Met Arg Thr Val His Ser Val Ile Lys				
218	223	228	233	
agg act cca agg aaa tat tta gca gaa att gtg tta att gac gat ttc				833
Arg Thr Pro Arg Lys Tyr Leu Ala Glu Ile Val Leu Ile Asp Asp Phe				
234	239	244	249	
agt aat aaa gaa cac tta aaa gaa aaa ctg gat gaa tat att aag ctg				881
Ser Asn Lys Glu His Leu Lys Glu Lys Leu Asp Glu Tyr Ile Lys Leu				
250	255	260	265	
tgg aat ggc cta gtg aag gta ttt cga aat gaa aga agg gaa ggt tta				929
Trp Asn Gly Leu Val Lys Val Phe Arg Asn Glu Arg Arg Glu Gly Leu				
266	271	276	281	
att caa gca cga agt att ggt gct cag aag gct aaa ctt gga cag gtt				977
Ile Gln Ala Arg Ser Ile Gly Ala Gln Lys Ala Lys Leu Gly Gln Val				
282	287	292	297	

ttg ata tac ctt gat gcc cac tgt gag gtg gca gtt aac tgg tat gca	1025
Leu Ile Tyr Leu Asp Ala His Cys Glu Val Ala Val Asn Trp Tyr Ala	
298 303 308 313	
cca ctt gta gct ccc ata tct aag gac aga acc att tgc act gtg ccg	1073
Pro Leu Val Ala Pro Ile Ser Lys Asp Arg Thr Ile Cys Thr Val Pro	
314 319 324 329	
ctt ata gat gtc ata aat ggc aac aca tat gaa att ata ccc caa ggg	1121
Leu Ile Asp Val Ile Asn Gly Asn Thr Tyr Glu Ile Ile Pro Gln Gly	
330 335 340 345	
ggg ggt gat gaa gat ggg tat gcc cga gga gca tgg gat tgg agt atg	1169
Gly Gly Asp Glu Asp Gly Tyr Ala Arg Gly Ala Trp Asp Trp Ser Met	
346 351 356 361	
ctc tgg aaa cgg gtg cct ctg acc cct caa gag aag aga ctg aga aag	1217
Leu Trp Lys Arg Val Pro Leu Thr Pro Gln Glu Lys Arg Leu Arg Lys	
362 367 372 377	
aca aaa act gaa ccg tat cgg tcc cca gcc atg gct ggg gga tta tgt	1265
Thr Lys Thr Glu Pro Tyr Arg Ser Pro Ala Met Ala Gly Gly Leu Cys	
378 383 388 393	
gcc att gaa cga gag ttc ttc ttt gaa ttg ggt ctc tat gat cca ggt	1313
Ala Ile Glu Arg Glu Phe Phe Phe Glu Leu Gly Leu Tyr Asp Pro Gly	
394 399 404 409	
ctc cag att tgg ggt ggt gaa aac ttt gag atc tca tac aag ata tgg	1361
Leu Gln Ile Trp Gly Gly Glu Asn Phe Glu Ile Ser Tyr Lys Ile Trp	
410 415 420 425	
cag tgt ggt ggc aaa tta tta ttt gtt cct tgt tct cgt gtt gga cat	1409
Gln Cys Gly Gly Lys Leu Leu Phe Val Pro Cys Ser Arg Val Gly His	
426 431 436 441	
atc tac cgt ctt gag ggc tgg caa gga aat cct ccg ccc att tat gtt	1457
Ile Tyr Arg Leu Glu Gly Trp Gln Gly Asn Pro Pro Pro Ile Tyr Val	
442 447 452 457	
ggg tct tct cca act ctg aag aat tat gtt aga gtt gtg gag gtt tgg	1505
Gly Ser Ser Pro Thr Leu Lys Asn Tyr Val Arg Val Val Glu Val Trp	
458 463 468 473	
tgg gat gaa tat aaa gac tac ttc tat gct agt cgt cct gaa tcg cag	1553
Trp Asp Glu Tyr Lys Asp Tyr Phe Tyr Ala Ser Arg Pro Glu Ser Gln	
474 479 484 489	
gca tta cca tat ggg gat ata tcg gag ctg aaa aaa ttt cga gaa gat	1601
Ala Leu Pro Tyr Gly Asp Ile Ser Glu Leu Lys Lys Phe Arg Glu Asp	
490 495 500 505	
cac aac tgc aaa agt ttt aag tgg ttc atg gaa gaa ata gct tat gat	1649
His Asn Cys Lys Ser Phe Lys Trp Phe Met Glu Glu Ile Ala Tyr Asp	
506 511 516 521	

atc acc tca cac tac cct ttg cca ccc aaa aat gtt gac tgg gga gaa	1697
Ile Thr Ser His Tyr Pro Leu Pro Pro Lys Asn Val Asp Trp Gly Glu	
522 527 532 537	
atc aga ggc ttc gaa act gct tac tgc att gat agc atg gga aaa aca	1745
Ile Arg Gly Phe Glu Thr Ala Tyr Cys Ile Asp Ser Met Gly Lys Thr	
538 543 548 553	
aat gga ggc ttt gtt gaa cta gga ccc tgc cac agg atg gga ggg aat	1793
Asn Gly Gly Phe Val Glu Leu Gly Pro Cys His Arg Met Gly Gly Asn	
554 559 564 569	
cag ctt ttc aga atc aat gaa gca aat caa ctc atg cag tat gac cag	1841
Gln Leu Phe Arg Ile Asn Glu Ala Asn Gln Leu Met Gln Tyr Asp Gln	
570 575 580 585	
tgt ttg aca aag gga gct gat gga tca aaa gtt atg att aca cac tgt	1889
Cys Leu Thr Lys Gly Ala Asp Gly Ser Lys Val Met Ile Thr His Cys	
586 591 596 601	
aat cta aat gaa ttt aag gaa tgg cag tac ttc aag aac ctg cac aga	1937
Asn Leu Asn Glu Phe Lys Glu Trp Gln Tyr Phe Lys Asn Leu His Arg	
602 607 612 617	
ttt act cat att cct tca gga aag tgt tta gat cgc tca gag gtc ctg	1985
Phe Thr His Ile Pro Ser Gly Lys Cys Leu Asp Arg Ser Glu Val Leu	
618 623 628 633	
cat caa gta ttc atc tcc aat tgt gac tcc agt aaa acg act caa aaa	2033
His Gln Val Phe Ile Ser Asn Cys Asp Ser Ser Lys Thr Thr Gln Lys	
634 639 644 649	
tggt gaa atg aat aac atc cat agt gtt tag a gagaaaaaaaa taaaccaata	2084
Trp Glu Met Asn Asn Ile His Ser Val *	
650 655	
acctacctac tgacaagtaa atttatacag gactgaaaac cgcttgaaac ctgctgcaac	2144
tattgttatt aactctgtat agctccaaac ctggaacctc ctgatcagtt tgaaggacat	2204
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Glu Ile Leu Asn Leu Thr Trp Trp Pro Leu Phe Arg Asp Val Ser Phe
186 191 196 201

tac att gtt gac ttg atc atg ctg atc ata ttt ttc ctg gat aat gtc 1035
Tyr Ile Val Asp Leu Ile Met Leu Ile Ile Phe Phe Leu Asp Asn Val
202 207 212 217

atc atg tgg tgg gaa agc ttg ctt ctc tta aca gct tat ttt tgc tat 1083
Ile Met Trp Trp Glu Ser Leu Leu Leu Leu Thr Ala Tyr Phe Cys Tyr
218 223 228 233

gtg gtt ttc atg aaa ttc aac gtc caa gta gaa aaa tgg gtg aag caa 1131
Val Val Phe Met Lys Phe Asn Val Gln Val Glu Lys Trp Val Lys Gln
234 239 244 249

atg ata aac cgc aat aag gtc gtc aag gtg aca gca cca gaa gcc caa 1179
Met Ile Asn Arg Asn Lys Val Val Lys Val Thr Ala Pro Glu Ala Gln
250 255 260 265

gca aag cca tct gca gcc agg gac aag gat gaa cca act cta ccg gct 1227
Ala Lys Pro Ser Ala Ala Arg Asp Lys Asp Glu Pro Thr Leu Pro Ala
266 271 276 281

aag ccg cgt ctc cag cga ggt gga agc tct gcc tcc ctc cac aac agt 1275
Lys Pro Arg Leu Gln Arg Gly Gly Ser Ser Ala Ser Leu His Asn Ser
282 287 292 297

ctc atg agg aat agc atc ttc caa ctc atg ata cac acc ctt gac cca 1323
Leu Met Arg Asn Ser Ile Phe Gln Leu Met Ile His Thr Leu Asp Pro
298 303 308 313

ctc gcc gaa gaa ctt gga tca tat gga aaa cta aaa tat tat gac aca 1371
Leu Ala Glu Glu Leu Gly Ser Tyr Gly Lys Leu Lys Tyr Tyr Asp Thr
314 319 324 329

atg act gaa gaa ggg agg ttc aga gaa aag gct tca att ctc cac aag 1419
Met Thr Glu Glu Gly Arg Phe Arg Glu Lys Ala Ser Ile Leu His Lys
330 335 340 345

atc gcc aag aag aaa tgt cat gtg gat gag aac gag cgg cag aat ggg 1467
Ile Ala Lys Lys Lys Cys His Val Asp Glu Asn Glu Arg Gln Asn Gly
346 351 356 361

gct gcc aac cac gtg gaa aaa att gag ctt cca aac agc acc agc aca 1515
Ala Ala Asn His Val Glu Lys Ile Glu Leu Pro Asn Ser Thr Ser Thr
362 367 372 377

gat gtt gaa atg aca cca tcc agt gat gct tca gaa cct gta caa aat 1563
Asp Val Glu Met Thr Pro Ser Ser Asp Ala Ser Glu Pro Val Gln Asn
378 383 388 393

gga aat ctc tcc cac aac att gaa ggt gca gaa gcc cag acc gct gat 1611
Gly Asn Leu Ser His Asn Ile Glu Gly Ala Glu Ala Gln Thr Ala Asp

394	399	404	409	
gag gag gag gac cag cct ctc agc ctt gcc tgg cct tct gaa acc cgc				1659
Glu Glu Glu Asp Gln Pro Leu Ser Leu Ala Trp Pro Ser Glu Thr Arg				
410	415	420	425	
aag caa gtc acg ttt ctg att gtt ttc ccc ata gtg ttt cct ctc tgg				1707
Lys Gln Val Thr Phe Leu Ile Val Phe Pro Ile Val Phe Pro Leu Trp				
426	431	436	441	
att acg tta cct gac gtt cgc aaa cct tca tgc agg aag ttt ttt ccc				1755
Ile Thr Leu Pro Asp Val Arg Lys Pro Ser Ser Arg Lys Phe Phe Pro				
442	447	452	457	
atc acg ttc ttt ggc tcc att acc tgg att gca gta ttc tct tac ttg				1803
Ile Thr Phe Phe Gly Ser Ile Thr Trp Ile Ala Val Phe Ser Tyr Leu				
458	463	468	473	
atg gtc tgg tgg gcg cac cag gtt gga gag aca att ggc atc agt gaa				1851
Met Val Trp Trp Ala His Gln Val Gly Glu Thr Ile Gly Ile Ser Glu				
474	479	484	489	
gag att atg ggc ctg acc atc ttg gct gct ggg acc tcc atc cct gat				1899
Glu Ile Met Gly Leu Thr Ile Leu Ala Ala Gly Thr Ser Ile Pro Asp				
490	495	500	505	
ctt atc acc agt gtc ata gtg gcc cgg aag ggg cta ggg gac atg gct				1947
Leu Ile Thr Ser Val Ile Val Ala Arg Lys Gly Leu Gly Asp Met Ala				
506	511	516	521	
gtg tcc agc tct gtt gga agc aac att ttt gac atc act gta ggg ctc				1995
Val Ser Ser Ser Val Gly Ser Asn Ile Phe Asp Ile Thr Val Gly Leu				
522	527	532	537	
cca ctg ccc tgg ctc ctg tac acc gtc att cac aga ttc cag cca gtg				2043
Pro Leu Pro Trp Leu Leu Tyr Thr Val Ile His Arg Phe Gln Pro Val				
538	543	548	553	
gct gtc agc agc aat ggc ctt ttc tgt gcc atc gtc ctt ctc ttc atc				2091
Ala Val Ser Ser Asn Gly Leu Phe Cys Ala Ile Val Leu Leu Phe Ile				
554	559	564	569	
atg ctg ctc ttc gtc atc ctc tct atc gcc ctc tgc aag tgg cga atg				2139
Met Leu Leu Phe Val Ile Leu Ser Ile Ala Leu Cys Lys Trp Arg Met				
570	575	580	585	
aac aaa atc ctg ggc ttc atc atg ttt ggc ctc tac ttt gtg ttc ctg				2187
Asn Lys Ile Leu Gly Phe Ile Met Phe Gly Leu Tyr Phe Val Phe Leu				
586	591	596	601	
gtg gtg agc gtt ctc cta gaa gac aga att ctt aca tgc ccc gtc tcc				2235
Val Val Ser Val Leu Leu Glu Asp Arg Ile Leu Thr Cys Pro Val Ser				
602	607	612	617	
atc tag caggaaaagc catatcttgc accagcagca tgaatggtcc ctccacactc				2291
Ile *				
618				

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tctgtttcct catctatcaa tgaagatgat actatgaacc caataaggct gttaaaacag	180
gtttttttatt acctaccacg gggggtgta catctctgac gtacagaagg aggacgcct	240
ctccacctat cgctgcatca ccaagcacia gtatagcggg gagaccggc agagcaatgg	300
ggcacgcctc tctgtgacag accctgctga gtgatcccc accatcctgg atggcttcca	360
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tatccccgcc atccgctggc tcaaggatgg ccggcccctc ccggctgaca gccgctggac	480
caagcgcctc acagggtgta ccatcagcga cttgcggacc gaggacagcg gcacctacat	540
ttgtgaggtc accaacacct tcggttcggc agaggccaca ggcatcctc	595
	atg gtc
	Met Val
	1

att gat ccc ctt cat gtg acc ctg aca cca aag aag ctg aag acc ggc	643
Ile Asp Pro Leu His Val Thr Leu Thr Pro Lys Lys Leu Lys Thr Gly	
3 8 13 18	

att ggc agc acg gtc atc ctc tcc tgt gcc ctg acg ggc tcc cca gag	691
Ile Gly Ser Thr Val Ile Leu Ser Cys Ala Leu Thr Gly Ser Pro Glu	
19 24 29 34	

ttc acc atc cgc tgg tat cgc aac acg gag ctg gtg ctg cct gac gag	739
Phe Thr Ile Arg Trp Tyr Arg Asn Thr Glu Leu Val Leu Pro Asp Glu	
35 40 45 50	

gcc atc tcc atc cgc ggg ctc agc aac gag acg ctg ctc atc acc tcg	787
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Ala	Ile	Ser	Ile	Arg	Gly	Leu	Ser	Asn	Glu	Thr	Leu	Leu	Ile	Thr	Ser		
51					56					61					66		
gcc	cag	aag	agc	cat	tcc	ggg	gcc	tac	cag	tgc	ttc	gct	acc	cgc	aag	835	
Ala	Gln	Lys	Ser	His	Ser	Gly	Ala	Tyr	Gln	Cys	Phe	Ala	Thr	Arg	Lys		
67					72					77					82		
gcc	cag	acc	gcc	cag	gac	ttt	gcc	atc	att	gca	ctt	gag	gat	ggc	acg	883	
Ala	Gln	Thr	Ala	Gln	Asp	Phe	Ala	Ile	Ile	Ala	Leu	Glu	Asp	Gly	Thr		
83					88					93					98		
ccc	cgc	atc	gtc	tgc	tcc	ttc	agc	gag	aag	gtg	gtc	aac	ccc	ggg	gag	931	
Pro	Arg	Ile	Val	Ser	Ser	Phe	Ser	Glu	Lys	Val	Val	Asn	Pro	Gly	Glu		
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Gln	Phe	Ser	Leu	Met	Cys	Ala	Ala	Lys	Gly	Ala	Pro	Pro	Pro	Thr	Val		
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acc	tgg	gcc	ctc	gac	gat	gag	ccc	atc	gtg	cgg	gat	ggc	agc	cac	cgc	1027	
Thr	Trp	Ala	Leu	Asp	Asp	Glu	Pro	Ile	Val	Arg	Asp	Gly	Ser	His	Arg		
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acc	aac	cag	tac	acc	atg	tgc	gac	ggc	acc	acc	atc	agc	cac	atg	aac	1075	
Thr	Asn	Gln	Tyr	Thr	Met	Ser	Asp	Gly	Thr	Thr	Ile	Ser	His	Met	Asn		
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Arg	Asn	Leu	Val	Gly	Ser	Ala	Glu	Tyr	Gln	Ala	Arg	Ile	Asn	Val	Arg		
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Gly	Pro	Pro	Ser	Ile	Arg	Ala	Met	Arg	Asn	Ile	Thr	Ala	Val	Ala	Gly		
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cgg	gac	acc	ctt	atc	aac	tgc	agg	gtc	atc	ggc	tat	ccc	tac	tac	tcc	1267	
Arg	Asp	Thr	Leu	Ile	Asn	Cys	Arg	Val	Ile	Gly	Tyr	Pro	Tyr	Tyr	Ser		
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atc	aag	tgg	tac	aag	gat	gcc	ctg	ctg	ctg	cca	gac	aac	cac	cgc	cag	1315	
Ile	Lys	Trp	Tyr	Lys	Asp	Ala	Leu	Leu	Leu	Pro	Asp	Asn	His	Arg	Gln		
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gtg	gtg	ttt	gag	aat	ggg	acc	ctc	aag	ctg	act	gac	gtg	cag	aag	ggc	1363	
Val	Val	Phe	Glu	Asn	Gly	Thr	Leu	Lys	Leu	Thr	Asp	Val	Gln	Lys	Gly		
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atg	gat	gag	ggg	gag	tac	ctg	tgc	agt	gtc	ctc	atc	cag	ccc	cag	ctc	1411	
Met	Asp	Glu	Gly	Glu	Tyr	Leu	Cys	Ser	Val	Leu	Ile	Gln	Pro	Gln	Leu		
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tcc	atc	agc	cag	agc	gtt	cac	gta	gcc	gtc	aaa	gtg	ccc	cct	ctg	atc	1459	
Ser	Ile	Ser	Gln	Ser	Val	His	Val	Ala	Val	Lys	Val	Pro	Pro	Leu	Ile		

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Gln Pro Phe Glu Phe Pro Pro Ala Ser Ile Gly Gln Leu Leu Tyr Ile				
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ccc tgt gtg gtg tcc tcg ggg gac atg ccc atc cgt atc acc tgg agg				1555
Pro Cys Val Val Ser Ser Gly Asp Met Pro Ile Arg Ile Thr Trp Arg				
307	312	317	322	
aag gac gga cag gtg atc atc tca ggc tcg ggc gtg acc atc gag agc				1603
Lys Asp Gly Gln Val Ile Ile Ser Gly Ser Gly Val Thr Ile Glu Ser				
323	328	333	338	
aag gaa ttc atg agc tcc ctg cag atc tct agc gtc tcc ctc aag cac				1651
Lys Glu Phe Met Ser Ser Leu Gln Ile Ser Ser Val Ser Leu Lys His				
339	344	349	354	
aac ggc aac tat aca tgc atc gcc agc aac gca gcc gcc acc gtg agc				1699
Asn Gly Asn Tyr Thr Cys Ile Ala Ser Asn Ala Ala Ala Thr Val Ser				
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cgg gag cgc cag ctc atc gtg cgt gtg ccc cct cga ttt gtg gtg caa				1747
Arg Glu Arg Gln Leu Ile Val Arg Val Pro Pro Arg Phe Val Val Gln				
371	376	381	386	
ccc aac aac cag gat ggc atc tac ggc aaa gct ggt gtg ctc aac tgc				1795
Pro Asn Asn Gln Asp Gly Ile Tyr Gly Lys Ala Gly Val Leu Asn Cys				
387	392	397	402	
tcg gtg gac ggc tac ccc cca ccc aag gtc atg tgg aag cat gcc aag				1843
Ser Val Asp Gly Tyr Pro Pro Pro Lys Val Met Trp Lys His Ala Lys				
403	408	413	418	
ggg agc ggg aac ccc cag cag tac cac cct gtg ccc ctc act ggc cgc				1891
Gly Ser Gly Asn Pro Gln Gln Tyr His Pro Val Pro Leu Thr Gly Arg				
419	424	429	434	
atc cag atc ctg ccc aac agc tcg ctg ctg atc cgc cac gtc cta gaa				1939
Ile Gln Ile Leu Pro Asn Ser Ser Leu Leu Ile Arg His Val Leu Glu				
435	440	445	450	
gag gac atc ggc tac tac ctc tgc cag gcc agc aac ggc gta ggc acc				1987
Glu Asp Ile Gly Tyr Tyr Leu Cys Gln Ala Ser Asn Gly Val Gly Thr				
451	456	461	466	
gac atc agc aag tcc atg ttc ctc aca gtc aag atc ccg gcc atg atc				2035
Asp Ile Ser Lys Ser Met Phe Leu Thr Val Lys Ile Pro Ala Met Ile				
467	472	477	482	
act tcc cac ccc aac acc acc atc gcc atc aag ggc cat gcg aag gag				2083
Thr Ser His Pro Asn Thr Thr Ile Ala Ile Lys Gly His Ala Lys Glu				
483	488	493	498	
cta aac tgc acg gca cgg ggt gag cgg ccc atc atc atc cgc tgg gag				2131
Leu Asn Cys Thr Ala Arg Gly Glu Arg Pro Ile Ile Ile Arg Trp Glu				
499	504	509	514	

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Lys Gly Asp Thr Val Ile Asp Pro Asp Arg Val Met Arg Tyr Ala Ile	
515 520 525 530	
gcc acc aag gac aac ggc gac gag gtc gtc tcc aca ctg aag ctc aag	2227
Ala Thr Lys Asp Asn Gly Asp Glu Val Val Ser Thr Leu Lys Leu Lys	
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Pro Ala Asp Arg Gly Asp Ser Val Phe Phe Ser Cys His Ala Ile Asn	
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Ser Tyr Gly Glu Asp Arg Gly Leu Ile Gln Leu Thr Val Gln Glu Pro	
563 568 573 578	
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Asn Leu Arg Trp Thr Gln Arg Phe Asp Gly Asn Ser Ile Ile Thr Gly	
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Phe Asp Ile Glu Tyr Lys Asn Lys Ser Asp Ser Trp Asp Phe Lys Gln	
611 616 621 626	
tcc aca cgc aac atc tcc ccc acc atc aac cag gcc aac att gtg gac	2515
Ser Thr Arg Asn Ile Ser Pro Thr Ile Asn Gln Ala Asn Ile Val Asp	
627 632 637 642	
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Leu His Pro Ala Ser Val Tyr Ser Ile Arg Met Tyr Ser Phe Asn Lys	
643 648 653 658	
att ggc cgc agt gaa cca agc aag gag ctc acc atc agc act gag gag	2611
Ile Gly Arg Ser Glu Pro Ser Lys Glu Leu Thr Ile Ser Thr Glu Glu	
659 664 669 674	
gcc gct ccc gat ggg ccc ccc atg gat gtt acc ttg cag cca gtg acc	2659
Ala Ala Pro Asp Gly Pro Pro Met Asp Val Thr Leu Gln Pro Val Thr	
675 680 685 690	
tca cag agc atc cag gtg acc tgg aag gca ccc aag aag gag ctg cag	2707
Ser Gln Ser Ile Gln Val Thr Trp Lys Ala Pro Lys Lys Glu Leu Gln	
691 696 701 706	
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Asn Gly Val Ile Arg Gly Tyr Gln Ile Gly Tyr Arg Glu Asn Ser Pro	
707 712 717 722	
ggc agc aac ggg cag tac agc atc gtg gag atg aag gcc acg ggg gac	2803
Gly Ser Asn Gly Gln Tyr Ser Ile Val Glu Met Lys Ala Thr Gly Asp	
723 728 733 738	

agc gag gtc tac acc ctg gac aac ctc aag aag ttc gcc cag tat ggg	2851
Ser Glu Val Tyr Thr Leu Asp Asn Leu Lys Lys Phe Ala Gln Tyr Gly	
739 744 749 754	
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Val Val Val Gln Ala Phe Asn Arg Ala Gly Thr Gly Pro Ser Ser Ser	
755 760 765 770	
gag atc aat gcc acc act ctg gag gat gtg ccc agc cag ccc cct gag	2947
Glu Ile Asn Ala Thr Thr Leu Glu Asp Val Pro Ser Gln Pro Pro Glu	
771 776 781 786	
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Asn Val Arg Ala Leu Ser Ile Thr Ser Asp Val Ala Val Ile Ser Trp	
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Ser Glu Pro Pro Arg Ser Thr Leu Asn Gly Val Leu Lys Gly Tyr Arg	
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Val Ile Phe Trp Ser Leu Tyr Val Asp Gly Glu Trp Gly Glu Met Gln	
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Asn Ile Thr Thr Thr Arg Glu Arg Val Glu Leu Arg Gly Met Glu Lys	
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Phe Thr Asn Tyr Ser Val Gln Val Leu Ala Tyr Thr Gln Ala Gly Asp	
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883 888 893 898	
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Val Val Ser Trp Leu Pro Pro Thr Lys Pro Asn Gly Val Ile Arg Lys	
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Tyr Thr Ile Phe Cys Ser Ser Pro Gly Ser Gly Gln Pro Ala Pro Ser	
915 920 925 930	
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Glu Tyr Glu Thr Ser Pro Glu Gln Leu Phe Tyr Arg Ile Ala His Leu	
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Asn Arg Gly Gln Gln Tyr Leu Leu Trp Val Ala Ala Val Thr Ser Ala	
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Gly	Arg	Gly	Asn	Ser	Ser	Glu	Lys	Val	Thr	Ile	Glu	Pro	Ala	Gly	Lys		
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Ala	Pro	Ala	Lys	Ile	Ile	Ser	Phe	Gly	Gly	Thr	Val	Thr	Thr	Pro	Trp		
979					984					989					994		
atg	aaa	gat	gtt	cgg	ctg	cct	tgc	aat	tca	gtg	gga	gat	cca	gcc	cct	3619	
Met	Lys	Asp	Val	Arg	Leu	Pro	Cys	Asn	Ser	Val	Gly	Asp	Pro	Ala	Pro		
995					1000					1005					1010		
gct	gtg	aag	tgg	acc	aag	gac	agt	gaa	gac	tgc	gcc	att	cca	gtg	tcc	3667	
Ala	Val	Lys	Trp	Thr	Lys	Asp	Ser	Glu	Asp	Ser	Ala	Ile	Pro	Val	Ser		
1011					1016					1021					1026		
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Met	Asp	Gly	His	Arg	Leu	Ile	His	Thr	Asn	Gly	Thr	Leu	Leu	Leu	Arg		
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Pro	Asp	Gln	Pro	Arg	Leu	Thr	Val	Ser	Lys	Thr	Ser	Ala	Ser	Ser	Ile		
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Phe	Val	Leu	Gln	Tyr	Ser	Val	Asp	Asn	Ser	Glu	Glu	Trp	Lys	Asp	Val		
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Ser	Phe	Ser	Lys	Asp	Gln	His	Leu	Phe	Thr	His	Ile	Asn	Ser	Thr	His		
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Ala Ile Val Leu Glu Tyr Arg Pro Lys Gly Thr Trp Ala Trp Gln Gly				
1203	1208	1213	1218	
ctc cgg gcc aac agc tcc ggg gag gtg ttt ctg acg gaa ctg cga gag				4291
Leu Arg Ala Asn Ser Ser Gly Glu Val Phe Leu Thr Glu Leu Arg Glu				
1219	1224	1229	1234	
gcc acg tgg tac gag ctg cgc atg agg gct tgc aac agt gcg ggc tgc				4339
Ala Thr Trp Tyr Glu Leu Arg Met Arg Ala Cys Asn Ser Ala Gly Cys				
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ggc aat gaa aca gcc cag ttc gcc acc ctg gac tac gat ggc agc acc				4387
Gly Asn Glu Thr Ala Gln Phe Ala Thr Leu Asp Tyr Asp Gly Ser Thr				
1251	1256	1261	1266	
att cca ccc atc aag tct gct caa ggt gaa ggg gat gat gtg aag aag				4435
Ile Pro Pro Ile Lys Ser Ala Gln Gly Glu Gly Asp Asp Val Lys Lys				
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ctg ttc acc atc ggc tgc cct gtc atc ctg gcc aca ctg ggg gtg gca				4483
Leu Phe Thr Ile Gly Cys Pro Val Ile Leu Ala Thr Leu Gly Val Ala				
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Leu Leu Phe Ile Val Arg Lys Lys Arg Lys Glu Lys Arg Leu Lys Arg				
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Leu Arg Asp Ala Lys Ser Leu Ala Glu Met Leu Ile Ser Lys Asn Asn				
1315	1320	1325	1330	
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Arg Ser Phe Asp Thr Pro Val Lys Gly Pro Pro Gln Gly Pro Arg Leu				
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His Ile Asp Ile Pro Arg Val Gln Leu Leu Ile Glu Asp Lys Glu Gly				
1347	1352	1357	1362	
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Ile Lys Gln Leu Gly Asp Asp Lys Ala Thr Ile Pro Val Thr Asp Ala				
1363	1368	1373	1378	
gag ttc agc caa gct gtc aac cca cag agc ttc tgt act ggc gtc tcc				4771
Glu Phe Ser Gln Ala Val Asn Pro Gln Ser Phe Cys Thr Gly Val Ser				
1379	1384	1389	1394	
ttg cac cac cca acc ctc atc cag agc aca gga ccc ctc atc gac atg				4819
Leu His His Pro Thr Leu Ile Gln Ser Thr Gly Pro Leu Ile Asp Met				
1395	1400	1405	1410	
tct gac atc cgg cca gga acc aat cca gtg tcc agg aag aat gtg aag				4867
Ser Asp Ile Arg Pro Gly Thr Asn Pro Val Ser Arg Lys Asn Val Lys				
1411	1416	1421	1426	

tca gcc cac agc acc cgg aac cgg tac tca agc cag tgg acc ctg acc	4915
Ser Ala His Ser Thr Arg Asn Arg Tyr Ser Ser Gln Trp Thr Leu Thr	
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Lys Cys Gln Ala Ser Thr Pro Ala Arg Thr Leu Thr Ser Asp Trp Arg	
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Thr Val Gly Ser Gln His Gly Val Thr Val Thr Glu Ser Asp Ser Tyr	
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Ser Ala Ser Leu Ser Gln Asp Thr Asp Lys Gly Arg Asn Ser Met Val	
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Glu His Ala Lys Leu Glu Glu Gln Leu Gln His Ala Lys Phe Glu Ile	
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Thr Glu Cys Phe Ile Ser Asp Ser Ser Ser Asp Gln Met Thr Thr Gly	
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Pro Gly Ile Cys Arg Phe Thr Ala Ser Pro Pro Lys Pro Gln Asp Ala	
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gac cgg ggc aaa aac gtg gct gtg ccc atc cct cac cgg gcc aac aag	5347
Asp Arg Gly Lys Asn Val Ala Val Pro Ile Pro His Arg Ala Asn Lys	
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Ala Ser Ile Arg Asn Leu Ala Arg Thr Tyr His Thr Gln Ala Arg His	
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ctg acc ctg gac cct gcc agc aag tcc ttg ggc ctt ccc cac cca ggg	5539
Leu Thr Leu Asp Pro Ala Ser Lys Ser Leu Gly Leu Pro His Pro Gly	
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Pro Ala Glu Pro Pro Thr Ala Pro Ser Ala Ala Pro Pro Ala Pro Ser	
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Met Arg Arg	
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Ala Leu Ser Asn Arg Ile Arg Leu Gln Val Ser Lys Ser Pro Leu Trp	
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Pro Lys Glu Asn Leu Asp Pro Val Val Val Gln Glu Gly Ala Pro Leu	
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Thr Leu Gln Cys Asn Pro Pro Pro Gly Leu Pro Ser Pro Val Ile Phe	
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Trp Met Ser Ser Ser Met Glu Pro Ile Thr Gln Asp Lys Arg Val Ser	
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Gln Gly His Asn Gly Asp Leu Tyr Phe Ser Asn Val Met Leu Gln Asp	
100 105 110 115	
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Met Gln Thr Asp Tyr Ser Cys Asn Ala Arg Phe His Phe Thr His Thr	
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Ile Gln Gln Lys Asn Pro Phe Thr Leu Lys Val Leu Thr Thr Arg Gly	
132 137 142 147	
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Val Ala Glu Arg Thr Pro Ser Phe Met Tyr Pro Gln Gly Thr Ala Ser	
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Ser Gln Met Val Leu Arg Gly Met Asp Leu Leu Leu Glu Cys Ile Ala	
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Ser Gly Val Pro Thr Pro Asp Ile Ala Trp Tyr Lys Lys Gly Gly Asp	
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ctc cca tct gat aag gcc aag ttt gag aac ttt aat aag gcc ctg cgt	800
Leu Pro Ser Asp Lys Ala Lys Phe Glu Asn Phe Asn Lys Ala Leu Arg	
196 201 206 211	
atc aca aat gtc tct gag gaa gac tcc ggg gag tat ttc tgc ctg gcc	848
Ile Thr Asn Val Ser Glu Glu Asp Ser Gly Glu Tyr Phe Cys Leu Ala	
212 217 222 227	
tcc aac aag atg ggc agc atc cgg cac acg atc tcg gtg aga gta aag	896
Ser Asn Lys Met Gly Ser Ile Arg His Thr Ile Ser Val Arg Val Lys	
228 233 238 243	
gct gct ccc tac tgg ctg gac gaa ccc aag aac ctt att ctg gct cct	944
Ala Ala Pro Tyr Trp Leu Asp Glu Pro Lys Asn Leu Ile Leu Ala Pro	
244 249 254 259	
ggc gag gat ggg aga ctg gtg tgt cga gcc aat gga aac ccc aaa ccc	992
Gly Glu Asp Gly Arg Leu Val Cys Arg Ala Asn Gly Asn Pro Lys Pro	
260 265 270 275	

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Thr Val Gln Trp Met Val Asn Gly Glu Pro Leu Gln Ser Ala Pro Pro	
276 281 286 291	
aac cca aac cgt gag gtg gcc gga gac acc atc atc ttc cgg gac acc	1088
Asn Pro Asn Arg Glu Val Ala Gly Asp Thr Ile Ile Phe Arg Asp Thr	
292 297 302 307	
cag atc agc agc agg gct gtg tac cag tgc aac acc tcc aac gag cat	1136
Gln Ile Ser Ser Arg Ala Val Tyr Gln Cys Asn Thr Ser Asn Glu His	
308 313 318 323	
ggc tac ctg ctg gcc aac gcc ttt gtc agt gtg ctg gat gtg ccg cct	1184
Gly Tyr Leu Leu Ala Asn Ala Phe Val Ser Val Leu Asp Val Pro Pro	
324 329 334 339	
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Arg Met Leu Ser Pro Arg Asn Gln Leu Ile Arg Val Ile Leu Tyr Asn	
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Arg Thr Arg Leu Asp Cys Pro Phe Phe Gly Ser Pro Ile Pro Thr Leu	
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Arg Trp Phe Lys Asn Gly Gln Gly Ser Asn Leu Asp Gly Gly Asn Tyr	
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cat gtt tat gag aac ggc agt ctg gaa att aag atg atc cgc aaa gag	1376
His Val Tyr Glu Asn Gly Ser Leu Glu Ile Lys Met Ile Arg Lys Glu	
388 393 398 403	
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Asp Gln Gly Ile Tyr Thr Cys Val Ala Thr Asn Ile Leu Gly Lys Ala	
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Glu Asn Gln Val Arg Leu Glu Val Lys Asp Pro Thr Arg Ile Tyr Arg	
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Met Pro Glu Asp Gln Val Ala Arg Arg Gly Thr Thr Val Gln Leu Glu	
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Cys Arg Val Lys His Asp Pro Ser Leu Lys Leu Thr Val Ser Trp Leu	
452 457 462 467	
aag gat gac gag ccg ctc tat att gga aac agg atg aag aag gaa gac	1616
Lys Asp Asp Glu Pro Leu Tyr Ile Gly Asn Arg Met Lys Lys Glu Asp	
468 473 478 483	
gat ttc gtg acc atc ttt ggg gtg gca gag cgg gac cag ggc agt tac	1664
Asp Phe Val Thr Ile Phe Gly Val Ala Glu Arg Asp Gln Gly Ser Tyr	
484 489 494 499	
acg tgt gtc gcc agc acc gag cta gac caa gac ctg gcc aag gcc tac	1712

Thr Cys Val Ala Ser	Thr Glu Leu Asp Gln	Asp Leu Ala Lys Ala Tyr	
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ctc acc gtg cta gga	cgg cca gac cgg ccc	cgg gac ctg gag ctg acc	1760
Leu Thr Val Leu Gly	Arg Pro Asp Arg Pro	Arg Asp Leu Glu Leu Thr	
516	521	526	531
gac ctg gcc gag agg	agc gtg cgg ctg acc	tgg atc ccc ggg gat gct	1808
Asp Leu Ala Glu Arg	Ser Val Arg Leu Thr	Trp Ile Pro Gly Asp Ala	
532	537	542	547
aac aac agc ccc atc	aca gac tac gtc gtc	cag ttt gaa gaa gac cag	1856
Asn Asn Ser Pro Ile	Thr Asp Tyr Val Val	Gln Phe Glu Glu Asp Gln	
548	553	558	563
ttc caa cct ggg gtc	tgg cat gac cat tcc	aag tac ccc ggc agc gtt	1904
Phe Gln Pro Gly Val	Trp His Asp His Ser	Lys Tyr Pro Gly Ser Val	
564	569	574	579
aac tca gcc gtc ctc	cgg ctg tcc ccg tat	gtc aac tac cag ttc cgt	1952
Asn Ser Ala Val Leu	Arg Leu Ser Pro Tyr	Val Asn Tyr Gln Phe Arg	
580	585	590	595
gtc att gcc atc aac	gag gtt ggg agc agc	cac ccc agc ctc cca tcc	2000
Val Ile Ala Ile Asn	Glu Val Gly Ser Ser	His Pro Ser Leu Pro Ser	
596	601	606	611
gag cgc tac cga acc	agt gga gca ccc ccc	gag tcc aat cct ggt gac	2048
Glu Arg Tyr Arg Thr	Ser Gly Ala Pro Pro	Glu Ser Asn Pro Gly Asp	
612	617	622	627
gtg aag gga gag ggg	acc aga aag aac aac	atg gag atc acg tgg acg	2096
Val Lys Gly Glu Gly	Thr Arg Lys Asn Asn	Met Glu Ile Thr Trp Thr	
628	633	638	643
ccc atg aat gcc acc	tcg gcc ttt ggc ccc	aac ctg cgc tac att gtc	2144
Pro Met Asn Ala Thr	Ser Ala Phe Gly Pro	Asn Leu Arg Tyr Ile Val	
644	649	654	659
aag tgg agg cgg aga	gag act cga gag gcc	tgg aac aac gtc aca gtg	2192
Lys Trp Arg Arg Arg	Glu Thr Arg Glu Ala	Trp Asn Asn Val Thr Val	
660	665	670	675
tgg ggc tct cgc tac	gtg gtg ggg cag acc	cca gtc tac gtg ccc tat	2240
Trp Gly Ser Arg Tyr	Val Val Gly Gln Thr	Pro Val Tyr Val Pro Tyr	
676	681	686	691
gag atc cga gtc cag	gct gaa aat gac ttc	ggg aag ggc cct gag cca	2288
Glu Ile Arg Val Gln	Ala Glu Asn Asp Phe	Gly Lys Gly Pro Glu Pro	
692	697	702	707
gag tcc gtc atc ggt	tac tcc gga gaa gat	tat ccc agg gct gcg ccc	2336
Glu Ser Val Ile Gly	Tyr Ser Gly Glu Asp	Tyr Pro Arg Ala Ala Pro	
708	713	718	723
act gaa gtt aaa gtc	cga gtc atg aac agc	aca gcc atc agc ctt cag	2384
Thr Glu Val Lys Val	Arg Val Met Asn Ser	Thr Ala Ile Ser Leu Gln	

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Trp Asn Arg Val Tyr Ser Asp Thr Val Gln Gly Gln Leu Arg Glu Tyr				
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cga gcc tac tac tgg agg gag agc agc ttg ctg aag aac ctg tgg gtg				2480
Arg Ala Tyr Tyr Trp Arg Glu Ser Ser Leu Leu Lys Asn Leu Trp Val				
756	761	766	771	
tct cag aag aga cag caa gcc agc ttc cct ggt gac cgc ctc cgt ggc				2528
Ser Gln Lys Arg Gln Gln Ala Ser Phe Pro Gly Asp Arg Leu Arg Gly				
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gtg gtg tcc cgc ctc ttc ccc tac agt aac tac aag ctg gag atg gtt				2576
Val Val Ser Arg Leu Phe Pro Tyr Ser Asn Tyr Lys Leu Glu Met Val				
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Val Val Asn Gly Arg Gly Asp Gly Pro Arg Ser Glu Thr Lys Glu Phe				
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acc acc ccg gaa gga gta ccc agt gcc cct agg cgt ttc cga gtc cgg				2672
Thr Thr Pro Glu Gly Val Pro Ser Ala Pro Arg Arg Phe Arg Val Arg				
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Gln Pro Asn Leu Glu Thr Ile Asn Leu Glu Trp Asp His Pro Glu His				
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cca aat ggg atc atg att gga tac act ctc aaa tat gtg gcc ttt aac				2768
Pro Asn Gly Ile Met Ile Gly Tyr Thr Leu Lys Tyr Val Ala Phe Asn				
852	857	862	867	
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Gly Thr Lys Val Gly Lys Gln Ile Val Glu Asn Phe Ser Pro Asn Gln				
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acc aag ttc acg gtg caa aga acg gac ccc gtg tca cgc tac cgc ttt				2864
Thr Lys Phe Thr Val Gln Arg Thr Asp Pro Val Ser Arg Tyr Arg Phe				
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Thr Leu Ser Ala Arg Thr Gln Val Gly Ser Gly Glu Ala Val Thr Glu				
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gag tca cca gca ccc ccg aat gaa ggt agg tgc atg gca gca gcc cct				2960
Glu Ser Pro Ala Pro Pro Asn Glu Gly Arg Cys Met Ala Ala Ala Pro				
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Gly Val Lys Gly Pro Ser *				
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Met Gln Thr Asp Tyr Ser Cys Asn Ala Arg Phe His Phe Thr His Thr	
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atc cag cag aag aac cct ttc acc ctc aag gtc ctc acc acc cga gga	608
Ile Gln Gln Lys Asn Pro Phe Thr Leu Lys Val Leu Thr Thr Arg Gly	
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Val Ala Glu Arg Thr Pro Ser Phe Met Tyr Pro Gln Gly Thr Ala Ser	

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164	169	174	179	
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Ser Gly Val Pro Thr Pro Asp Ile Ala Trp Tyr Lys Lys Gly Gly Asp				
180	185	190	195	
ctc cca tct gat aag gcc aag ttt gag aac ttt aat aag gcc ctg cgt				800
Leu Pro Ser Asp Lys Ala Lys Phe Glu Asn Phe Asn Lys Ala Leu Arg				
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Ile Thr Asn Val Ser Glu Glu Asp Ser Gly Glu Tyr Phe Cys Leu Ala				
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Ser Asn Lys Met Gly Ser Ile Arg His Thr Ile Ser Val Arg Val Lys				
228	233	238	243	
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ggc gag gat ggg aga ctg gtg tgt cga gcc aat gga aac ccc aaa ccc				992
Gly Glu Asp Gly Arg Leu Val Cys Arg Ala Asn Gly Asn Pro Lys Pro				
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Gln Ile Ser Ser Arg Ala Val Tyr Gln Cys Asn Thr Ser Asn Glu His				
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Gly Tyr Leu Leu Ala Asn Ala Phe Val Ser Val Leu Asp Val Pro Pro				
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340	345	350	355	
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356	361	366	371	
cga tgg ttt aag aat ggg caa gga agc aac ctg gat ggt ggc aac tac				1328
Arg Trp Phe Lys Asn Gly Gln Gly Ser Asn Leu Asp Gly Gly Asn Tyr				
372	377	382	387	

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Thr Cys Val Ala Ser Thr Glu Leu Asp Gln Asp Leu Ala Lys Ala Tyr	
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Pro Asn Leu Glu Thr	Ile Asn Leu Glu Trp	Asp His Pro Glu His Pro	
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Leu Leu Leu Pro Leu Leu Ser Ala Leu Val Ala Ala Ala Ile Asp Ala
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Pro Lys Thr Cys Ser Pro Lys Gln Phe Ala Cys Arg Asp Gln Ile Thr
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Cys Gln Pro Asn Glu His Asn Cys Leu Gly Thr Glu Leu Cys Val Pro	
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Cys Gln His His Cys Val Pro Thr Leu Asp Gly Pro Thr Cys Tyr Cys	
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Lys Leu Val Asp Ser Lys Ile Val Phe Pro His Gly Ile Thr Leu Asp	
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Tyr Asn Gly Ala Gln Asp Trp Ile Tyr Ser Gly Ser Tyr Trp Asp Arg	
413 418 423 428	
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Asn Tyr Phe Asn Leu Pro Asp Ile Tyr *	
429 434	
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tcc ctt agt cga atc aag agc aac gtg gat ggg cgg tac ctg gtg gac 96
 Ser Leu Ser Arg Ile Lys Ser Asn Val Asp Gly Arg Tyr Leu Val Asp
 17 22 27 32

ggc gtc cct ttc agc tgc tgc aat cct agc tcg cca cgg ccc tgc atc 144
 Gly Val Pro Phe Ser Cys Cys Asn Pro Ser Ser Pro Arg Pro Cys Ile
 33 38 43 48

cag tat cag atc acc aac aac tca gca cac tac agt tac gac cac cag 192
 Gln Tyr Gln Ile Thr Asn Asn Ser Ala His Tyr Ser Tyr Asp His Gln
 49 54 59 64

acg gag gag ctc aac ctg tgg gtg cgt ggc tgc agg gct gcc ctg ctg 240
 Thr Glu Glu Leu Asn Leu Trp Val Arg Gly Cys Arg Ala Ala Leu Leu
 65 70 75 80

agc tac tac agc agc ctc atg aac tcc atg ggt gtc gtc acg ctc ctc 288
 Ser Tyr Tyr Ser Ser Leu Met Asn Ser Met Gly Val Val Thr Leu Leu
 81 86 91 96

att tgg ctc ttc gag gtg acc att aca att ggg ctg cgc tac cta cag 336
 Ile Trp Leu Phe Glu Val Thr Ile Thr Ile Gly Leu Arg Tyr Leu Gln
 97 102 107 112

acg tcg ctg gat ggt gtg tcc aac ccc gag gaa tct gag agc gag agc 384
 Thr Ser Leu Asp Gly Val Ser Asn Pro Glu Glu Ser Glu Ser Glu Ser
 113 118 123 128

gag ggc tgg ctg ctg gag aag agc gtg ccg gag acc tgg aag gcc ttt 432
 Glu Gly Trp Leu Leu Glu Lys Ser Val Pro Glu Thr Trp Lys Ala Phe
 129 134 139 144

ctg gag agt gtg aag aag ctg ggc aag ggc aac cag gtg act gtg gct 480
 Leu Glu Ser Val Lys Lys Leu Gly Lys Gly Asn Gln Val Thr Val Ala
 145 150 155 160

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Ile Asn Lys Asn Ile Ser Ser Asp Pro Leu Pro Arg Ala Val Asp Asn	
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Glu Phe Glu Thr Val Ala Thr Gln Leu Leu Lys Arg Thr Gln Ala Met	
177 182 187 192	
ctt aac aaa tac aga tgc ctg ctc cta gaa gat gcc atg cga atc aat	624
Leu Asn Lys Tyr Arg Cys Leu Leu Leu Glu Asp Ala Met Arg Ile Asn	
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Pro Ser Ala Glu Met Val Met Ile Asp Arg Met Phe Asn Gln Glu Glu	
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Arg Ala Ser Leu Ser Arg Asp Lys Arg Leu Ala Leu Val Asp Pro Glu	
225 230 235 240	
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Gly Phe Gln Ala Asp Phe Cys Cys Ser Phe Lys Leu Asp Lys Ala Ala	
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His Glu Thr Gln Phe Gly Arg Ser Asp Gln His Gly Ser Lys Ala Ser	
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Ser Ser Leu Gln Pro Pro Ala Lys Ala Gln Gly Arg Asp Arg Ala Lys	
273 278 283 288	
acc ggt gtg acg gaa ccc atg aat cat gac cag ttt cat cta gtg cct	912
Thr Gly Val Thr Glu Pro Met Asn His Asp Gln Phe His Leu Val Pro	
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Cys Leu Gly Arg Ala Leu Lys Phe Asp Lys Val Gly Leu Val Gln Tyr	
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Gln Ser Thr Ser Glu Glu Lys Ala Ser Arg Arg Glu Pro Leu Lys Ala	
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Ser Asp His Gly Thr Glu Ser Lys Leu Ser Ser Ile Leu Ala Asp Ser	
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Asn	Ser	Pro	Lys	Asn	Glu	Val	Leu	His	Thr	Asp	Ile	Met	Lys	Gly	Ser	
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Phe	Lys	Asn	Ile	Leu	Glu	Leu	Lys	Lys	Ala	Gly	Arg	Gln	Pro	Gln	Ser	
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Asp	Pro	Thr	Val	Ser	Gly	Ser	Val	Glu	Leu	Asp	Phe	Pro	Asn	Phe	Ser	
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cct	atg	gct	tca	cag	gaa	aac	tgc	ctg	gaa	aag	ttc	atc	ccg	gac	cac	1440
Pro	Met	Ala	Ser	Gln	Glu	Asn	Cys	Leu	Glu	Lys	Phe	Ile	Pro	Asp	His	
465					470					475					480	
agt	gac	gtt	gtc	atg	gat	gat	gat	gat	gac	tcg	tgt	ctc	ctt	gat	ctt	1488
Ser	Asp	Val	Val	Met	Asp	Asp	Asp	Asp	Asp	Ser	Cys	Leu	Leu	Asp	Leu	
481					486					491					496	
att	gga	gac	cca	caa	gca	ttg	aac	tat	ttt	cta	cat	gga	cct	agt	aat	1536
Ile	Gly	Asp	Pro	Gln	Ala	Leu	Asn	Tyr	Phe	Leu	His	Gly	Pro	Ser	Asn	
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Lys	Ser	Ser	Asn	Asp	Asp	Leu	Thr	Asn	Ala	Gly	Tyr	Ser	Ala	Ala	Asn	
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tca	aat	tca	att	ttc	gcc	aac	tct	agt	aat	gct	gat	cct	aag	tca	tcc	1632
Ser	Asn	Ser	Ile	Phe	Ala	Asn	Ser	Ser	Asn	Ala	Asp	Pro	Lys	Ser	Ser	
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ctc	aaa	ggt	gta	agc	aac	cag	ctt	gga	gaa	ggg	ccc	agt	gat	gga	ctg	1680
Leu	Lys	Gly	Val	Ser	Asn	Gln	Leu	Gly	Glu	Gly	Pro	Ser	Asp	Gly	Leu	
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cca	ctt	tca	agt	agc	ctc	cag	ttt	ctt	gaa	gat	gaa	ctc	gag	tct	tct	1728
Pro	Leu	Ser	Ser	Ser	Leu	Gln	Phe	Leu	Glu	Asp	Glu	Leu	Glu	Ser	Ser	
561					566					571					576	
cct	ctt	cct	gat	ctc	act	gag	gac	caa	cct	ttc	gac	att	ctt	cag	aaa	1776
Pro	Leu	Pro	Asp	Leu	Thr	Glu	Asp	Gln	Pro	Phe	Asp	Ile	Leu	Gln	Lys	
577					582					587					592	
tcc	ttg	caa	gag	gcc	aat	atc	act	gaa	cag	aca	ttg	gca	gaa	gag	gca	1824
Ser	Leu	Gln	Glu	Ala	Asn	Ile	Thr	Glu	Gln	Thr	Leu	Ala	Glu	Glu	Ala	
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tat	ttg	gat	gcc	agt	ata	ggt	tca	agc	caa	cag	ttt	gca	caa	gct	cag	1872
Tyr	Leu	Asp	Ala	Ser	Ile	Gly	Ser	Ser	Gln	Gln	Phe	Ala	Gln	Ala	Gln	

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Leu His Pro Ser Ser Ser Ala Ser Phe Thr Gln Ala Ser Asn Val Ser				
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aat tac tca ggt cag acg ctg cag cct ata ggg gtg acg cat gtg cct				1968
Asn Tyr Ser Gly Gln Thr Leu Gln Pro Ile Gly Val Thr His Val Pro				
641	646	651	656	
gtt gga gca tcg ttt gca agc aat aca gtg ggt gta caa cat ggc ttt				2016
Val Gly Ala Ser Phe Ala Ser Asn Thr Val Gly Val Gln His Gly Phe				
657	662	667	672	
atg caa cat gtg ggg atc agt gtt ccc agc cag cat ttg tct aat agc				2064
Met Gln His Val Gly Ile Ser Val Pro Ser Gln His Leu Ser Asn Ser				
673	678	683	688	
agt cag att agt ggt tct ggt caa ata cag tta att ggg tca ttt ggt				2112
Ser Gln Ile Ser Gly Ser Gly Gln Ile Gln Leu Ile Gly Ser Phe Gly				
689	694	699	704	
aat cat cct tcc atg atg act att aat aac cta gat gga tct caa atc				2160
Asn His Pro Ser Met Met Thr Ile Asn Asn Leu Asp Gly Ser Gln Ile				
705	710	715	720	
ata tta aag ggc agc ggg cag caa gcc cca tca aat gtg agt gga ggg				2208
Ile Leu Lys Gly Ser Gly Gln Gln Ala Pro Ser Asn Val Ser Gly Gly				
721	726	731	736	
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Leu Leu Val His Arg Gln Thr Pro Asn Gly Asn Ser Leu Phe Gly Asn				
737	742	747	752	
tct agt tcc agt cca gta gca cag cct gtt acc gtt cca ttt aac agc				2304
Ser Ser Ser Ser Pro Val Ala Gln Pro Val Thr Val Pro Phe Asn Ser				
753	758	763	768	
aca aat ttt caa aca tct tta cct gtg cat aac atc atc ata caa agg				2352
Thr Asn Phe Gln Thr Ser Leu Pro Val His Asn Ile Ile Ile Gln Arg				
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Gly Leu Ala Pro Asn Ser Asn Lys Val Pro Ile Asn Ile Gln Pro Lys				
785	790	795	800	
cct atc cag atg ggt cag caa aat aca tac aat gtg aac aat ttg gga				2448
Pro Ile Gln Met Gly Gln Gln Asn Thr Tyr Asn Val Asn Asn Leu Gly				
801	806	811	816	
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Ile Gln Gln His His Val Gln Gln Gly Ile Ser Phe Ala Ser Ala Ser				
817	822	827	832	
tca ccc cag ggc tca gta gtt ggt cca cac atg tct gtg aac att gta				2544
Ser Pro Gln Gly Ser Val Val Gly Pro His Met Ser Val Asn Ile Val				
833	838	843	848	

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Asn Gln Gln Asn Thr Arg Lys Pro Val Thr Ser Gln Ala Val Ser Ser	
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Thr Gly Gly Ser Ile Val Ile His Ser Pro Met Gly Gln Pro His Ala	
865 870 875 880	
ccc caa agt cag ttc ctt ata cct aca agc ctt tct gtc agt tcc aac	2688
Pro Gln Ser Gln Phe Leu Ile Pro Thr Ser Leu Ser Val Ser Ser Asn	
881 886 891 896	
tcg gta cac cac gtc cag act ata aat ggg caa ctt ctt caa act caa	2736
Ser Val His His Val Gln Thr Ile Asn Gly Gln Leu Leu Gln Thr Gln	
897 902 907 912	
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Pro Ser Gln Leu Ile Ser Gly Gln Val Ala Ser Glu His Val Met Leu	
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Asn Arg Asn Ser Ser Asn Met Leu Arg Thr Asn Gln Pro Tyr Thr Gly	
929 934 939 944	
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Pro Met Leu Asn Asn Gln Asn Thr Ala Val His Leu Val Ser Gly Gln	
945 950 955 960	
aca ttt gct gcc tct gga agt cca gtg ata gcc aat cat gcc tct cct	2928
Thr Phe Ala Ala Ser Gly Ser Pro Val Ile Ala Asn His Ala Ser Pro	
961 966 971 976	
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Gln Leu Val Gly Gly Gln Met Pro Leu Gln Gln Ala Ser Pro Thr Val	
977 982 987 992	
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Leu His Leu Ser Pro Gly Gln Ser Ser Val Ser Gln Gly Arg Pro Gly	
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Phe Ala Thr Met Pro Ser Val Thr Ser Met Ser Gly Pro Ser Arg Phe	
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Pro Ala Val Ser Ser Ala Ser Thr Ala His Pro Ser Leu Gly Ser Ala	
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Gln Pro Asn Arg Thr Pro Val Pro Val Ser Val Ser His Arg Leu Pro	
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Val Ser Ser Ser Lys Ser Thr Ser Thr Phe Ser Asn Thr Pro Gly Thr	
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Gly Thr Gln Gln Gln Phe Phe Cys Gln Ala Gln Lys Lys Cys Leu Asn	
1089 1094 1099 1104	
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Gln Thr Ser Pro Ile Ser Ala Pro Lys Thr Thr Asp Gly Leu Arg Gln	
1105 1110 1115 1120	
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Ala Gln Ile Pro Gly Leu Leu Ser Thr Thr Leu Pro Gly Gln Asp Ser	
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Gly Ser Lys Val Ile Ser Ala Ser Leu Gly Thr Ala Gln Pro Gln Gln	
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Ser His Ser Gly Gly Gln Lys Arg Pro Ala Ala Lys Gln Leu Thr Lys	
1169 1174 1179 1184	
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Thr Pro Asp Lys Ser His Phe Arg Ser Leu Ser Asp Ala Val Gln Arg	
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1249 1254 1259 1264	
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His Gly Ser Lys Ala Ser Ser Ser Leu Gln Pro Pro Ala Lys Ala Gln	
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attcaaacia ccaaccctga tttcctgctt ctccttttca tgagtgttcc tgtgggtctct      180
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                               Met Ala Gly Pro Arg Pro
                               1

cgg tgg cgc gac cag ctg ctg ttc atg agc atc ata gtc ctc gtg att      283
Arg Trp Arg Asp Gln Leu Leu Phe Met Ser Ile Ile Val Leu Val Ile
  7                12                17                22

gtg gtc atc tgc ctg atg tta tac gct ctt ctc tgg gag gct ggc aac      331
Val Val Ile Cys Leu Met Leu Tyr Ala Leu Leu Trp Glu Ala Gly Asn
  23                28                33                38

ctc act gac ctg ccc aac ctg aga atc ggc ttc tat aac ttc tgc ctg      379
Leu Thr Asp Leu Pro Asn Leu Arg Ile Gly Phe Tyr Asn Phe Cys Leu
  39                44                49                54

tgg aat gag gac acc agc acc cta cag tgt cac cag ttc cct gag ctg      427
Trp Asn Glu Asp Thr Ser Thr Leu Gln Cys His Gln Phe Pro Glu Leu
  55                60                65                70

gaa gcc ctg ggg gtg cct cgg gtt ggc ctg ggc ctg gcc agg ctt ggc      475
Glu Ala Leu Gly Val Pro Arg Val Gly Leu Gly Leu Ala Arg Leu Gly
  71                76                81                86

gtg tac ggg tcc ctg gtc ctc acc ctc ttt gcc ccc cag cct ctc ctc      523
Val Tyr Gly Ser Leu Val Leu Thr Leu Phe Ala Pro Gln Pro Leu Leu
  87                92                97                102

cta gcc cag tgc aac agt gat gag aga gcg tgg cgg ctg gca gtg ggc      571
Leu Ala Gln Cys Asn Ser Asp Glu Arg Ala Trp Arg Leu Ala Val Gly
  103                108                113                118

ttc ctg gct gtg tcc tct gtg ctg ctg gcc ggc ggc ctg ggc ctc ttc      619
Phe Leu Ala Val Ser Ser Val Leu Leu Ala Gly Gly Leu Gly Leu Phe
  119                124                129                134

ctc tcc tat gtg tgg aag tgg gtc agg ctc tcc ctc ccg ggg cct ggg      667
Leu Ser Tyr Val Trp Lys Trp Val Arg Leu Ser Leu Pro Gly Pro Gly

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Phe Leu Ala Leu Gly Ser Ala Gln Ala Leu Leu Ile Leu Leu Leu Ile				
151	156	161	166	
gcc atg gct gtg ttc cct ctg agg gct gag agg gct gag agc aag ctt				763
Ala Met Ala Val Phe Pro Leu Arg Ala Glu Arg Ala Glu Ser Lys Leu				
167	172	177	182	
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Glu Ser Cys *				
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cgg ggg gcg aga aat gcc cgc gtc ctc cgg ggg att ctc gca gga gcc 98
Arg Gly Ala Arg Asn Ala Arg Val Leu Arg Gly Ile Leu Ala Gly Ala
13             18             23             28

aca gct aac aag gct tct cat aac agg acc cgg gcc ctg caa agc cac 146
Thr Ala Asn Lys Ala Ser His Asn Arg Thr Arg Ala Leu Gln Ser His
29             34             39             44

agc tcc cca gag ggc aag gag gaa cct gaa ccc cta tcc ccg gag ctg 194
Ser Ser Pro Glu Gly Lys Glu Glu Pro Glu Pro Leu Ser Pro Glu Leu
45             50             55             60

gaa tac att ccc aga aag agg ggc aag aac ccc atg aaa gct gtg gga 242
Glu Tyr Ile Pro Arg Lys Arg Gly Lys Asn Pro Met Lys Ala Val Gly
61             66             71             76

ctg gcc tgg tac agc ctg tac acc cgc acc tgg ctc ggg tac ctc ttc 290
Leu Ala Trp Tyr Ser Leu Tyr Thr Arg Thr Trp Leu Gly Tyr Leu Phe
77             82             87             92

tac cga cag cag ctg cgc agg gct cgg aat cgc tac cct aaa ggc cac 338
Tyr Arg Gln Gln Leu Arg Arg Ala Arg Asn Arg Tyr Pro Lys Gly His
93             98             103            108

tcg aaa acc cag ccc cgc ctc ttc aat gga gtg aag gtg ctt ccc atc 386

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Pro	Val	Leu	Ser	Asp	Asn	Tyr	Ser	Tyr	Leu	Ile	Ile	Asp	Thr	Gln	Ala		
125					130					135					140		
cag	ctg	gct	gtg	gct	gtg	gac	cct	tca	gac	cct	cgg	gct	gtg	cag	gct	482	
Gln	Leu	Ala	Val	Ala	Val	Asp	Pro	Ser	Asp	Pro	Arg	Ala	Val	Gln	Ala		
141					146					151					156		
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Ser	Ile	Glu	Lys	Glu	Gly	Val	Thr	Leu	Val	Ala	Ile	Leu	Cys	Thr	His		
157					162					167					172		
aag	cac	tgg	gac	cac	agt	gga	ggg	aac	cgt	gac	ctc	agc	cgg	cgg	cac	578	
Lys	His	Trp	Asp	His	Ser	Gly	Gly	Asn	Arg	Asp	Leu	Ser	Arg	Arg	His		
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cgg	gac	tgt	cgg	gtg	tac	ggg	agc	cct	cag	gac	ggc	atc	ccc	tac	ctc	626	
Arg	Asp	Cys	Arg	Val	Tyr	Gly	Ser	Pro	Gln	Asp	Gly	Ile	Pro	Tyr	Leu		
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Thr	His	Pro	Leu	Cys	His	Gln	Asp	Val	Val	Ser	Val	Gly	Arg	Leu	Gln		
205					210					215					220		
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Ile	Arg	Ala	Leu	Ala	Thr	Pro	Gly	His	Thr	Gln	Gly	His	Leu	Val	Tyr		
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253					258					263					268		
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Glu	Thr	Met	Leu	Ser	Ser	Leu	Asp	Thr	Val	Leu	Gly	Leu	Gly	Asp	Asp		
269					274					279					284		
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285					290					295					300		
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Trp	Val	Gln	Arg	Gln	Arg	Leu	Glu	Arg	Lys	Gly	Thr	Cys	Pro	Ser	Thr		
317					322					327					332		
ctg	gga	gag	gag	cgc	tcc	tac	aac	ccg	ttc	ctg	aga	acc	cac	tgc	ctg	1058	
Leu	Gly	Glu	Glu	Arg	Ser	Tyr	Asn	Pro	Phe	Leu	Arg	Thr	His	Cys	Leu		

333	338	343	348	
gcg cta cag gag gct ctg ggg ccg ggg ccg ggc ccc act ggg gat gat				1106
Ala Leu Gln Glu Ala Leu Gly Pro Gly Pro Gly Pro Thr Gly Asp Asp				
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Asp Tyr Ser Arg Ala Gln Leu Leu Glu Glu Leu Arg Arg Leu Lys Asp				
365	370	375	380	
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Met His Lys Ser Lys *				
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ttgggctgag cagaggacga c atg ttg ctt ttc gtg gag cag gta gca tct 171

Met Leu Leu Phe Val Glu Gln Val Ala Ser
1 5

aaa gga act ggt tta aat cct aat gcc aaa gta tgg caa gaa att gct 219

Lys Gly Thr Gly Leu Asn Pro Asn Ala Lys Val Trp Gln Glu Ile Ala
11 16 21 26

cct gga aat act gat gcc acc cca gta act cat gga act gaa agc tct 267

Pro Gly Asn Thr Asp Ala Thr Pro Val Thr His Gly Thr Glu Ser Ser
27 32 37 42

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Trp His Glu Ile Ala Ala Thr Ser Gly Ala His Pro Glu Gly Asn Ala
43 48 53 58

gag ctc tca gaa gat ata tgt aaa gaa tat gaa gta atg tat tct tca 363

Glu Leu Ser Glu Asp Ile Cys Lys Glu Tyr Glu Val Met Tyr Ser Ser
59 64 69 74

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Ser Cys Glu Thr Thr Arg Asn Thr Thr Gly Ile Glu Glu Ser Thr Asp
75 80 85 90

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Gly Met Ile Leu Gly Pro Glu Asp Leu Ser Tyr Gln Ile Tyr Asp Val
91 96 101 106

tcc gga gaa agc aat tca gca gtt tct aca gaa gac cta aaa gaa tgt 507

Ser Gly Glu Ser Asn Ser Ala Val Ser Thr Glu Asp Leu Lys Glu Cys
107 112 117 122

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123 128 133 138

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Phe Lys Ser Glu Asn Cys Pro Lys Val Ile Ser Cys Glu Phe Ala His	
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Tyr Arg Leu Met Asp Ser Ser Ile Tyr Ser His Pro Ile Gln Thr Gln	
283 288 293 298	
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Gln Gln Tyr Ser Val Tyr Ser Ile Val Pro Gln Ser Trp Ser Pro Asn	
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395 400 405 410	
gaa cgg cat aac ccc aca gta act ggg cat cag gag caa act tac ctt	1419
Glu Arg His Asn Pro Thr Val Thr Gly His Gln Glu Gln Thr Tyr Leu	
411 416 421 426	
cag aag gag act tcc act ttg cag gtg gaa cag aat ggg gac tat ggt	1467
Gln Lys Glu Thr Ser Thr Leu Gln Val Glu Gln Asn Gly Asp Tyr Gly	
427 432 437 442	
agg ggc agg taa gaa aataaagtac ctgaaaacct ttgataataa tgtgatcatc	1522
Arg Gly Arg *	
443	
ctgaataatt gaagaacgtg atcttcataa taattaaatg agcatttaatt tattggtata	1582
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ctgaccgcaa cccctacccc cgcccaccag c atg gcc cgg cac gtg ttc cta	172
Met Ala Arg His Val Phe Leu	
1 5	
acg ggg ccc cca gga gtt gga aaa aca aca ttg atc cat aaa gcc agt	220
Thr Gly Pro Pro Gly Val Gly Lys Thr Thr Leu Ile His Lys Ala Ser	
8 13 18 23	
gag gtt tta aaa tcc tct ggt gtg cct gtt gat gga ttt tat acc gaa	268
Glu Val Leu Lys Ser Ser Gly Val Pro Val Asp Gly Phe Tyr Thr Glu	
24 29 34 39	

gaa gtc aga cag gga ggg aga aga ata gga ttc gat gtc gtc acg ttg	316
Glu Val Arg Gln Gly Gly Arg Arg Ile Gly Phe Asp Val Val Thr Leu	
40 45 50 55	
tcc ggc acc cgg ggg cct tta tcg aga gtt ggg tta gag cct cca cct	364
Ser Gly Thr Arg Gly Pro Leu Ser Arg Val Gly Leu Glu Pro Pro Pro	
56 61 66 71	
gga aaa cgt gaa tgc cga gtt ggg cag tat gtg gtc gac ctg act tct	412
Gly Lys Arg Glu Cys Arg Val Gly Gln Tyr Val Val Asp Leu Thr Ser	
72 77 82 87	
ttt gag cag ttg gca cta ccc gtc ttg agg aat gcc gac tgc agc agt	460
Phe Glu Gln Leu Ala Leu Pro Val Leu Arg Asn Ala Asp Cys Ser Ser	
88 93 98 103	
ggc cca ggg caa aga gtg tgc gtc atc gat gag att ggg aag atg gag	508
Gly Pro Gly Gln Arg Val Cys Val Ile Asp Glu Ile Gly Lys Met Glu	
104 109 114 119	
ctc ttc agt cag ctt ttc att caa gct gtt cgt cag acg ctg tct acc	556
Leu Phe Ser Gln Leu Phe Ile Gln Ala Val Arg Gln Thr Leu Ser Thr	
120 125 130 135	
cca ggg act ata atc ctt ggc aca atc cca gtt cct aaa gga aag cca	604
Pro Gly Thr Ile Ile Leu Gly Thr Ile Pro Val Pro Lys Gly Lys Pro	
136 141 146 151	
ctg gct ctt gta gaa gaa atc aga aac aga aag gat gtg aag gtg ttt	652
Leu Ala Leu Val Glu Glu Ile Arg Asn Arg Lys Asp Val Lys Val Phe	
152 157 162 167	
aat gtc acc aag gaa aac aga aac cac ctt ctg cca gat atc gtg acg	700
Asn Val Thr Lys Glu Asn Arg Asn His Leu Leu Pro Asp Ile Val Thr	
168 173 178 183	
tgc gtg cag agc agc agg aag tga agacacgtgc attcctgcct tccgtgaagg	754
Cys Val Gln Ser Ser Arg Lys *	
184 189	
agtgccagtc tcaagaggag cctgatggag ccctgcctgt cgaggctgta tgcctatggg	814
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taaaagatca aaaaaaaaaa a	895

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<400> 51

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1

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Glu Pro Val Gly Cys Cys Gly Glu Cys Arg Gly Ser Ser Val Asp Pro
2 7 12 17

cgg agc acc ttc gtg ttg agt aac ctg gcg gag gtg gtg gag cgt gtg 154
Arg Ser Thr Phe Val Leu Ser Asn Leu Ala Glu Val Val Glu Arg Val
18 23 28 33

ctc acc ttc ctg ccc gcc aag gcg ttg ctg cgg gtg gcc tgc gtg tgc 202
Leu Thr Phe Leu Pro Ala Lys Ala Leu Leu Arg Val Ala Cys Val Cys
34 39 44 49

cgc tta tgg agg gag tgt gtg cgc aga gta ttg cgg acc cat cgg agc 250
Arg Leu Trp Arg Glu Cys Val Arg Arg Val Leu Arg Thr His Arg Ser
50 55 60 65

gta acc tgg atc tcc gca ggc ctg gcg gag gcc ggc cac ctg gag ggg 298
Val Thr Trp Ile Ser Ala Gly Leu Ala Glu Ala Gly His Leu Glu Gly
66 71 76 81

cat tgc ttg gtt cgc gtg gta gca gag gag ctt gag aat gtt cgc atc 346
His Cys Leu Val Arg Val Val Ala Glu Glu Leu Glu Asn Val Arg Ile
82 87 92 97

tta cca cat aca gtt ctt tac atg gct gat tca gaa act ttc att agt 394
Leu Pro His Thr Val Leu Tyr Met Ala Asp Ser Glu Thr Phe Ile Ser
98 103 108 113

ctg gaa gag tgt cgt ggc cat aag aga gca agg aaa aga act agt atg 442
Leu Glu Glu Cys Arg Gly His Lys Arg Ala Arg Lys Arg Thr Ser Met
114 119 124 129

gaa aca gca ctt gcc ctt gag aag cta ttc ccc aaa caa tgc caa gtc 490
Glu Thr Ala Leu Ala Leu Glu Lys Leu Phe Pro Lys Gln Cys Gln Val
130 135 140 145

ctt ggg att gtg acc cca gga att gta gtg act cca atg gga tca ggt 538
Leu Gly Ile Val Thr Pro Gly Ile Val Val Thr Pro Met Gly Ser Gly
146 151 156 161

agc aat cga cct cag gaa ata gaa att gga gaa tct ggt ttt gct tta 586
Ser Asn Arg Pro Gln Glu Ile Glu Ile Gly Glu Ser Gly Phe Ala Leu
162 167 172 177

tta ttc cct caa att gaa gga ata aaa ata caa ccc ttt cat ttt att 634
Leu Phe Pro Gln Ile Glu Gly Ile Lys Ile Gln Pro Phe His Phe Ile
178 183 188 193

aag gat cca aag aat tta aca tta gaa aga cat caa ctc act gaa gta 682
Lys Asp Pro Lys Asn Leu Thr Leu Glu Arg His Gln Leu Thr Glu Val
194 199 204 209

ggt ctt tta gat aac cct gaa ctt cgt gtg gtc ctt gtc ttt ggt tat	730
Gly Leu Leu Asp Asn Pro Glu Leu Arg Val Val Leu Val Phe Gly Tyr	
210 215 220 225	
aat tgc tgt aag gtg gga gcc agt aat tat ctg cag caa gta gtc agc	778
Asn Cys Cys Lys Val Gly Ala Ser Asn Tyr Leu Gln Gln Val Val Ser	
226 231 236 241	
act ttc agt gat atg aat atc atc ttg gct gga gcc cag gtg gac aac	826
Thr Phe Ser Asp Met Asn Ile Ile Leu Ala Gly Gly Gln Val Asp Asn	
242 247 252 257	
ctg tca tca ctg act tct gaa aag aac cct ctg gat att gat gcc tcg	874
Leu Ser Ser Leu Thr Ser Glu Lys Asn Pro Leu Asp Ile Asp Ala Ser	
258 263 268 273	
ggt gtg gtt gga ctg tca ttt agt gga cac cga atc cag agt gcc act	922
Gly Val Val Gly Leu Ser Phe Ser Gly His Arg Ile Gln Ser Ala Thr	
274 279 284 289	
gtg ctc ctc aac gag gac gtc agt gat gag aag act gct gag gct gcg	970
Val Leu Leu Asn Glu Asp Val Ser Asp Glu Lys Thr Ala Glu Ala Ala	
290 295 300 305	
atg cag cgc ctc aaa gcg gcc aac att cca gag cat aac acc att ggc	1018
Met Gln Arg Leu Lys Ala Ala Asn Ile Pro Glu His Asn Thr Ile Gly	
306 311 316 321	
ttc atg ttt gca tgc gtt gcc agg gcc ttt cag tat tac aga gcc aag	1066
Phe Met Phe Ala Cys Val Gly Arg Gly Phe Gln Tyr Tyr Arg Ala Lys	
322 327 332 337	
ggg aat gtt gag gct gat gca ttt aga aag ttt ttt cct agt gtt ccc	1114
Gly Asn Val Glu Ala Asp Ala Phe Arg Lys Phe Phe Pro Ser Val Pro	
338 343 348 353	
tta ttc ggc ttc ttt gga aat gga gaa att gga tgt gat cgg ata gtc	1162
Leu Phe Gly Phe Phe Gly Asn Gly Glu Ile Gly Cys Asp Arg Ile Val	
354 359 364 369	
act ggg aac ttt ata ttg agg aaa tgt aat gag gta aaa gat gat gat	1210
Thr Gly Asn Phe Ile Leu Arg Lys Cys Asn Glu Val Lys Asp Asp Asp	
370 375 380 385	
ctg ttt cat agc tat aca aca ata atg gca ctc ata cat ctg ggg tca	1258
Leu Phe His Ser Tyr Thr Thr Ile Met Ala Leu Ile His Leu Gly Ser	
386 391 396 401	
tct aaa taa taattaaagt ggctttcata ataaaaaaaaa aaaa	1301
Ser Lys *	
402	

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<220>
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<400> 52

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gga ata ttg gca ggg ggg gcc cgg gag gcg tca tgc agg tac ccc gcg      104
Gly Ile Leu Ala Gly Gly Ala Arg Glu Ala Ser Cys Arg Tyr Pro Ala
  4                               9                               14                               19

ctg ggg cct cgc ctc gcc gct cac ttt cca gcg cag cgg ccg ccg cag      152
Leu Gly Pro Arg Leu Ala Ala His Phe Pro Ala Gln Arg Pro Pro Gln
  20                               25                               30                               35

cgg aca ctc cag aac ggc ctg gcc ctg cag cgg tgc ctg cac gcg acg      200
Arg Thr Leu Gln Asn Gly Leu Ala Leu Gln Arg Cys Leu His Ala Thr
  36                               41                               46                               51

gcg acc cgg gct ctc ccg ctc att ccc atc gtg gtg gag cag acg ggt      248
Ala Thr Arg Ala Leu Pro Leu Ile Pro Ile Val Val Glu Gln Thr Gly
  52                               57                               62                               67

cgc ggc gag cgc gcc tat gac atc tac tcg cgg ctg ctg cgg gag cgc      296
Arg Gly Glu Arg Ala Tyr Asp Ile Tyr Ser Arg Leu Leu Arg Glu Arg
  68                               73                               78                               83

atc gtg tgc gtc atg ggc ccg atc gat gac agc gtt gcc agc ctt gtt      344
Ile Val Cys Val Met Gly Pro Ile Asp Asp Ser Val Ala Ser Leu Val
  84                               89                               94                               99

atc gca cag ctc ctc ttc ctg ctt ctc gcc gcc ggc acc cca ggc atg      392
Ile Ala Gln Leu Leu Phe Leu Leu Leu Ala Ala Gly Thr Pro Gly Met
  100                               105                               110                               115

cgc cac tcg ctc ccc aac tcc cgt atc atg atc cac cag ccc tca gga      440
Arg His Ser Leu Pro Asn Ser Arg Ile Met Ile His Gln Pro Ser Gly
  116                               121                               126                               131

ggc gcc cgg ggc caa gcc aca gac att gcc atc cag gca gag gag atc      488
Gly Ala Arg Gly Gln Ala Thr Asp Ile Ala Ile Gln Ala Glu Glu Ile
  132                               137                               142                               147

atg aag ctc aag aag cag ctc tat aac atc tac gcc aag cac acc aaa      536
Met Lys Leu Lys Lys Gln Leu Tyr Asn Ile Tyr Ala Lys His Thr Lys
  148                               153                               158                               163

cag agc ctg cag gtg atc gag tcc gcc atg gag agg gac cgc tac atg      584
Gln Ser Leu Gln Val Ile Glu Ser Ala Met Glu Arg Asp Arg Tyr Met
  164                               169                               174                               179

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agc ccc atg gag gcc cag gag ttt ggc atc tta gac aag gtt ctg gtc	632
Ser Pro Met Glu Ala Gln Glu Phe Gly Ile Leu Asp Lys Val Leu Val	
180 185 190 195	
cac cct ccc cag gac ggt gag gat gag ccc acg ctg gtg cag aag gag	680
His Pro Pro Gln Asp Gly Glu Asp Glu Pro Thr Leu Val Gln Lys Glu	
196 201 206 211	
cct gta gaa gca gcg ccg gca gca gaa cct gtc cca gct agc acc tga	728
Pro Val Glu Ala Ala Pro Ala Ala Glu Pro Val Pro Ala Ser Thr *	
212 217 222 227	
gagctggggcc tcctctccag aatcatgttg agggggccaga ggctgccag acccccagct	788
gggccctgct cacccttgt tgctgggctt ggaggggcct cttgaggaac ttttaatttg	848
caggggtgcc cgctatggac ggggcattcc agctgagaca ctgtgatttt aaattaaatc	908
tttgtgtct ttaaaaaaaaa aaaa	932

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 <211> 670
 <212> DNA
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<220>
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 <222> (88) .. (312)

<400> 53

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Met Leu Thr Ser Leu Ser Arg Pro	
1 5	
ata act acc atg gct ctc agt gcc ttg gtg tac cct ggg atg tgt ggc	159
Ile Thr Thr Met Ala Leu Ser Ala Leu Val Tyr Pro Gly Met Cys Gly	
9 14 19 24	
ctt ctg gcc aag cat ctg tca ttt cat att gtt gga gca ttc ctt ata	207
Leu Leu Ala Lys His Leu Ser Phe His Ile Val Gly Ala Phe Leu Ile	
25 30 35 40	
acc ctg ggg ttg cag ctc tct gta agt ttg ctg tgg cct gac caa gaa	255
Thr Leu Gly Leu Gln Leu Ser Val Ser Leu Leu Trp Pro Asp Gln Glu	
41 46 51 56	
aga agg cat atg cag att tct aca gaa att ata att gaa tta aag aat	303
Arg Arg His Met Gln Ile Ser Thr Glu Ile Ile Ile Glu Leu Lys Asn	
57 62 67 72	
ttg agg tga ggaaggc taatatctct cagagtacaa agtgattttg gaacataaag	359

Leu Arg *

73

tattttctttg ggttgaatta cataaaagtt tgtcactgta cctgtgttcc tgaactatct 419
 gtgaaacatg aatatgtggg ctaagaaatt gtttatctta ataaataatt aacaaaccct 479
 ttaaacgggt aaaaaaaaa agtcatgggc agtctttttt catatgtata gaccctaac 539
 tactaccgtt aagcaaattc cagacttcat aatttggggg aagtaactat cagatttcat 599
 ctgtactaga atcgtggcaa agtaccattc cacctgctct cgtgccgaat tcttggcctc 659
 gagggccaaa t 670

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 Met Ser Gly Arg Leu Trp Ser Lys Ala Ile Phe Ala Gly Tyr Lys Arg
 1 5 10 15
 ggt ctc cgg aac caa agg gag cac aca gct ctt ctt aaa att gaa ggt 153
 Gly Leu Arg Asn Gln Arg Glu His Thr Ala Leu Leu Lys Ile Glu Gly
 17 22 27 32
 gtt tac gcc cga gat gaa aca gaa ttc tat ttg ggc aag aga tgc gct 201
 Val Tyr Ala Arg Asp Glu Thr Glu Phe Tyr Leu Gly Lys Arg Cys Ala
 33 38 43 48
 tat gta tat aaa gca aag aac aac aca gtc act cct ggc ggc aaa cca 249
 Tyr Val Tyr Lys Ala Lys Asn Asn Thr Val Thr Pro Gly Gly Lys Pro
 49 54 59 64
 aac aaa acc aga gtc atc tgg gga aaa gta act cgg gcc cat gga aac 297
 Asn Lys Thr Arg Val Ile Trp Gly Lys Val Thr Arg Ala His Gly Asn
 65 70 75 80
 agt ggc atg gtt cgt gcc aaa ttc cga agc aat ctt cct gct aag gcc 345
 Ser Gly Met Val Arg Ala Lys Phe Arg Ser Asn Leu Pro Ala Lys Ala
 81 86 91 96
 att gga cac aga atc cga gtg atg ctg tac ccc tca agg att taa act 393
 Ile Gly His Arg Ile Arg Val Met Leu Tyr Pro Ser Arg Ile *
 97 102 107

aacgaagt

401

<210> 55
 <211> 5759
 <212> DNA
 <213> Homo sapiens

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<400> 55

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gagcaaaagt tgcacagcta aaccaggggc tcattcccag gacagac atg cag tta	176
	Met Gln Leu
	1
tgg att ccg aaa gac aag tca agg aca ctg atg aca ttg aaa gtc cta	224
Trp Ile Pro Lys Asp Lys Ser Arg Thr Leu Met Thr Leu Lys Val Leu	
4 9 14 19	
aac gca gta tcc gag aca gtg gct aca tcg act gct ggg att ccg agc	272
Asn Ala Val Ser Glu Thr Val Ala Thr Ser Thr Ala Gly Ile Pro Ser	
20 25 30 35	
gca gcg act ccc tct ctc ctc ctc gcc acg gca gag atg att cct tcg	320
Ala Ala Thr Pro Ser Leu Leu Leu Ala Thr Ala Glu Met Ile Pro Ser	
36 41 46 51	
aca gcc tgg att cct ttg gct ctc gct cgt cgg cag acg cct tca cca	368
Thr Ala Trp Ile Pro Leu Ala Leu Ala Arg Arg Gln Thr Pro Ser Pro	
52 57 62 67	
gat gta gtc ctc agg gga agc agc gat ggg aga gga agc gac tct gaa	416
Asp Val Val Leu Arg Gly Ser Ser Asp Gly Arg Gly Ser Asp Ser Glu	
68 73 78 83	
tcc gac ttg cct cat cgg aag ctg cca gat gtg aag aag gat gac atg	464
Ser Asp Leu Pro His Arg Lys Leu Pro Asp Val Lys Lys Asp Asp Met	
84 89 94 99	
tct gca cgg cgg act tcc cat ggt gag ccg aaa tca gca gtg cct ttt	512
Ser Ala Arg Arg Thr Ser His Gly Glu Pro Lys Ser Ala Val Pro Phe	
100 105 110 115	
aac cag tac ctc ccg aac aaa agc aat cag acg gcc tac gtc ccc gcg	560
Asn Gln Tyr Leu Pro Asn Lys Ser Asn Gln Thr Ala Tyr Val Pro Ala	
116 121 126 131	
cct ctg aga aag aag aaa gca gag aga gag gaa tac cgc aag agc tgg	608
Pro Leu Arg Lys Lys Lys Ala Glu Arg Glu Glu Tyr Arg Lys Ser Trp	

132	137	142	147	
agt acc gcc acc tcc ccg ctg ggt ggg gag agg ccc ttc aga tac ggt				656
Ser Thr Ala Thr Ser Pro Leu Gly Gly Glu Arg Pro Phe Arg Tyr Gly				
148	153	158	163	
ccg aga act cct gtg tct gat gac gca gag agc acc agc atg ttt gac				704
Pro Arg Thr Pro Val Ser Asp Asp Ala Glu Ser Thr Ser Met Phe Asp				
164	169	174	179	
atg cgg tgt gag gag gag gcc gcg gtg cag ccg cac agc agg gcc cgc				752
Met Arg Cys Glu Glu Glu Ala Ala Val Gln Pro His Ser Arg Ala Arg				
180	185	190	195	
cag gag cag ctg cag ctg ata aat aac cag ctg agg gaa gag gac gac				800
Gln Glu Gln Leu Gln Leu Ile Asn Asn Gln Leu Arg Glu Glu Asp Asp				
196	201	206	211	
aaa tgg caa gat gac ctg gct cgt tgg aag agt cgt aga aga agt gtt				848
Lys Trp Gln Asp Asp Leu Ala Arg Trp Lys Ser Arg Arg Arg Ser Val				
212	217	222	227	
tct cag gac tta atc aag aaa gag gaa gaa agg aaa aaa atg gag aag				896
Ser Gln Asp Leu Ile Lys Lys Glu Glu Glu Arg Lys Lys Met Glu Lys				
228	233	238	243	
tta ctg gct gga gaa gat ggg aca agt gaa cga agg aaa agc atc aaa				944
Leu Leu Ala Gly Glu Asp Gly Thr Ser Glu Arg Arg Lys Ser Ile Lys				
244	249	254	259	
acc tac aga gaa att gtt caa gaa aaa gag cgg aga gag aga gag ctg				992
Thr Tyr Arg Glu Ile Val Gln Glu Lys Glu Arg Arg Glu Arg Glu Leu				
260	265	270	275	
cat gaa gca tat aag aac gct cgg tcc cag gag gag gca gag ggg atc				1040
His Glu Ala Tyr Lys Asn Ala Arg Ser Gln Glu Glu Ala Glu Gly Ile				
276	281	286	291	
ctt caa cag tac att gag agg ttc acc atc agt gag gct gtt ctc gaa				1088
Leu Gln Gln Tyr Ile Glu Arg Phe Thr Ile Ser Glu Ala Val Leu Glu				
292	297	302	307	
cgc ttg gag atg cca aaa att ctg gaa aga agc cat tca aca gag cca				1136
Arg Leu Glu Met Pro Lys Ile Leu Glu Arg Ser His Ser Thr Glu Pro				
308	313	318	323	
aat tta tcc tcc ttc ctg aat gac ccc aat ccc atg aaa tac ctg cgg				1184
Asn Leu Ser Ser Phe Leu Asn Asp Pro Asn Pro Met Lys Tyr Leu Arg				
324	329	334	339	
caa cag tca ctg cct cca ccc aaa ttc act gcc act gtt gaa acc acc				1232
Gln Gln Ser Leu Pro Pro Pro Lys Phe Thr Ala Thr Val Glu Thr Thr				
340	345	350	355	
att gct cgt gcc agt gtt ctg gat acc agc atg tca gca ggc agt ggg				1280
Ile Ala Arg Ala Ser Val Leu Asp Thr Ser Met Ser Ala Gly Ser Gly				
356	361	366	371	

tct cca agc aaa act gtc act ccc aaa gca gtg cct atg ctg aca ccc	1328
Ser Pro Ser Lys Thr Val Thr Pro Lys Ala Val Pro Met Leu Thr Pro	
372 377 382 387	
aag cct tac tcc cag ccc aaa aat tct caa gat gtt ctg aag acc ttt	1376
Lys Pro Tyr Ser Gln Pro Lys Asn Ser Gln Asp Val Leu Lys Thr Phe	
388 393 398 403	
aag gta gac ggg aaa gtc agt gtg aat gga gag acg gtt cat aga gag	1424
Lys Val Asp Gly Lys Val Ser Val Asn Gly Glu Thr Val His Arg Glu	
404 409 414 419	
gag gag aag gaa aga gag tgt ccc acg gtg gca cct gcc cac tcc tta	1472
Glu Glu Lys Glu Arg Glu Cys Pro Thr Val Ala Pro Ala His Ser Leu	
420 425 430 435	
acc aaa tcc cag atg ttt gaa ggt gtg gcc aga gtg cac ggg tct cca	1520
Thr Lys Ser Gln Met Phe Glu Gly Val Ala Arg Val His Gly Ser Pro	
436 441 446 451	
ctg gag ctg aaa caa gac aac ggt agc atc gag atc aac ata aag aag	1568
Leu Glu Leu Lys Gln Asp Asn Gly Ser Ile Glu Ile Asn Ile Lys Lys	
452 457 462 467	
cca aac tct gtt ccc caa gag ctc gca gca acc act gag aaa acg gaa	1616
Pro Asn Ser Val Pro Gln Glu Leu Ala Ala Thr Thr Glu Lys Thr Glu	
468 473 478 483	
ccg aat agt caa gag gac aag aat gat ggt gga aaa tca aga aaa ggg	1664
Pro Asn Ser Gln Glu Asp Lys Asn Asp Gly Gly Lys Ser Arg Lys Gly	
484 489 494 499	
aat ata gaa ctt gcc tca tca gaa cca cag cat ttt aca aca act gtg	1712
Asn Ile Glu Leu Ala Ser Ser Glu Pro Gln His Phe Thr Thr Thr Val	
500 505 510 515	
act cga tgc agc ccg acc gtg gcc ttt gtg gaa ttt ccc tcc agc ccc	1760
Thr Arg Cys Ser Pro Thr Val Ala Phe Val Glu Phe Pro Ser Ser Pro	
516 521 526 531	
cag ctg aag aat gat gtg tcg gaa gaa aaa gac cag aag aaa cca gaa	1808
Gln Leu Lys Asn Asp Val Ser Glu Glu Lys Asp Gln Lys Lys Pro Glu	
532 537 542 547	
aat gaa atg agt gga aag gtg gag ttg gtg ctg tca caa aag gtg gta	1856
Asn Glu Met Ser Gly Lys Val Glu Leu Val Leu Ser Gln Lys Val Val	
548 553 558 563	
aag cca aaa tct cca gaa ccc gaa gca acg ctg aca ttt cca ttt ctg	1904
Lys Pro Lys Ser Pro Glu Pro Glu Ala Thr Leu Thr Phe Pro Phe Leu	
564 569 574 579	
gac aaa atg cct gaa gcc aac caa cta cat ttg cca aat ctc aat tct	1952
Asp Lys Met Pro Glu Ala Asn Gln Leu His Leu Pro Asn Leu Asn Ser	
580 585 590 595	

caa gtg gat tct cca agc agt gag aag tca cct gtt acg aca cct ttt	2000
Gln Val Asp Ser Pro Ser Ser Glu Lys Ser Pro Val Thr Thr Pro Phe	
596 601 606 611	
aag ttc tgg gca tgg gac cca gaa gag gag cgc agg cga cag gaa aaa	2048
Lys Phe Trp Ala Trp Asp Pro Glu Glu Glu Arg Arg Arg Gln Glu Lys	
612 617 622 627	
tgg caa cag gaa cag gaa cgt ttg ctc cag gag aga tac cag aag gag	2096
Trp Gln Gln Glu Gln Glu Arg Leu Leu Gln Glu Arg Tyr Gln Lys Glu	
628 633 638 643	
cag gac aag ctg aaa gaa gag tgg gaa aag gcc caa aag gag gtg gaa	2144
Gln Asp Lys Leu Lys Glu Glu Trp Glu Lys Ala Gln Lys Glu Val Glu	
644 649 654 659	
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Leu Gly Asn Cys Gln Asp Glu Lys Gln Asp Arg Arg Trp Lys Lys Ser	
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Met Glu Pro Gly Asn
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Ala Trp Glu Cys Gly Ser Ser Arg Gly Pro Trp Gly Leu Leu Arg Tyr
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Thr Phe Ala Pro Val Arg Ala Ser Arg Pro Trp Ala Cys Leu Pro Lys
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ggc tca cta agc cag agg cca aag gtg ccc cct ccc gtt cac cta cca 533
Gly Ser Leu Ser Gln Arg Pro Lys Val Pro Pro Pro Val His Leu Pro
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Pro Lys Ser Ser Cys Pro Pro Arg Ala Gly Gly Gly Gly Ala Gln Gly
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agg cgg gtt cca tgt aca tat tta tca ccc ctt tca cat agc ccc aag 629
Arg Arg Val Pro Cys Thr Tyr Leu Ser Pro Leu Ser His Ser Pro Lys
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671

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 Arg Met Thr Phe Gly Thr Ala Ser Glu Leu Ala Ser Val Cys Met Pro
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 Arg Asn Lys *
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Glu Pro Ala Pro Glu Pro Glu Pro Glu Pro Lys Pro Gly Ala Gly Thr
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Ser Glu Ala Phe Ser Arg Leu Trp Thr Asp Val Met Gly Ile Leu Asp
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Pro Thr Ser Leu Gln Leu Arg Ser Gln Ile Glu Glu Ser Leu Gly Phe
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Cys Ser Ala Val Ser Thr Pro Glu Val Glu Arg Lys Asn Pro Leu His
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Ile Thr Met Ser Asp Glu Glu Arg Ile Gln Leu Met Met Met Val Lys				
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Asp Gly Ser Tyr Pro Thr Phe Asp Gly Ser Ser Asn Cys Asn Ser Arg				
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Glu Gln Ser Asp Asp Glu Thr Glu Glu Ser Val Lys Phe Lys Arg Leu				
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His Lys Leu Val Asn Ser Thr Arg Arg Val Arg Lys Lys Leu Ile Arg				
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Val Glu Glu Met Lys Lys Pro Ser Thr Glu Gly Gly Glu Glu His Val				
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Phe Glu Asn Ser Pro Val Leu Asp Glu Arg Ser Ala Leu Tyr Ser Gly				
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Cys Ser Phe Gly Gly Phe Asp Leu Thr Asn Arg Ser Leu His Val Gly	
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His	Ser	Leu	Asp	Asp	Leu	Gln	Val	Glu	Pro	Gly	Ala	Glu	Gln	Asp	Val	
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Pro	Thr	Glu	Val	Thr	Glu	Pro	Pro	Pro	Gln	Ile	Val	Pro	Glu	Val	Pro	
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Pro	Asp	Ala	Pro	Cys	Leu	Pro	Val	Lys	Arg	Gly	Ser	Pro	Ala	Ser	Pro	
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Phe Lys Leu Pro Pro Gly Pro Glu Ala Met *				
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Ser Leu Ser Leu Ala Asp Leu Cys Val Trp Ala Thr Leu Lys Gly Asn	
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Ala Ala Trp Gln Glu Gln Leu Lys Gln Lys Lys Ala Pro Val His Val	
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Ile Met Lys Tyr Ala Glu Lys Leu Ile Gln Glu Gly Lys Ala Tyr Val	
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Ile Trp Glu Tyr Ser	Arg Leu Asn Leu Asn	Asn Thr Val Leu Ser	Lys	
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Tyr Val Asn Lys Asn Ser Lys His Glu Glu Leu Met Leu Gly Asp Pro	
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Arg Arg Leu Leu Ser Val Asn Ile Arg Val Arg Ala Asp Leu Arg Asp				
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Asn Tyr Ser Pro Gly Trp Lys Phe Asn His Trp Glu Leu Lys Gly Val				
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Pro Ile Arg Leu Glu Val Gly Pro Arg Asp Met Lys Ser Cys Gln Phe				
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Val Ala Val Arg Arg Asp Thr Gly Glu Lys Leu Thr Val Ala Glu Asn				
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Glu Ala Glu Thr Lys Leu Gln Ala Ile Leu Glu Asp Ile Gln Val Thr				
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Leu Phe Thr Arg Ala Ser Glu Asp Leu Lys Thr His Met Val Val Ala				
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Asn Thr Met Glu Asp Phe Gln Lys Ile Leu Asp Ser Gly Lys Ile Val				
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Gln Ile Pro Phe Cys Gly Glu Ile Asp Cys Glu Asp Trp Ile Lys Lys				
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Met Pro Phe Pro Val Thr	
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Glu Glu Glu Leu Gln Arg Arg Ile Leu Ile Leu Gly Lys Leu Asn Asn	
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Tyr Arg Leu Gly Val His Thr Lys Gly Ala Asp Ile Asp Ala Leu Cys	
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Asn Ala Leu Asp Lys Gln Glu Glu Leu Thr Pro Leu Gly Val His Leu	
678 683 688 693	
gca cga tta ccc gtt gag cca cat att gga aaa atg att ctt ttt gga	2227
Ala Arg Leu Pro Val Glu Pro His Ile Gly Lys Met Ile Leu Phe Gly	
694 699 704 709	
gca ctg ttc tgc tgc tta gac cca gta ctc act att gct gct agt ctc	2275
Ala Leu Phe Cys Cys Leu Asp Pro Val Leu Thr Ile Ala Ala Ser Leu	
710 715 720 725	
agt ttc aaa gat cca ttt gtc att cca ctg gga aaa gaa aag att gca	2323
Ser Phe Lys Asp Pro Phe Val Ile Pro Leu Gly Lys Glu Lys Ile Ala	
726 731 736 741	
gat gca aga aga aag gaa ttg gca aag gat act aga agt gat cac tta	2371
Asp Ala Arg Arg Lys Glu Leu Ala Lys Asp Thr Arg Ser Asp His Leu	
742 747 752 757	
aca gtt gtg aat gcg ttt gag ggc tgg gaa gag gct agg cga cgt ggt	2419
Thr Val Val Asn Ala Phe Glu Gly Trp Glu Glu Ala Arg Arg Arg Gly	
758 763 768 773	
ttc aga tac gaa aag gac tat tgc tgg gaa tat ttt ctg tct tca aac	2467
Phe Arg Tyr Glu Lys Asp Tyr Cys Trp Glu Tyr Phe Leu Ser Ser Asn	
774 779 784 789	
aca ctg cag atg ctg cat aac atg aaa gga cag ttt gct gag cat ctt	2515
Thr Leu Gln Met Leu His Asn Met Lys Gly Gln Phe Ala Glu His Leu	
790 795 800 805	
ctt gga gct gga ttt gta agc agt aga aat cct aaa gat cca gaa tct	2563
Leu Gly Ala Gly Phe Val Ser Ser Arg Asn Pro Lys Asp Pro Glu Ser	
806 811 816 821	
aat ata aat tca gat aat gag aag ata att aaa gct gtc atc tgt gct	2611
Asn Ile Asn Ser Asp Asn Glu Lys Ile Ile Lys Ala Val Ile Cys Ala	
822 827 832 837	
ggg tta tat ccc aaa gtt gct aaa att cga cta aat ttg ggt aaa aaa	2659
Gly Leu Tyr Pro Lys Val Ala Lys Ile Arg Leu Asn Leu Gly Lys Lys	

838	843	848	853	
aga aaa atg gta aaa gtt tac aca aaa acc gat ggc ctg gtt gct gtt				2707
Arg Lys Met Val Lys Val Tyr Thr Lys Thr Asp Gly Leu Val Ala Val				
854	859	864	869	
cat cct aaa tct gtt aat gtg gag caa aca gac ttt cac tac aac tgg				2755
His Pro Lys Ser Val Asn Val Glu Gln Thr Asp Phe His Tyr Asn Trp				
870	875	880	885	
ctt atc tat cac cta aag atg aga aca agc agt ata tac ttg tat gac				2803
Leu Ile Tyr His Leu Lys Met Arg Thr Ser Ser Ile Tyr Leu Tyr Asp				
886	891	896	901	
tgc aca gag gtt tcc cca tac tgt ctc ttg ttt ttt gga ggt gac att				2851
Cys Thr Glu Val Ser Pro Tyr Cys Leu Leu Phe Phe Gly Gly Asp Ile				
902	907	912	917	
tcc atc cag aag gat aac gat cag gaa act att gct gta gat gag tgg				2899
Ser Ile Gln Lys Asp Asn Asp Gln Glu Thr Ile Ala Val Asp Glu Trp				
918	923	928	933	
att gta ttt cag tct cca gca aga att gcc cat ctt gtt aag gaa tta				2947
Ile Val Phe Gln Ser Pro Ala Arg Ile Ala His Leu Val Lys Glu Leu				
934	939	944	949	
aga aag gaa cta gat att ctt ctg caa gag aag att gaa agt cct cat				2995
Arg Lys Glu Leu Asp Ile Leu Leu Gln Glu Lys Ile Glu Ser Pro His				
950	955	960	965	
cct gta gac tgg aat gac act aaa tcc aga gac tgt gca gta ctg tca				3043
Pro Val Asp Trp Asn Asp Thr Lys Ser Arg Asp Cys Ala Val Leu Ser				
966	971	976	981	
gct att ata gac ttg atc aaa aca cag gaa aag gca act ccc agg aac				3091
Ala Ile Ile Asp Leu Ile Lys Thr Gln Glu Lys Ala Thr Pro Arg Asn				
982	987	992	997	
ttt ccg cca cga ttc cag gat gga tat tac agc tga cagc ttttcagggg				3141
Phe Pro Pro Arg Phe Gln Asp Gly Tyr Tyr Ser *				
998	1003	1008		
tggtctgaaa agccagtttg acagccattc ttcattcattg tttaaatttt ggctggatgc				3201
caaaccctgg gacatgaaca attttcatgt gtaaggtaga agccttcagt aggtagtaaa				3261
gacttaatgt gcatgacttg atgttatatg tagagatata tatatatata tatatatacc				3321
ataaaagcaa tatgttctct gatcatatac tctgctgtgg tcatgcccac tctttgggag				3381
tatattccct ttatatatat tgagtattgt accacttgag aaattccttt gttctgttat				3441
acaaaattaa tctttctgct cataatgatt gatgatacca ccagtaaaaa taggatgttt				3501
accccaaac aagtgtcaat taagaatttg aacacaacca catttttttaa aatgaaactt				3561
ctatcggaag taaattaatt tgttgtaata aagtccagta tttaataaaa tgtacaatgt				3621

taaatctcaa aaaaaaaaaa aaaaaaaaaa actcggcgca agctta

3667

<210> 62
<211> 1047
<212> DNA
<213> Homo sapiens

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<222> (308)..(454)

<400> 62

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ataagcttgc ggccgcatat cttttttttt tttttttttt ttaagtattt atatttttat 120

tccactctaa cacctcagag taaagaactg atgggcaggc atcggttctt gctgacaatt 180

gccaaaccggc atgagattgc tgagctgagg tggactctcc agacactgga actggaactc 240

caggcccaat ggctcttggg aagaatgctg caacgtgaga cccttgagag agactgactt 300

gttgaag atg aag aga aaa cca aga gcc tcc agt cca gtt gtt gaa gag 349
Met Lys Arg Lys Pro Arg Ala Ser Ser Pro Val Val Glu Glu
1 5 10

caa cca cga gcc aac acc aag gag aca agg aag aag aag tcc ttc tct 397
Gln Pro Arg Ala Asn Thr Lys Glu Thr Arg Lys Lys Lys Ser Phe Ser
15 20 25 30

caa ccg atg acc gca agc aca aag aag agt ccc aag ata gcg aag aaa 445
Gln Pro Met Thr Ala Ser Thr Lys Lys Ser Pro Lys Ile Ala Lys Lys
31 36 41 46

gga aaa taa ctcaagg gagagccagg aagaaaaatg ctccacaaaa atccatggct 501
Gly Lys *
47

ttaagaatac ttgaggaagg gagcaggcca acaccctctg gccacagtga ccagctgaat 561

gaggaactct aacagaatga gctgcagttg gagcaacaga ggggacatag ctggaacaac 621

agagcgaggg gacacagccg gagcaacaga gtgggaggat gccaacatt tcaactctct 681

ccctgagcag cgagtaattt cagggcaagc ccagagacta ggatccatct gagaagtctt 741

cagaggtctg acccagagta ctcaacaaca ggatacgtcc catggtgatg aaaataaaat 801

gaatcttgtg ttcaccgttg tattcctcac gacttaagtt aaaaacctga tgaaaagtgg 861

ttaatctcca taatgggtgt tagctccatc gcaggagca tgaggttggg cagacagagt 921

cgggcaaggt tatggagaag acttaatcca tccacaagag gtccgagtat gttgatgaag 981

tgatgacagt actgtttcaa gaacatcaac cctgccgcag tgcggacgcg tgggtcgacc 1041
 cgggaa 1047

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 <211> 1386
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (89) .. (838)

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 cggtggcctc ggtcccggta agccaggc atg aag atc aca agg cag aaa cat 112
 Met Lys Ile Thr Arg Gln Lys His
 1 5
 gcc aag aag cat ctt ggc ttc ttc cgc aac aac ttc gga gtc cgc gag 160
 Ala Lys Lys His Leu Gly Phe Phe Arg Asn Asn Phe Gly Val Arg Glu
 9 14 19 24
 ccg tac cag atc ctg ctg gac ggc acc ttc tgt cag gcg gcg ctg cgg 208
 Pro Tyr Gln Ile Leu Leu Asp Gly Thr Phe Cys Gln Ala Ala Leu Arg
 25 30 35 40
 ggc cgc atc cag ctg cgg gag cag ctg ccc cgc tac ctc atg ggg gag 256
 Gly Arg Ile Gln Leu Arg Glu Gln Leu Pro Arg Tyr Leu Met Gly Glu
 41 46 51 56
 acg cag ctg tgc acc aca aga tgt gtg tta aaa gag cta gaa aca ttg 304
 Thr Gln Leu Cys Thr Thr Arg Cys Val Leu Lys Glu Leu Glu Thr Leu
 57 62 67 72
 gga aag gac tta tat ggg gca aaa ctg att gca caa aaa tgc caa gtt 352
 Gly Lys Asp Leu Tyr Gly Ala Lys Leu Ile Ala Gln Lys Cys Gln Val
 73 78 83 88
 cga aat tgt cct cat ttc aag aat gca gtg agt gga tca gaa tgt ctg 400
 Arg Asn Cys Pro His Phe Lys Asn Ala Val Ser Gly Ser Glu Cys Leu
 89 94 99 104
 ctt tcc atg gtt gaa gag gga aat cct cat cat tat ttt gtg gca aca 448
 Leu Ser Met Val Glu Glu Gly Asn Pro His His Tyr Phe Val Ala Thr
 105 110 115 120
 cag gat cag aat ttg tct gtg aaa gta aaa aag aag cct gga gtt cct 496
 Gln Asp Gln Asn Leu Ser Val Lys Val Lys Lys Lys Pro Gly Val Pro
 121 126 131 136
 ctc atg ttt att att cag aac act atg gtt ttg gac aaa cct tct ccc 544

Leu Met Phe Ile Ile Gln Asn Thr Met Val Leu Asp Lys Pro Ser Pro	
137 142 147 152	
aaa aca att gcc ttt gta aaa gca gtg gag tca ggt cag ctt gtc tca	592
Lys Thr Ile Ala Phe Val Lys Ala Val Glu Ser Gly Gln Leu Val Ser	
153 158 163 168	
gtg cat gag aaa gaa agt atc aaa cat ctc aaa gag gaa cag ggt tta	640
Val His Glu Lys Glu Ser Ile Lys His Leu Lys Glu Glu Gln Gly Leu	
169 174 179 184	
gtg aaa aac act gaa cag agt aga aga aaa aag cgc aag aaa ata agt	688
Val Lys Asn Thr Glu Gln Ser Arg Arg Lys Lys Arg Lys Lys Ile Ser	
185 190 195 200	
ggg ccc aat cct ctt agt tgt ttg aag aaa aag aaa aag gca ccg gac	736
Gly Pro Asn Pro Leu Ser Cys Leu Lys Lys Lys Lys Lys Ala Pro Asp	
201 206 211 216	
aca caa tca tct gct tct gaa aag aaa aga aaa aga aaa aga att cgg	784
Thr Gln Ser Ser Ala Ser Glu Lys Lys Arg Lys Arg Lys Arg Ile Arg	
217 222 227 232	
aac aga tct aac cca aaa gta ctt tct gag aag cag aat gca gaa gga	832
Asn Arg Ser Asn Pro Lys Val Leu Ser Glu Lys Gln Asn Ala Glu Gly	
233 238 243 248	
gaa tga atcctttgga tactttcaag gacattcaaa tgtgaaaatg aattttttac	888
Glu *	
249	
aactagaagt atttataata aaagaccaaa cttatttttg taaatgaacc catatgcttt	948
actaaaatta attataaaat aaaaacagt accagtctag ccagcatgga aaaccccatc	1008
tctactaaaa tacaaaaatt agctgggcat gatgggtgcac agttgtaatt ccagctactc	1068
aggaggctga ggcattgagaa tcgcttgaac ctgggaggca gagattgcag tgagcccagt	1128
tcgtgtcact tcaactccagc ctgggcaaca gaggtagaac atgtctcaaa aaaaaaata	1188
aaaacagtga atgggtgtag gtgtgatgga attcacttta cttactaaat ggtttcggga	1248
ggttgtttct ccaggtaaaa ttgtgcctc tctgggtcca tccccacctt caaacattat	1308
atgcaaacag ttttaaaaaa ttttacagtt ctaaaagggc ttgtgacaaa aaagaggcag	1368
tcctctttca cattgaca	1386

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<211> 1503

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (125)..(1474)

<400> 64

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tatctggagc agtcggggcg ggcaggccca gctgagaggt gcgcgggcga ggacagcggc	120
agcg atg cgg gaa tgc ata tca gtc cac gtg ggc caa gcg gga gtt cag	169
Met Arg Glu Cys Ile Ser Val His Val Gly Gln Ala Gly Val Gln	
1 5 10	
att ggc aat gcc tgc tgg gag ctc ttc tgc ctg gaa cac ggc atc cag	217
Ile Gly Asn Ala Cys Trp Glu Leu Phe Cys Leu Glu His Gly Ile Gln	
16 21 26 31	
gca gac ggc act ttt gat gct caa gct agc aag atc aac gat gat gac	265
Ala Asp Gly Thr Phe Asp Ala Gln Ala Ser Lys Ile Asn Asp Asp Asp	
32 37 42 47	
tcc ttc acc acc ttt ttc agc gag act ggc aat ggg aag cat gtg ccc	313
Ser Phe Thr Thr Phe Phe Ser Glu Thr Gly Asn Gly Lys His Val Pro	
48 53 58 63	
cgg gcc gtc atg ata gat ctg gag cct act gta gtg gat gag gtt cgg	361
Arg Ala Val Met Ile Asp Leu Glu Pro Thr Val Val Asp Glu Val Arg	
64 69 74 79	
gca gga acc tac cgc cag ctc ttc cat cca gag cag ctg atc aca gga	409
Ala Gly Thr Tyr Arg Gln Leu Phe His Pro Glu Gln Leu Ile Thr Gly	
80 85 90 95	
aag gag gat gca gcc aac aac tat gcc cgg ggc cac tac acg gtg ggc	457
Lys Glu Asp Ala Ala Asn Asn Tyr Ala Arg Gly His Tyr Thr Val Gly	
96 101 106 111	
aag gag agc att gac ctg gtg ctg gac cgc ata cgg aag ctg aca gat	505
Lys Glu Ser Ile Asp Leu Val Leu Asp Arg Ile Arg Lys Leu Thr Asp	
112 117 122 127	
gct tgc tct ggc ctg cag ggc ttc ctg att ttc cac agt ttt ggt ggg	553
Ala Cys Ser Gly Leu Gln Gly Phe Leu Ile Phe His Ser Phe Gly Gly	
128 133 138 143	
ggc act ggc tcc ggc ttc act tct ctg ctg atg gaa cgc ctc tcc ctg	601
Gly Thr Gly Ser Gly Phe Thr Ser Leu Leu Met Glu Arg Leu Ser Leu	
144 149 154 159	
gat tat ggc aag aaa tcc aag ctg gag ttt gcc atc tac cca gcc ccc	649
Asp Tyr Gly Lys Lys Ser Lys Leu Glu Phe Ala Ile Tyr Pro Ala Pro	
160 165 170 175	
cag gtc tct act gca gtg gtg gag ccc tac aac tcc atc ctg acc acc	697
Gln Val Ser Thr Ala Val Val Glu Pro Tyr Asn Ser Ile Leu Thr Thr	
176 181 186 191	

cac acc aca ctg gaa cat tca gat tgt gct ttc atg gtg gac aac gaa His Thr Thr Leu Glu His Ser Asp Cys Ala Phe Met Val Asp Asn Glu 192 197 202 207	745
gcc atc tat gac atc tgc cgc agg aac ctt gac att gag cgc cct acc Ala Ile Tyr Asp Ile Cys Arg Arg Asn Leu Asp Ile Glu Arg Pro Thr 208 213 218 223	793
tat acc aac ctc aac cgc ctc atc agt cag att gtg tcc tca atc act Tyr Thr Asn Leu Asn Arg Leu Ile Ser Gln Ile Val Ser Ser Ile Thr 224 229 234 239	841
gct tct ctc cgc ttt gac ggg gcc ctc aat gtg gac ctc act gag ttc Ala Ser Leu Arg Phe Asp Gly Ala Leu Asn Val Asp Leu Thr Glu Phe 240 245 250 255	889
cag acc aac ctg gtg ccc tac ccc cgc atc cac ttc ccg ctg gtc acc Gln Thr Asn Leu Val Pro Tyr Pro Arg Ile His Phe Pro Leu Val Thr 256 261 266 271	937
tac gcg ccc atc atc tct gcc gag aaa gcc tat cac gaa cag ctc tct Tyr Ala Pro Ile Ile Ser Ala Glu Lys Ala Tyr His Glu Gln Leu Ser 272 277 282 287	985
gtg gcc gag ata acc agc tcc tgc ttt gag ccc aac agc cag atg gtg Val Ala Glu Ile Thr Ser Ser Cys Phe Glu Pro Asn Ser Gln Met Val 288 293 298 303	1033
aag tgc gac ccg aga cat ggc aag tac atg gcc tgc tgc atg ctc tac Lys Cys Asp Pro Arg His Gly Lys Tyr Met Ala Cys Cys Met Leu Tyr 304 309 314 319	1081
cgg ggc gac gtg gtg ccc aag gat gtg aat gtc gct att gct gcc atc Arg Gly Asp Val Val Pro Lys Asp Val Asn Val Ala Ile Ala Ala Ile 320 325 330 335	1129
aag acc aag agg acc atc cag ttt gta gac tgg tgt ccc aca ggc ttc Lys Thr Lys Arg Thr Ile Gln Phe Val Asp Trp Cys Pro Thr Gly Phe 336 341 346 351	1177
aag gtg ggc atc aac tac cag ccc ccg acc gtg gtc ccc ggg gga gac Lys Val Gly Ile Asn Tyr Gln Pro Pro Thr Val Val Pro Gly Gly Asp 352 357 362 367	1225
ctg gcc aag gtg cag cgg gcc gtc tgc atg ctc agc aac acc acg gcc Leu Ala Lys Val Gln Arg Ala Val Cys Met Leu Ser Asn Thr Thr Ala 368 373 378 383	1273
att gcg gag gcc tgg gcc cgc ctc gac cac aag ttc gac ctc atg tac Ile Ala Glu Ala Trp Ala Arg Leu Asp His Lys Phe Asp Leu Met Tyr 384 389 394 399	1321
gcc aag cgg gcc ttt gtg cat tgg tat gtg gga gag ggg atg gaa gaa Ala Lys Arg Ala Phe Val His Trp Tyr Val Gly Glu Gly Met Glu Glu 400 405 410 415	1369
gga gaa ttt tct gag gcc agg gaa gac tta gct gcc ctg gag aag gat	1417

Gly Glu Phe Ser Glu Ala Arg Glu Asp Leu Ala Ala Leu Glu Lys Asp
 416 421 426 431

tat gaa gaa gtg ggg act gat tcg ttt gaa gaa gaa aat gaa ggg gag 1465
 Tyr Glu Glu Val Gly Thr Asp Ser Phe Glu Glu Asn Glu Gly Glu
 432 437 442 447

gaa ttt taa atatatacct tcccccttgaa aaaaaaaat 1503
 Glu Phe *
 448

<210> 65
 <211> 5376
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (109)..(2679)

<400> 65

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tcggcagcag ctggaattca cgttccttca gaagatatcc ctgaaact atg gac gaa 117
 Met Asp Glu
 1

gat tct tcg ttg aga gat tat act gta agc ttg gac tct gac atg gat 165
 Asp Ser Ser Leu Arg Asp Tyr Thr Val Ser Leu Asp Ser Asp Met Asp
 4 9 14 19

gat gca tct aaa ttt ctt cag gat tat gat att cga act ggc aac acc 213
 Asp Ala Ser Lys Phe Leu Gln Asp Tyr Asp Ile Arg Thr Gly Asn Thr
 20 25 30 35

agg gaa gct ttg agt cct tgt cca agt act gta agt acc aag tct cag 261
 Arg Glu Ala Leu Ser Pro Cys Pro Ser Thr Val Ser Thr Lys Ser Gln
 36 41 46 51

cca ggc agc agt gct tct tct agt tct gga gtt aaa atg acc agc ttt 309
 Pro Gly Ser Ser Ala Ser Ser Ser Ser Gly Val Lys Met Thr Ser Phe
 52 57 62 67

gct gaa caa aaa ttc agg aaa ctg aat cat acc gat gga aaa agt agt 357
 Ala Glu Gln Lys Phe Arg Lys Leu Asn His Thr Asp Gly Lys Ser Ser
 68 73 78 83

gga agc agt tct caa aaa act aca cca gaa ggc tct gaa ctt aat att 405
 Gly Ser Ser Ser Gln Lys Thr Thr Pro Glu Gly Ser Glu Leu Asn Ile
 84 89 94 99

cct cat gtg gtt gct tgg gca caa att cca gaa gaa aca ggg ctt cca 453
 Pro His Val Val Ala Trp Ala Gln Ile Pro Glu Glu Thr Gly Leu Pro

100	105	110	115	
cag gga cgg gac act acc cag ctg ttg gcc tct gaa atg gtg cat ctt				501
Gln Gly Arg Asp Thr	Gln Leu Leu Ala	Ser Glu Met Val His	Leu	
116	121	126	131	
agg atg aaa cta gaa gaa aag agg cgt gct ata gaa gcc cag aaa aag				549
Arg Met Lys Leu Glu Glu Lys Arg Arg Ala Ile Glu Ala Gln Lys Lys				
132	137	142	147	
aaa atg gaa gct gct ttt acc aaa cag aga cag aaa atg gga agg aca				597
Lys Met Glu Ala Ala Phe Thr Lys Gln Arg Gln Lys Met Gly Arg Thr				
148	153	158	163	
gca ttc ctt act gta gtg aaa aag aaa ggg gat ggg ata tct cct cta				645
Ala Phe Leu Thr Val Val Lys Lys Lys Gly Asp Gly Ile Ser Pro Leu				
164	169	174	179	
cga gag gaa gcg gcg ggt gca gaa gat gag aaa gta tat act gat cga				693
Arg Glu Glu Ala Ala Gly Ala Glu Asp Glu Lys Val Tyr Thr Asp Arg				
180	185	190	195	
gca aaa gaa aag gaa tca caa aaa act gat gga caa agg agc aag tca				741
Ala Lys Glu Lys Glu Ser Gln Lys Thr Asp Gly Gln Arg Ser Lys Ser				
196	201	206	211	
ctg gca gat ata aaa gag agc atg gag aat cct caa gcc aaa tgg cta				789
Leu Ala Asp Ile Lys Glu Ser Met Glu Asn Pro Gln Ala Lys Trp Leu				
212	217	222	227	
aag tct cca act aca cct att gat cct gag aag cag tgg aac ctg gca				837
Lys Ser Pro Thr Thr Pro Ile Asp Pro Glu Lys Gln Trp Asn Leu Ala				
228	233	238	243	
agc ccc tca gaa gaa act tta aat gaa gga gag att tta gaa tat acc				885
Ser Pro Ser Glu Glu Thr Leu Asn Glu Gly Glu Ile Leu Glu Tyr Thr				
244	249	254	259	
aaa tcc att gaa aag tta aat tca tcc ctg cat ttt cta caa caa gaa				933
Lys Ser Ile Glu Lys Leu Asn Ser Ser Leu His Phe Leu Gln Gln Glu				
260	265	270	275	
atg caa cgc ttg tca ctt cag cag gag atg tta atg cag atg aga gag				981
Met Gln Arg Leu Ser Leu Gln Gln Glu Met Leu Met Gln Met Arg Glu				
276	281	286	291	
caa caa tct tgg gtg att tca cct cca caa ccc tct cca cag aaa cag				1029
Gln Gln Ser Trp Val Ile Ser Pro Pro Gln Pro Ser Pro Gln Lys Gln				
292	297	302	307	
att cga gat ttt aag cct tct aag cag gca ggc ctg tca tca gcc att				1077
Ile Arg Asp Phe Lys Pro Ser Lys Gln Ala Gly Leu Ser Ser Ala Ile				
308	313	318	323	
gca cca ttc tcc tca gac tcc cct cgt cct act cac cca tct cca cag				1125
Ala Pro Phe Ser Ser Asp Ser Pro Arg Pro Thr His Pro Ser Pro Gln				
324	329	334	339	

tct tct aac agg aaa agt gca tct ttt tct gtt aaa agt caa agg act	1173
Ser Ser Asn Arg Lys Ser Ala Ser Phe Ser Val Lys Ser Gln Arg Thr	
340 345 350 355	
cct agg cca aat gag tta aaa ata aca cct ttg aat cga acc ttg aca	1221
Pro Arg Pro Asn Glu Leu Lys Ile Thr Pro Leu Asn Arg Thr Leu Thr	
356 361 366 371	
cct cct cgg tct gtg gat agc ctt cct cgg tta agg agg ttt tca cca	1269
Pro Pro Arg Ser Val Asp Ser Leu Pro Arg Leu Arg Arg Phe Ser Pro	
372 377 382 387	
agt caa gtt cct att caa act agg tca ttt gta tgt ttt ggg gat gat	1317
Ser Gln Val Pro Ile Gln Thr Arg Ser Phe Val Cys Phe Gly Asp Asp	
388 393 398 403	
gga gaa cct cag tta aag gaa tcc aaa cct aaa gag gaa gtt aaa aag	1365
Gly Glu Pro Gln Leu Lys Glu Ser Lys Pro Lys Glu Glu Val Lys Lys	
404 409 414 419	
gag gaa ttg gaa tcc aaa ggg act ttg gaa cag cgt gga cat aat cca	1413
Glu Glu Leu Glu Ser Lys Gly Thr Leu Glu Gln Arg Gly His Asn Pro	
420 425 430 435	
gaa gaa aag gaa atc aaa cct ttt gag tca aca gtc tct gaa gtc cta	1461
Glu Glu Lys Glu Ile Lys Pro Phe Glu Ser Thr Val Ser Glu Val Leu	
436 441 446 451	
tca ctg cct gtc aca gag act gta tgt ctg aca cca aat gag gac caa	1509
Ser Leu Pro Val Thr Glu Thr Val Cys Leu Thr Pro Asn Glu Asp Gln	
452 457 462 467	
ttg aat caa ccc aca gaa ccc cct cct aaa ccc gtt ttc cca ccc act	1557
Leu Asn Gln Pro Thr Glu Pro Pro Pro Lys Pro Val Phe Pro Pro Thr	
468 473 478 483	
gct cca aaa aat gtt aat ctg att gaa gtt tcc ctc tca gat ttg aaa	1605
Ala Pro Lys Asn Val Asn Leu Ile Glu Val Ser Leu Ser Asp Leu Lys	
484 489 494 499	
ccc cct gaa aag gct gat gta cct gtt gaa aaa tat gat gga gaa agt	1653
Pro Pro Glu Lys Ala Asp Val Pro Val Glu Lys Tyr Asp Gly Glu Ser	
500 505 510 515	
gat aaa gaa caa ttt gat gat gac cag aaa gta tgc tgt gga ttc ttt	1701
Asp Lys Glu Gln Phe Asp Asp Asp Gln Lys Val Cys Cys Gly Phe Phe	
516 521 526 531	
ttt aag gat gat caa aaa gca gaa aat gat atg gca atg aaa cgg gca	1749
Phe Lys Asp Asp Gln Lys Ala Glu Asn Asp Met Ala Met Lys Arg Ala	
532 537 542 547	
gct ttg ttg gag aaa aga tta aga agg gaa aag gaa act cag ctc cgg	1797
Ala Leu Leu Glu Lys Arg Leu Arg Arg Glu Lys Glu Thr Gln Leu Arg	
548 553 558 563	

aaa caa cag ttg gaa gca gaa atg gag cat aag aag gag gaa aca agg Lys Gln Gln Leu Glu Ala Glu Met Glu His Lys Lys Glu Glu Thr Arg 564 569 574 579	1845
cgt aaa act gag gaa gaa cgt cag aag aaa gaa gat gag aga gca cgc Arg Lys Thr Glu Glu Glu Arg Gln Lys Lys Glu Asp Glu Arg Ala Arg 580 585 590 595	1893
aga gaa ttt att agg caa gaa tat atg agg cgg aaa caa ctg aaa cta Arg Glu Phe Ile Arg Gln Glu Tyr Met Arg Arg Lys Gln Leu Lys Leu 596 601 606 611	1941
atg gaa gat atg gat aca gta att aaa ccc cgt cct caa gta gta aaa Met Glu Asp Met Asp Thr Val Ile Lys Pro Arg Pro Gln Val Val Lys 612 617 622 627	1989
caa aaa aaa cag cga cca aaa tct att cac aga gat cat att gaa tcc Gln Lys Lys Gln Arg Pro Lys Ser Ile His Arg Asp His Ile Glu Ser 628 633 638 643	2037
ccc aaa aca cca ata aag ggt cct cca gtc tct agc ctt tct ttg gca Pro Lys Thr Pro Ile Lys Gly Pro Pro Val Ser Ser Leu Ser Leu Ala 644 649 654 659	2085
tcg ctg aac acg ggt gat aac gag agt gta cat tca ggc aag agg acg Ser Leu Asn Thr Gly Asp Asn Glu Ser Val His Ser Gly Lys Arg Thr 660 665 670 675	2133
cca aga tca gag tct gta gaa ggc ttc tta tct cca agt cgt tgt ggc Pro Arg Ser Glu Ser Val Glu Gly Phe Leu Ser Pro Ser Arg Cys Gly 676 681 686 691	2181
agt cga aat gga gaa aaa gac tgg gag aat gca tca aca act tct tca Ser Arg Asn Gly Glu Lys Asp Trp Glu Asn Ala Ser Thr Thr Ser Ser 692 697 702 707	2229
gtg gct tct gga aca gaa tat aca gga cca aag ctc tac aaa gaa ccc Val Ala Ser Gly Thr Glu Tyr Thr Gly Pro Lys Leu Tyr Lys Glu Pro 708 713 718 723	2277
agt gca aaa tcc aat aag cac ata ata caa aat gct tta gct cat tgc Ser Ala Lys Ser Asn Lys His Ile Ile Gln Asn Ala Leu Ala His Cys 724 729 734 739	2325
tgt ttg gct gga aaa gta aat gaa ggt cag aag aaa aaa ata ctg gag Cys Leu Ala Gly Lys Val Asn Glu Gly Gln Lys Lys Lys Ile Leu Glu 740 745 750 755	2373
gaa atg gag aaa tca gat gcc aac aac ttc tta atc ttg ttc cgg gat Glu Met Glu Lys Ser Asp Ala Asn Asn Phe Leu Ile Leu Phe Arg Asp 756 761 766 771	2421
tca gga tgc cag ttc aga tct tta tac act tat tgc cca gaa act gaa Ser Gly Cys Gln Phe Arg Ser Leu Tyr Thr Tyr Cys Pro Glu Thr Glu 772 777 782 787	2469
gaa atc aat aaa ctg act ggg ata ggc cct aaa tct atc act aaa aaa	2517

[illegible]

cttgaatgat tatgtgaccc tggtatatatt cagtgtttgtg acaaattgtgt aaactagcgg	3915
gggaagacag tattgtatca taaatgagat gcgtagtttg ttttctttca tgggaagtag	3975
agataaaaaat atatacatatt ctctaattga gttgttttaga gaaagaacta atgtctcata	4035
tgatgtattt acttatttta aaaaaagaa taggaatgag atgtccctga gctgtacttt	4095
tctattatta taaggccttt aggcatcagt gcattctgggt tatcaacatt ttctcaaattg	4155
ctgtcaatat tttactgtaa tttatgttct tatatttatg tatatttggt aaaactgtaa	4215
aaaaatttca cagatttttt tccaatacct gtgcaagata catgtgtagc tcaaaactat	4275
ttgtgatcta ctgtttgcat gtaagagacc aggatatgta actcttatat ttttaagtga	4335
tacatattgt gtatataaca tatggatatt aaaaatgggg aattgcacat tttacctttt	4395
ggacagtaat ttctatcaca gttagaagga aatgatagtc aaatacacgt ttagattaaa	4455
actagtttaa aaaattataa atgaatctaa tcaaaatgtg aatagtagtc aaaaggataa	4515
tttaataagc attttacgtt actaaatttg ttcatttcaa tattaactaa atttccctca	4575
tcaaagcaat ctttgtgata ttacttcgct attaaataaa gaaaattgga tgcaagacaa	4635
tggagaaact ttaaaactaa acaggaccac cttttattct taaatttggtg tgtgtccaac	4695
agttgaattg aatgtctata aggtctaaag gtagaatgtg aatattgcc aagagttcat	4755
tgctctcagt ataagatttt actttattaa tgcagaagga atatggatat atttctttaa	4815
gtctgcagat ttttttatta tgggtgcagct tttttttaat tatgttttta aaattataca	4875
gttgaaaaat atgccatttc ataaagtctg aggattttcg tcaaccttac tgaaacacac	4935
tgggtgcttc atcatcagag gtcaaattat tatgataact attccattaa gtttgccaaa	4995
catttgctgt ggttaccagt gcagcctgtc aaattctgct atttgacaca gctttggaaa	5055
gatttagttc ttgggtttttc cgttttgtat tagaatgact gttacagttt tatttggctg	5115
tttaaagcca aattcagcta ttttaattatg gtttcatgga cactgttgag caatgtacag	5175
tgtatgggtg gtttacctgt ccactctaga gcattgctta cagggtttttt gttttttaag	5235
atgctgtgct gtaaaatact gtcatacttg ctatttcctg gtacagtgtg gtttttcccc	5295
tttcatttga ataaaagcat ggcaccaaatt gactcctttt ctgtttcttg aataaaatgt	5355
agtttttggt aaaattattt g	5376

<210> 66

<211> 1180

<212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (196)..(1077)

<400> 66

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gcggccgcgg gcttgggggc ttgcgcgggg ccgggcgggc ggcgcccccg gctgctcccc	120
ccgcccggcg gacccgcgcc ccgcccgggg agcgggtggtg agagccccga ctccccggac	180
gccgcccggc gtgcc atg ggg ttc ccg gcc gcg gcg ctg ctc tgc gcg ctg	231
Met Gly Phe Pro Ala Ala Ala Leu Leu Cys Ala Leu	
1 5 10	
tgc tgc ggc ctc ctg gcc ccg gct gcc cgc gcc ggc tac tcc gag gag	279
Cys Cys Gly Leu Leu Ala Pro Ala Ala Arg Ala Gly Tyr Ser Glu Glu	
13 18 23 28	
cgc tgc agc tgg agg ggc agc ggc ctc acc cag gag ccc ggc agc gtg	327
Arg Cys Ser Trp Arg Gly Ser Gly Leu Thr Gln Glu Pro Gly Ser Val	
29 34 39 44	
ggg cag ctg gcc ctg gcc tgt gcg gag ggc gcg gtt gag tgg ctg tac	375
Gly Gln Leu Ala Leu Ala Cys Ala Glu Gly Ala Val Glu Trp Leu Tyr	
45 50 55 60	
ccg gct ggg gcg ctg cgc ctg acc ctg ggc ggc ccc gat ccc aga gcg	423
Pro Ala Gly Ala Leu Arg Leu Thr Leu Gly Gly Pro Asp Pro Arg Ala	
61 66 71 76	
cgg ccc ggc atc gcc tgt ctg cgg ccg gtg cgg ccc ttc gcg ggc gcc	471
Arg Pro Gly Ile Ala Cys Leu Arg Pro Val Arg Pro Phe Ala Gly Ala	
77 82 87 92	
cag gtc ttc gcg gag cgc gca ggg ggc gcc ctg gag ctg ctg ctg gct	519
Gln Val Phe Ala Glu Arg Ala Gly Gly Ala Leu Glu Leu Leu Leu Ala	
93 98 103 108	
gag ggc ccg ggc ccg gca ggg ggc cgc tgc gtg cgc tgg ggt ccc cgc	567
Glu Gly Pro Gly Pro Ala Gly Gly Arg Cys Val Arg Trp Gly Pro Arg	
109 114 119 124	
gag cgc cgg gcc ctc ttc ctg cag gcc acg ccg cac cag gac atc agc	615
Glu Arg Arg Ala Leu Phe Leu Gln Ala Thr Pro His Gln Asp Ile Ser	
125 130 135 140	
cgc cgc gtg gcc gcc ttc cgc ttt gag ctg cgc gag gac ggg cgc ccc	663
Arg Arg Val Ala Ala Phe Arg Phe Glu Leu Arg Glu Asp Gly Arg Pro	
141 146 151 156	
gag ctg ccc ccg cag gcc cac ggt ctc ggc gta gac ggt gcc tgc agg	711
Glu Leu Pro Pro Gln Ala His Gly Leu Gly Val Asp Gly Ala Cys Arg	
157 162 167 172	

ccc tgc agc gac gct gag ctg ctc ctg gcc gca tgc acc agc gac ttc	759
Pro Cys Ser Asp Ala Glu Leu Leu Leu Ala Ala Cys Thr Ser Asp Phe	
173 178 183 188	
gta att cac ggg atc atc cat ggg gtc acc cat gac gtg gag ctg cag	807
Val Ile His Gly Ile Ile His Gly Val Thr His Asp Val Glu Leu Gln	
189 194 199 204	
gag tct gtc atc act gtg gtg gcc gcc cgt gtc ctc cgc cag aca ccg	855
Glu Ser Val Ile Thr Val Val Ala Ala Arg Val Leu Arg Gln Thr Pro	
205 210 215 220	
ccg ctg ttc cag gcg ggg cga tcc ggg gac cag ggg ctg acc tcc att	903
Pro Leu Phe Gln Ala Gly Arg Ser Gly Asp Gln Gly Leu Thr Ser Ile	
221 226 231 236	
cgt acc cca ctg cgc tgt ggc gtc cac ccg ggc cca ggc acc ttc ctc	951
Arg Thr Pro Leu Arg Cys Gly Val His Pro Gly Pro Gly Thr Phe Leu	
237 242 247 252	
ttc atg ggc tgg agc cgc ttt ggg gag gcc cgg ctg ggc tgt gcc cca	999
Phe Met Gly Trp Ser Arg Phe Gly Glu Ala Arg Leu Gly Cys Ala Pro	
253 258 263 268	
cga ttc cag gag ttc cgc cgt gcc tac gag gct gcc cgt gct gcc cac	1047
Arg Phe Gln Glu Phe Arg Arg Ala Tyr Glu Ala Ala Arg Ala Ala His	
269 274 279 284	
ctc cac ccc tgc gag gtg gcg ctg cac tga g gggctgggtg ctggggaggg	1098
Leu His Pro Cys Glu Val Ala Leu His *	
285 290	
gctggttagga gggaggggtg gccactgct ttggaggtga tgggactatc aataagaact	1158
ctgttcacgc aaaaaaaaaa aa	1180

<210> 67
 <211> 1540
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (210)..(1322)

<220>
 <221> misc_feature
 <222> (1)...(1540)
 <223> n = a,t,c or g

<400> 67
 aggttcccc cnntttgacg actgagagca tgatgatata actatctatt cgatgatgaa 60

gataccccac caaacccaaa aaaagagatc tctcgaggat ccgaattcgc ggccgcgtcg	120
accgacacga ccattcatttg tcgacgccgc tgccaccgcc tgcctgagag aagtcgtcgc	180
ggccgacccc gtcgcctccg ccggctacc atg tcc gcc cag gcg cag atg cgg	233
Met Ser Ala Gln Ala Gln Met Arg	
1 5	
gcc ctg ctg gac cag ctc atg ggc acg gct cgg gac gac gaa acc aga	281
Ala Leu Leu Asp Gln Leu Met Gly Thr Ala Arg Asp Asp Glu Thr Arg	
9 14 19 24	
cag agg gtc aag ttt aca gat gac cgt gtc tgc aag agt cac ctt ctg	329
Gln Arg Val Lys Phe Thr Asp Asp Arg Val Cys Lys Ser His Leu Leu	
25 30 35 40	
gac tgc tgc ccc cat gac atc ctg gct ggg acg cgc atg gat tta gga	377
Asp Cys Cys Pro His Asp Ile Leu Ala Gly Thr Arg Met Asp Leu Gly	
41 46 51 56	
gaa tgt acc aaa atc cac gac ttg gcc ctc cga gca gat tat gag att	425
Glu Cys Thr Lys Ile His Asp Leu Ala Leu Arg Ala Asp Tyr Glu Ile	
57 62 67 72	
gca agt aaa gaa aga gac ctg ttt ttt gaa tta gat gca atg gat cac	473
Ala Ser Lys Glu Arg Asp Leu Phe Phe Glu Leu Asp Ala Met Asp His	
73 78 83 88	
ttg gag tcc ttt att gct gaa tgt gat cgg aga act gag ctc gcc aag	521
Leu Glu Ser Phe Ile Ala Glu Cys Asp Arg Arg Thr Glu Leu Ala Lys	
89 94 99 104	
aag cgg ctg gca gaa aca cag gag gaa atc agt gcg gaa gtt tct gca	569
Lys Arg Leu Ala Glu Thr Gln Glu Glu Ile Ser Ala Glu Val Ser Ala	
105 110 115 120	
aag gca gaa aaa gta cat gag tta aat gaa gaa ata gga aaa ctc ctt	617
Lys Ala Glu Lys Val His Glu Leu Asn Glu Glu Ile Gly Lys Leu Leu	
121 126 131 136	
gct aaa gcc gaa cag cta ggg gct gaa ggt aat gtg gat gaa tcc cag	665
Ala Lys Ala Glu Gln Leu Gly Ala Glu Gly Asn Val Asp Glu Ser Gln	
137 142 147 152	
aag att ctt atg gaa gtg gaa aaa gtt cgt gcg aag aaa aaa gaa gct	713
Lys Ile Leu Met Glu Val Glu Lys Val Arg Ala Lys Lys Lys Glu Ala	
153 158 163 168	
gag gaa gaa tac aga aat tcc atg cct gca tcc agt ttt cag cag caa	761
Glu Glu Glu Tyr Arg Asn Ser Met Pro Ala Ser Ser Phe Gln Gln Gln	
169 174 179 184	
aag ctg cgt gtc tgc gag gtc tgt tca gcc tac ctt ggt ctc cat gac	809
Lys Leu Arg Val Cys Glu Val Cys Ser Ala Tyr Leu Gly Leu His Asp	
185 190 195 200	
aat gac cgt cgc ctg gca gac cac ttc ggt ggc aag tta cac ttg ggg	857

Asn Asp Arg Arg Leu Ala Asp His Phe Gly Gly Lys Leu His Leu Gly	
201 206 211 216	
ttc att cag atc cga gag aag ctt gat cag ttg agg aaa act gtc gct	905
Phe Ile Gln Ile Arg Glu Lys Leu Asp Gln Leu Arg Lys Thr Val Ala	
217 222 227 232	
gaa aag cag gag aag aga aat cag gat cgc ttg agg agg aga gag gag	953
Glu Lys Gln Glu Lys Arg Asn Gln Asp Arg Leu Arg Arg Arg Glu Glu	
233 238 243 248	
agg gaa cgg gag gag cgt ctg agc agg agg tcg gga tca aga acc aga	1001
Arg Glu Arg Glu Glu Arg Leu Ser Arg Arg Ser Gly Ser Arg Thr Arg	
249 254 259 264	
gat cgc agg agg tca cgc tcc cgg gat cgg cgt cgg agg cgg tca aga	1049
Asp Arg Arg Arg Ser Arg Ser Arg Asp Arg Arg Arg Arg Arg Ser Arg	
265 270 275 280	
tct acc tcc cga gag cga cgg aaa ttg tcc cgg tcc cgg tcc cga gat	1097
Ser Thr Ser Arg Glu Arg Arg Lys Leu Ser Arg Ser Arg Ser Arg Asp	
281 286 291 296	
aga cat cgg cgc cac cgc agc cgt tcc cgg agc cac agc cgg gga cat	1145
Arg His Arg Arg His Arg Ser Arg Ser Arg Ser His Ser Arg Gly His	
297 302 307 312	
cgt cgg gct tcc cgg gac cga agt gcg aaa tac aag ttc tcc aga gag	1193
Arg Arg Ala Ser Arg Asp Arg Ser Ala Lys Tyr Lys Phe Ser Arg Glu	
313 318 323 328	
cgg gca tcc aga gag gag tcc tgg gag agc ggg cgg agc gag cga ggg	1241
Arg Ala Ser Arg Glu Glu Ser Trp Glu Ser Gly Arg Ser Glu Arg Gly	
329 334 339 344	
ccc ccg gac tgg agg ctt gag agc tcc aac ggg aag atg gct tca cgg	1289
Pro Pro Asp Trp Arg Leu Glu Ser Ser Asn Gly Lys Met Ala Ser Arg	
345 350 355 360	
agg tca gaa gag aag gag gcc ggc gag atc tga acccgtct cccgggtgct	1340
Arg Ser Glu Glu Lys Glu Ala Gly Glu Ile *	
361 366 371	
gtaaatagtc tgataaacgt tcacacagtc taaaattacc ctttatattt gctgaataca	1400
actcatcttt tgtagtttaa aattttotatt gttttggagc tagctgtgag tttctagaag	1460
tgtagacaggt tgctcctgtg ttccccgggtc atgttgagta ggaataaata aatctgatgc	1520
tgccctcctga aaaaaaaaaa	1540

<210> 68
 <211> 1363
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (210)..(1145)

<220>

<221> misc_feature

<222> (1)...(1363)

<223> n = a,t,c or g

<400> 68

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gataccccac caaacccaaa aaaagagatc tctcgaggat ccgaattcgc ggccgcgtcg 120

accgacacga ccattcatttg tcgacgccgc tgccaccgcc tgcttgagag aagtcgtcgc 180

ggccgacccc gtcgcctccg ccggctacc atg tcc gcc cag gcg cag atg cgg 233
Met Ser Ala Gln Ala Gln Met Arg
1 5

gcc ctg ctg gac cag ctc atg ggc acg gct cgg gac gac gaa acc aga 281
Ala Leu Leu Asp Gln Leu Met Gly Thr Ala Arg Asp Asp Glu Thr Arg
9 14 19 24

cag agg gtc aag ttt aca gat gac cgt gtc tgc aag agt cac ctt ctg 329
Gln Arg Val Lys Phe Thr Asp Asp Arg Val Cys Lys Ser His Leu Leu
25 30 35 40

gac tgc tgc ccc cat gac atc ctg gct ggg acg cgc atg gat tta gga 377
Asp Cys Cys Pro His Asp Ile Leu Ala Gly Thr Arg Met Asp Leu Gly
41 46 51 56

gaa tgt acc aaa atc cac gac ttg gcc ctc cga gca gat tat gag att 425
Glu Cys Thr Lys Ile His Asp Leu Ala Leu Arg Ala Asp Tyr Glu Ile
57 62 67 72

gca agt aaa gaa aga gac ctg ttt ttt gaa tta gat gca atg gat cac 473
Ala Ser Lys Glu Arg Asp Leu Phe Phe Glu Leu Asp Ala Met Asp His
73 78 83 88

ttg gag tcc ttt att gct gaa tgt gat cgg aga act gag ctc gcc aag 521
Leu Glu Ser Phe Ile Ala Glu Cys Asp Arg Arg Thr Glu Leu Ala Lys
89 94 99 104

aag cgg ctg gca gaa aca cag gag gaa atc agt gcg gaa gtt tct gca 569
Lys Arg Leu Ala Glu Thr Gln Glu Glu Ile Ser Ala Glu Val Ser Ala
105 110 115 120

aag gca gaa aaa gta cat gag tta aat gaa gaa ata gga aaa ctc ctt 617
Lys Ala Glu Lys Val His Glu Leu Asn Glu Glu Ile Gly Lys Leu Leu
121 126 131 136

gct aaa gcc gaa cag cta ggg gct gaa ggt aat gtg gat gaa tcc cag 665
Ala Lys Ala Glu Gln Leu Gly Ala Glu Gly Asn Val Asp Glu Ser Gln
137 142 147 152

aag att ctt atg gaa gtg gaa aaa gtt cgt gcg aag aaa aaa gaa gct	713
Lys Ile Leu Met Glu Val Glu Lys Val Arg Ala Lys Lys Lys Glu Ala	
153 158 163 168	
gag aaa act gtc gct gaa aag cag gag aag aga aat cag gat cgc ttg	761
Glu Lys Thr Val Ala Glu Lys Gln Glu Lys Arg Asn Gln Asp Arg Leu	
169 174 179 184	
agg agg aga gag gag agg gaa cgg gag gag cgt ctg agc agg agg tcg	809
Arg Arg Arg Glu Glu Arg Glu Arg Glu Glu Arg Leu Ser Arg Arg Ser	
185 190 195 200	
gga tca aga acc aga gat cgc agg agg tca cgc tcc cgg gat cgg cgt	857
Gly Ser Arg Thr Arg Asp Arg Arg Arg Ser Arg Ser Arg Asp Arg Arg	
201 206 211 216	
cgg agg cgg tca aga tct acc tcc cga gag cga cgg aaa ttg tcc cgg	905
Arg Arg Arg Ser Arg Ser Thr Ser Arg Glu Arg Arg Lys Leu Ser Arg	
217 222 227 232	
tcc cgg tcc cga gat aga cat cgg cgc cac cgc agc cgt tcc cgg agc	953
Ser Arg Ser Arg Asp Arg His Arg Arg His Arg Ser Arg Ser Arg Ser	
233 238 243 248	
cac agc cgg gga cat cgt cgg gct tcc cgg gac cga agt gcg aaa tac	1001
His Ser Arg Gly His Arg Arg Ala Ser Arg Asp Arg Ser Ala Lys Tyr	
249 254 259 264	
aag ttc tcc aga gag cgg gca tcc aga gag gag tcc tgg gag agc ggg	1049
Lys Phe Ser Arg Glu Arg Ala Ser Arg Glu Glu Ser Trp Glu Ser Gly	
265 270 275 280	
cgg agc gag cga ggg ccc ccg gac tgg agg ctt gag agc tcc aac ggg	1097
Arg Ser Glu Arg Gly Pro Pro Asp Trp Arg Leu Glu Ser Ser Asn Gly	
281 286 291 296	
aag atg gct tca cgg agg tca gaa gag aag gag gcc ggc gag atc tga	1145
Lys Met Ala Ser Arg Arg Ser Glu Glu Lys Glu Ala Gly Glu Ile *	
297 302 307 312	
accggtctcc cgggtgctgt aaatagtctg ataaacgttc acacagtcta aaattaccct	1205
ttatatattgc tgaatacaaac tcatcttttg tagtttaaaa tttctattgt tttggagcta	1265
gctgtgagtt tctagaagtg tacagagttg ctctgtgtt cccgggtcat gttgagtagg	1325
aataaataaa tctgatgctg cctcctgaaa aaaaaaaaa	1363

<210> 69
 <211> 3552
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (30)..(3218)

<400> 69

aatcacctcc atctgtccag agtttggct	atg agg cta ctg agt atg cca gga	53
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	1 5	
gcc cag gga gct gca gca gca ggg tct gaa ccc cct cca gcc acc acg	101	
Ala Gln Gly Ala Ala Ala Ala Gly Ser Glu Pro Pro Pro Ala Thr Thr		
9 14 19 24		
agc cca gag gga cag ccc aag gtc cac cga gcc cgc aaa acc atg tcc	149	
Ser Pro Glu Gly Gln Pro Lys Val His Arg Ala Arg Lys Thr Met Ser		
25 30 35 40		
aaa cca gga aat gga cag ccc ccg gtc cct gag aag cgg ccc cct gaa	197	
Lys Pro Gly Asn Gly Gln Pro Pro Val Pro Glu Lys Arg Pro Pro Glu		
41 46 51 56		
ata cag cat ttc cgc atg agt gat gat gtc cac tca ctg gga aag gtg	245	
Ile Gln His Phe Arg Met Ser Asp Asp Val His Ser Leu Gly Lys Val		
57 62 67 72		
acc tca gat ctg gcc aaa agg agg aag ctg aac tca gga ggt ggc ctg	293	
Thr Ser Asp Leu Ala Lys Arg Arg Lys Leu Asn Ser Gly Gly Gly Leu		
73 78 83 88		
tcg gag gag tta ggt tct gcc cgg cgt tca gga gaa gtg acc ctg acg	341	
Ser Glu Glu Leu Gly Ser Ala Arg Arg Ser Gly Glu Val Thr Leu Thr		
89 94 99 104		
aaa ggg gac ccc ggg tcc ctg gag gag tgg gag acg gtg gtg ggt gat	389	
Lys Gly Asp Pro Gly Ser Leu Glu Glu Trp Glu Thr Val Val Gly Asp		
105 110 115 120		
gac ttc agt ctc tac tat gat tcc tac tct gtg gat gag cgc gtg gac	437	
Asp Phe Ser Leu Tyr Tyr Asp Ser Tyr Ser Val Asp Glu Arg Val Asp		
121 126 131 136		
tcc gac agc aag tct gaa gtt gaa gct cta act gaa caa cta agt gaa	485	
Ser Asp Ser Lys Ser Glu Val Glu Ala Leu Thr Glu Gln Leu Ser Glu		
137 142 147 152		
gag gag gag gag gaa gag gag gaa gaa gaa gaa gag gaa gag gag gag	533	
Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu		
153 158 163 168		
gaa gag gaa gaa gaa gag gaa gat gag gag tca ggg aat cag tca gat	581	
Glu Glu Glu Glu Glu Glu Glu Asp Glu Glu Ser Gly Asn Gln Ser Asp		
169 174 179 184		
agg agt ggt tcc agt ggc cgg cgc aag gcc aag aag aaa tgg cga aaa	629	
Arg Ser Gly Ser Ser Gly Arg Arg Lys Ala Lys Lys Lys Trp Arg Lys		
185 190 195 200		

gac agc cca tgg gtg aag ccg tct cgg aaa cgg cgc aag cgg gag cct	677
Asp Ser Pro Trp Val Lys Pro Ser Arg Lys Arg Arg Lys Arg Glu Pro	
201 206 211 216	
ccg cgg gcc aag gag cca cga gga gtg aat ggt gtg ggc tcc tca ggc	725
Pro Arg Ala Lys Glu Pro Arg Gly Val Asn Gly Val Gly Ser Ser Gly	
217 222 227 232	
ccc agt gag tac atg gag gtc cct ctg ggg tcc ctg gag ctg ccc agc	773
Pro Ser Glu Tyr Met Glu Val Pro Leu Gly Ser Leu Glu Leu Pro Ser	
233 238 243 248	
gag ggg acc ctc tcc ccc aac cac gct ggg gtg tcc aat gac aca tct	821
Glu Gly Thr Leu Ser Pro Asn His Ala Gly Val Ser Asn Asp Thr Ser	
249 254 259 264	
tcg ctg gag aca gag cga ggg ttt gag gag ttg ccc ctg tgc agc tgc	869
Ser Leu Glu Thr Glu Arg Gly Phe Glu Glu Leu Pro Leu Cys Ser Cys	
265 270 275 280	
cgc atg gag gca ccc aag att gac cgc atc agc gag agg gcg ggg cac	917
Arg Met Glu Ala Pro Lys Ile Asp Arg Ile Ser Glu Arg Ala Gly His	
281 286 291 296	
aag tgc atg gcc act gag agt gtg gac gga gag ctg tca ggc tgc aat	965
Lys Cys Met Ala Thr Glu Ser Val Asp Gly Glu Leu Ser Gly Cys Asn	
297 302 307 312	
gcc gcc atc ctc aag cgg gag acc atg agg cca tcc agc cgt gtg gcc	1013
Ala Ala Ile Leu Lys Arg Glu Thr Met Arg Pro Ser Ser Arg Val Ala	
313 318 323 328	
ctg atg gtg ctc tgt gag acc cac cgc gcc cgc atg gtc aaa cac cac	1061
Leu Met Val Leu Cys Glu Thr His Arg Ala Arg Met Val Lys His His	
329 334 339 344	
tgc tgc ccg ggc tgc ggc tac ttc tgc acg gcg ggc acc ttc ctg gag	1109
Cys Cys Pro Gly Cys Gly Tyr Phe Cys Thr Ala Gly Thr Phe Leu Glu	
345 350 355 360	
tgc cac cct gac ttc cgt gtg gcc cac cgc ttc cac aag gcc tgt gtg	1157
Cys His Pro Asp Phe Arg Val Ala His Arg Phe His Lys Ala Cys Val	
361 366 371 376	
tct cag ctg aat ggg atg gtc ttc tgt ccc cac tgt ggg gag gat gct	1205
Ser Gln Leu Asn Gly Met Val Phe Cys Pro His Cys Gly Glu Asp Ala	
377 382 387 392	
tct gaa gct caa gag gtg acc atc ccc cgg ggt gac ggg gtg acc cca	1253
Ser Glu Ala Gln Glu Val Thr Ile Pro Arg Gly Asp Gly Val Thr Pro	
393 398 403 408	
ccg gcc ggc act gca gct cct gca ccc cca ccc ctg tcc cag gat gtc	1301
Pro Ala Gly Thr Ala Pro Ala Pro Pro Pro Leu Ser Gln Asp Val	
409 414 419 424	
ccc ggg aga gca gac act tct cag ccc agt gcc cgg atg cga ggg cat	1349

Pro Gly Arg Ala Asp Thr Ser Gln Pro Ser Ala Arg Met Arg Gly His	
425 430 435 440	
ggg gaa ccc cgg cgc ccg ccc tgc gat ccc ctg gct gac acc att gac	1397
Gly Glu Pro Arg Arg Pro Pro Cys Asp Pro Leu Ala Asp Thr Ile Asp	
441 446 451 456	
agc tca ggg ccc tcc ctg acc ctg ccc aat ggg ggc tgc ctt tca gcc	1445
Ser Ser Gly Pro Ser Leu Thr Leu Pro Asn Gly Gly Cys Leu Ser Ala	
457 462 467 472	
gtg ggg ctg cca ctg ggg cca ggc cgg gag gcc ctg gaa aag gcc ctg	1493
Val Gly Leu Pro Leu Gly Pro Gly Arg Glu Ala Leu Glu Lys Ala Leu	
473 478 483 488	
gtc atc cag gag tca gag agg cgg aag aag ctc cgt ttc cac cct cgg	1541
Val Ile Gln Glu Ser Glu Arg Arg Lys Lys Leu Arg Phe His Pro Arg	
489 494 499 504	
cag ttg tac ctg tcc gtg aag cag ggc gag ctg cag aag gtg atc ctg	1589
Gln Leu Tyr Leu Ser Val Lys Gln Gly Glu Leu Gln Lys Val Ile Leu	
505 510 515 520	
atg ctg ttg gac aac ctg gac ccc aac ttc cag agc gac cag cag agc	1637
Met Leu Leu Asp Asn Leu Asp Pro Asn Phe Gln Ser Asp Gln Gln Ser	
521 526 531 536	
aag cgc acg ccc ctg cat gca gcc gcc cag aag ggc tcc gtg gag atc	1685
Lys Arg Thr Pro Leu His Ala Ala Ala Gln Lys Gly Ser Val Glu Ile	
537 542 547 552	
tgc cat gtg ctg ctg cag gct gga gcc aac ata aat gca gtg gac aaa	1733
Cys His Val Leu Leu Gln Ala Gly Ala Asn Ile Asn Ala Val Asp Lys	
553 558 563 568	
cag cag cgg acg cca ctg atg gag gcc gtg gtg aac aac cac ctg gag	1781
Gln Gln Arg Thr Pro Leu Met Glu Ala Val Val Asn Asn His Leu Glu	
569 574 579 584	
gta gcc cgt tac atg gtg cag cgt ggt ggc tgt gtc tat agc aag gag	1829
Val Ala Arg Tyr Met Val Gln Arg Gly Gly Cys Val Tyr Ser Lys Glu	
585 590 595 600	
gag gac ggt tcc acc tgc ctc cac cac gca gcc aaa atc ggg aac ttg	1877
Glu Asp Gly Ser Thr Cys Leu His His Ala Ala Lys Ile Gly Asn Leu	
601 606 611 616	
gag atg gtc agc ctg ctg ctg agc aca gga cag gtg gac gtc aac gcc	1925
Glu Met Val Ser Leu Leu Leu Ser Thr Gly Gln Val Asp Val Asn Ala	
617 622 627 632	
cag gac agt ggg ggg tgg acg ccc atc atc tgg gct gca gag cac aag	1973
Gln Asp Ser Gly Gly Trp Thr Pro Ile Ile Trp Ala Ala Glu His Lys	
633 638 643 648	
cac atc gag gtg atc cgc atg cta ctg acg cgg ggc gcc gac gtc acc	2021
His Ile Glu Val Ile Arg Met Leu Leu Thr Arg Gly Ala Asp Val Thr	

649	654	659	664	
ctc act gac aac gag	gag aac atc tgc ctg	cac tgg gcc tcc ttc acg		2069
Leu Thr Asp Asn Glu	Glu Asn Ile Cys Leu	His Trp Ala Ser Phe Thr		
665	670	675	680	
ggc agc gcc gcc atc	gcc gaa gtc ctt ctg	aat gcg cgc tgt gac ctc		2117
Gly Ser Ala Ala Ile	Ala Glu Val Leu Leu	Asn Ala Arg Cys Asp Leu		
681	686	691	696	
cat gct gtc aac tac	cat ggg gac acc ccc	ctg cac atc gca gct cgg		2165
His Ala Val Asn Tyr	His Gly Asp Thr Pro	Leu His Ile Ala Ala Arg		
697	702	707	712	
gag agc tac cat gac	tgc gtg ctg tta ttc	ctg tca cgt ggg gcc aac		2213
Glu Ser Tyr His Asp	Cys Val Leu Leu Phe	Leu Ser Arg Gly Ala Asn		
713	718	723	728	
cct gag ctg cgg aac	aaa gag ggg gac aca	gca tgg gac ctg act ccc		2261
Pro Glu Leu Arg Asn	Lys Glu Gly Asp Thr	Ala Trp Asp Leu Thr Pro		
729	734	739	744	
gag cgc tcc gac gtg	tgg ttt gcg ctt caa	ctc aac cgc aag ctc cga		2309
Glu Arg Ser Asp Val	Trp Phe Ala Leu Gln	Leu Asn Arg Lys Leu Arg		
745	750	755	760	
ctt ggg gtg gga aat	cgg gcc atc cgc aca	gag aag atc atc tgc cgg		2357
Leu Gly Val Gly Asn	Arg Ala Ile Arg Thr	Glu Lys Ile Ile Cys Arg		
761	766	771	776	
gac gtg gct cgg ggc	tat gag aac gtg ccc	att ccc tgt gtc aac ggt		2405
Asp Val Ala Arg Gly	Tyr Glu Asn Val Pro	Ile Pro Cys Val Asn Gly		
777	782	787	792	
gtg gat ggg gag ccc	tgc cct gag gat tac	aag tac atc tca gag aac		2453
Val Asp Gly Glu Pro	Cys Pro Glu Asp Tyr	Lys Tyr Ile Ser Glu Asn		
793	798	803	808	
tgc gag acg tcc acc	atg aac atc gat cgc	aac atc acc cac ctg cag		2501
Cys Glu Thr Ser Thr	Met Asn Ile Asp Arg	Asn Ile Thr His Leu Gln		
809	814	819	824	
cac tgc acg tgt gtg	gac gac tgc tct agc	tcc aac tgc ctg tgc ggc		2549
His Cys Thr Cys Val	Asp Asp Cys Ser Ser	Ser Asn Cys Leu Cys Gly		
825	830	835	840	
cag ctc agc atc cgg	tgc tgg tat gac aag	gat ggg cga ttg ctc cag		2597
Gln Leu Ser Ile Arg	Cys Trp Tyr Asp Lys	Asp Gly Arg Leu Leu Gln		
841	846	851	856	
gaa ttt aac aag att	gag cct ccg ctg att	ttc gag tgt aac cag gcg		2645
Glu Phe Asn Lys Ile	Glu Pro Pro Leu Ile	Phe Glu Cys Asn Gln Ala		
857	862	867	872	
tgc tca tgc tgg aga	aac tgc aag aac cgg	gtc gta cag agt ggc atc		2693
Cys Ser Cys Trp Arg	Asn Cys Lys Asn Arg	Val Val Gln Ser Gly Ile		
873	878	883	888	

aag gtg cgg cta cag ctc tac cga aca gcc aag atg ggc tgg ggg gtc	2741
Lys Val Arg Leu Gln Leu Tyr Arg Thr Ala Lys Met Gly Trp Gly Val	
889 894 899 904	
cgc gcc ctg cag acc atc cca cag ggg acc ttc atc tgc gag tat gtc	2789
Arg Ala Leu Gln Thr Ile Pro Gln Gly Thr Phe Ile Cys Glu Tyr Val	
905 910 915 920	
ggg gag ctg atc tct gat gct gag gct gat gtg aga gag gat gat tct	2837
Gly Glu Leu Ile Ser Asp Ala Glu Ala Asp Val Arg Glu Asp Asp Ser	
921 926 931 936	
tac ctc ttc gac tta gac aac aag gat gga gag gtg tac tgc ata gat	2885
Tyr Leu Phe Asp Leu Asp Asn Lys Asp Gly Glu Val Tyr Cys Ile Asp	
937 942 947 952	
gcc cgt tac tat ggc aac atc agc cgc ctc ctc tgc cac ctg tgt gac	2933
Ala Arg Tyr Tyr Gly Asn Ile Ser Arg Leu Leu Cys His Leu Cys Asp	
953 958 963 968	
ccc aac atc att ccc gtc cgg gtc ttc atg ctg cac caa gac ctg cga	2981
Pro Asn Ile Ile Pro Val Arg Val Phe Met Leu His Gln Asp Leu Arg	
969 974 979 984	
ttt cca cgc atc gcc ttc ttc agt tcc cga gac atc cgg act ggg gag	3029
Phe Pro Arg Ile Ala Phe Phe Ser Ser Arg Asp Ile Arg Thr Gly Glu	
985 990 995 1000	
gag cta ggg ttt gac tat ggc gac cgc ttc tgg gac atc aaa agc aaa	3077
Glu Leu Gly Phe Asp Tyr Gly Asp Arg Phe Trp Asp Ile Lys Ser Lys	
1001 1006 1011 1016	
tat ttc acc tgc caa tgt ggc tct gag aag tgc aag cac tca gcc gaa	3125
Tyr Phe Thr Cys Gln Cys Gly Ser Glu Lys Cys Lys His Ser Ala Glu	
1017 1022 1027 1032	
gcc att gcc ctg gag cag agc cgt ctg gcc cgc ctg gac cca cac cct	3173
Ala Ile Ala Leu Glu Gln Ser Arg Leu Ala Arg Leu Asp Pro His Pro	
1033 1038 1043 1048	
gag ctg ctg ccc gag ctc ggc tcc ctg ccc cct gtc aac aca tga gaa	3221
Glu Leu Leu Pro Glu Leu Gly Ser Leu Pro Pro Val Asn Thr *	
1049 1054 1059	
cgaccacac cctctctccc cagcatggat ggccacagct cagccgcctc ctctgccacc	3281
agctgctcgc agcccatgcc tgggggtgct gccatcttct ctccccacca ccctttcaca	3341
cattcctgac cagagatccc agccaggccc tggaggtctg acagcccctc cctcccagag	3401
ctggttcctc cctgggaggg caacttcagg gctggccacc ccccggtgtc cccatcctca	3461
gttgaagttt gatgaattga agtcgggcct ctatgccaac tggttccttt tggttctcaat	3521
aaatgttggg tttggtaata aaaaaaaaaa a	3552

<210> 70
 <211> 1925
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (510)..(1562)

<220>
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 <222> (1)...(1925)
 <223> n = a,t,c or g

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 ccccgatgg cctcagccac ggaggacccc gttctggagc gttatttcaa aggccacaaa 180
 gctgcgatca cctccttggga cctcagcccc aacggcaagc aacttgctac tgcttcttgg 240
 gatacctttc tcatgctatg gaatttcaag ccacatgcta gagcttacag atatgtgggt 300
 cacaaggatg ttgtaaccag cgtgcagttt tctccacatg gaaacttatt ggcgtctgcc 360
 tcacgagaca gaaccgtgag actctggatt cctgataaga gaggaaaatt ctcagaattt 420
 aaagctcata cagctccagt tcgaagtgta gacttttcag ctgatggcca gtttctagct 480
 acagcttctg aagacaaatc cataaaagt atg gag cat gta tcg cca gcg ctt 533
 Met Glu His Val Ser Pro Ala Leu
 1 5
 cct gta ttc ctt gta tcg aca tac aca ctg ggt acg ctg tgc cca att 581
 Pro Val Phe Leu Val Ser Thr Tyr Thr Leu Gly Thr Leu Cys Pro Ile
 9 14 19 24
 tca ccc gat gga aga cta att gtg tca tgt agt gag gat aaa act att 629
 Ser Pro Asp Gly Arg Leu Ile Val Ser Cys Ser Glu Asp Lys Thr Ile
 25 30 35 40
 aaa att tgg gat acc aca aat aag caa tgt gtt aat aac ttc tca gat 677
 Lys Ile Trp Asp Thr Thr Asn Lys Gln Cys Val Asn Asn Phe Ser Asp
 41 46 51 56
 tcc gtt gga ttt gca aat ttt gtg gac ttt aac cct agt ggt aca tgc 725
 Ser Val Gly Phe Ala Asn Phe Val Asp Phe Asn Pro Ser Gly Thr Cys
 57 62 67 72
 ata gct tca gca ggt tct gat caa act gtg aaa gtc tgg gat gta aga 773
 Ile Ala Ser Ala Gly Ser Asp Gln Thr Val Lys Val Trp Asp Val Arg
 73 78 83 88

gtg aac aaa tta cta cag cat tac caa gtt cac agc ggt gga gtt aat	821
Val Asn Lys Leu Leu Gln His Tyr Gln Val His Ser Gly Gly Val Asn	
89 94 99 104	
tgc ata tca ttc cat cct tgc ggt aac tat ctc atc aca gct tct tca	869
Cys Ile Ser Phe His Pro Ser Gly Asn Tyr Leu Ile Thr Ala Ser Ser	
105 110 115 120	
gat ggt acc ctt aag att ctg gac ctc tta gaa gga agg ctc atc tat	917
Asp Gly Thr Leu Lys Ile Leu Asp Leu Leu Glu Gly Arg Leu Ile Tyr	
121 126 131 136	
aca ctt caa gga cat acg gga cct gtc ttt act gtt tca ttt tca aaa	965
Thr Leu Gln Gly His Thr Gly Pro Val Phe Thr Val Ser Phe Ser Lys	
137 142 147 152	
ggg gga gag cta ttt gca tca gga ggt gca gac aca cag gtc tta tta	1013
Gly Gly Glu Leu Phe Ala Ser Gly Gly Ala Asp Thr Gln Val Leu Leu	
153 158 163 168	
tgg agg act aac ttt gat gaa ttg cat tgt aaa ggt ctt acc aaa aga	1061
Trp Arg Thr Asn Phe Asp Glu Leu His Cys Lys Gly Leu Thr Lys Arg	
169 174 179 184	
aat ctc aaa aga tta cat ttt gat tca cca cca cat ctt ctt gat atc	1109
Asn Leu Lys Arg Leu His Phe Asp Ser Pro Pro His Leu Leu Asp Ile	
185 190 195 200	
tac cca aga aca cca cat ccc cat gag gaa aaa gtt gag act gta gaa	1157
Tyr Pro Arg Thr Pro His Pro His Glu Glu Lys Val Glu Thr Val Glu	
201 206 211 216	
att aat cca aag ctt gag gta atc gat ttg cag atc tct act ccc cct	1205
Ile Asn Pro Lys Leu Glu Val Ile Asp Leu Gln Ile Ser Thr Pro Pro	
217 222 227 232	
gtt atg gat atc ctt tct ttt gat tct acc aca aca aca gaa acc agt	1253
Val Met Asp Ile Leu Ser Phe Asp Ser Thr Thr Thr Thr Glu Thr Ser	
233 238 243 248	
ggg agg act ctg cca gac aag ggt gaa gag gcc tgt gga tat ttc ttg	1301
Gly Arg Thr Leu Pro Asp Lys Gly Glu Glu Ala Cys Gly Tyr Phe Leu	
249 254 259 264	
aac cct tcc tta atg tca cca gaa tgt ttg cca aca acc acg aaa aag	1349
Asn Pro Ser Leu Met Ser Pro Glu Cys Leu Pro Thr Thr Thr Lys Lys	
265 270 275 280	
aaa aca gaa gac atg agt gac ctc ccc tgt gaa agt caa agg agc ata	1397
Lys Thr Glu Asp Met Ser Asp Leu Pro Cys Glu Ser Gln Arg Ser Ile	
281 286 291 296	
cct ctc gct gtg act gat gct tta gag cat att atg gaa caa ctc aat	1445
Pro Leu Ala Val Thr Asp Ala Leu Glu His Ile Met Glu Gln Leu Asn	
297 302 307 312	

ggt ttg aca cag act ggt tca atc ttg gag cag cga ctg act ttg aca	1493
Val Leu Thr Gln Thr Val Ser Ile Leu Glu Gln Arg Leu Thr Leu Thr	
313 318 323 328	
 gag gat aag ctg aaa gac tgc ctt gaa aat cag caa aag ctt ttc agt	1541
Glu Asp Lys Leu Lys Asp Cys Leu Glu Asn Gln Gln Lys Leu Phe Ser	
329 334 339 344	
 gct gtc caa cag aaa agc tga at aaaaaattca ttttcatttg ttgggcagag	1594
Ala Val Gln Gln Lys Ser *	
345 350	
 gccaataaaa tgaacaaatg tacatacact caggaaggta gtacaagata ctccatacaa	1654
cacaaccatg tgctatttat catggcattt cttaaaaggg tgagcaacag aacaaaaggc	1714
agaaaaggca tacctaagga ctaatttaaa cacatatcaa tgtgaaggac taatttaa	1774
tactatcatt tatgattgca gtaataaagt gataagcatt caagcaactc tgtattttcc	1834
ccatattaat ttaaatgtcc attntcattt ataggccana tcctgccaag aaaagaaccc	1894
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 <222> (484) .. (837)

<400> 71

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gctccccggg aagcgttttg gccccaccg gaatggtgtc atctggttaa gaagcgcaag	120
tggcgctttg gagaaaccaa ccaagacccc ggggggggggt tgggccccaa tcctaattac	180
ccttctgtcc ccaacttcca gttagccaaa atataaagaa ggcaaatacct gtactgttgg	240
caaaaacagc caccacaaaag ttgttaaaaa gcaaaacaaa acacctcaag cttaaatttt	300
tgaaaaacaa tcctcacaca aagatactat caacaaatca cacaccaatt tatcttagaa	360
ggatcaagag atgaaaaaca gcaaaggata ttttcgtaat atgctagaat ctttgaatat	420
aatactgaag ttggcaacca aaagcaattc agaagttcaa cttagaacta atggctgtat	480
 ccg atg gca ctg tct att tta gat att aaa atg tca cca tct tgg tat	528
Met Ala Leu Ser Ile Leu Asp Ile Lys Met Ser Pro Ser Trp Tyr	
1 5 10	

ttt cac atg gct ata ggc att ata aac tgg aac act act gcg ggt tta	576
Phe His Met Ala Ile Gly Ile Ile Asn Trp Asn Thr Thr Ala Gly Leu	
16 21 26 31	
tct ggc act ctg tat cca aaa gtc ccc caa aag tac ata ctc ttt gac	624
Ser Gly Thr Leu Tyr Pro Lys Val Pro Gln Lys Tyr Ile Leu Phe Asp	
32 37 42 47	
tct gta att ctg ctt cta ggc atg tta aga aaa ata cgt cag gta tgc	672
Ser Val Ile Leu Leu Leu Gly Met Leu Arg Lys Ile Arg Gln Val Cys	
48 53 58 63	
caa aat gta tac atg aaa ggg tgt tca cca ata aca tta ttt aaa ata	720
Gln Asn Val Tyr Met Lys Gly Cys Ser Pro Ile Thr Leu Phe Lys Ile	
64 69 74 79	
gtt cac tac tgg cca ggc gca gta gct cat gcc tat aat cct agc act	768
Val His Tyr Trp Pro Gly Ala Val Ala His Ala Tyr Asn Pro Ser Thr	
80 85 90 95	
ttg gga ggc caa gtt ggg ggc aaa tca cct gag gtc agg agt tcg aga	816
Leu Gly Gly Gln Val Gly Gly Lys Ser Pro Glu Val Arg Ser Ser Arg	
96 101 106 111	
cca gcc tgg act aca tgg tga aa ccccatctct actaaaagaa caaaaattag	869
Pro Ala Trp Thr Thr Trp *	
112 117	
gtcgacgcgg ccgcgaattc ggatcctcga gagatctctt tttttggggtt tgggtggggta	929
tcttcatcgt cgaatcgta gttatat	956

<210> 72
 <211> 1615
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (215)..(1507)

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gctgaagcca gagatccact caaaagagca gatactggaa ctgctgggtgc tggagcagtt	180
cctgactatt ctgccaggag agacacagac ccag atg cag aag cac cat cca	232
Met Gln Lys His His Pro	
1	
cag agc att gag gag gct gtg gct ctg gta gaa cac ttg cag agg gaa	280
Gln Ser Ile Glu Glu Ala Val Ala Leu Val Glu His Leu Gln Arg Glu	

7	12	17	22	
tct ggt caa aca tgg aat ggg gtt gca gtc cat gag ctg gga aag gag				328
Ser Gly Gln Thr Trp Asn Gly Val Ala Val His Glu Leu Gly Lys Glu				
23	28	33	38	
gca gtg ctc ttg gga gaa aca gca gag gcc tca agt ttc ggg ctg aag				376
Ala Val Leu Leu Gly Glu Thr Ala Glu Ala Ser Ser Phe Gly Leu Lys				
39	44	49	54	
cca aca gag tcc caa cca gtg ggc gta tcc caa gat gaa gaa ttt tgg				424
Pro Thr Glu Ser Gln Pro Val Gly Val Ser Gln Asp Glu Glu Phe Trp				
55	60	65	70	
aat aca tac gag ggt ctg caa gaa cag ctc agc agg aat act cat aaa				472
Asn Thr Tyr Glu Gly Leu Gln Glu Gln Leu Ser Arg Asn Thr His Lys				
71	76	81	86	
gag act gag cct gtg tat gag agg gct gtg cct act caa cag att cta				520
Glu Thr Glu Pro Val Tyr Glu Arg Ala Val Pro Thr Gln Gln Ile Leu				
87	92	97	102	
gct ttt cct gag caa aca aac acc aaa gac tgg aca gtg aca cct gag				568
Ala Phe Pro Glu Gln Thr Asn Thr Lys Asp Trp Thr Val Thr Pro Glu				
103	108	113	118	
cac gtc ttg cct gag tcc cag agc ttg ttg aca ttt gaa gaa gtg gcc				616
His Val Leu Pro Glu Ser Gln Ser Leu Leu Thr Phe Glu Glu Val Ala				
119	124	129	134	
atg tat ttt tcc cag gaa gaa tgg gag tta ttg gat ccc act cag aag				664
Met Tyr Phe Ser Gln Glu Glu Trp Glu Leu Leu Asp Pro Thr Gln Lys				
135	140	145	150	
gcc ctc tac aat gat gta atg cag gaa aac tat gag act gtc atc tct				712
Ala Leu Tyr Asn Asp Val Met Gln Glu Asn Tyr Glu Thr Val Ile Ser				
151	156	161	166	
cta gca ttg ttt gtg ctc ccc aaa cct aaa gtg atc tcc tgt cta gag				760
Leu Ala Leu Phe Val Leu Pro Lys Pro Lys Val Ile Ser Cys Leu Glu				
167	172	177	182	
caa ggg gaa gag cca tgg gtt caa gta tcc ccg gag ttt aag gat agt				808
Gln Gly Glu Glu Pro Trp Val Gln Val Ser Pro Glu Phe Lys Asp Ser				
183	188	193	198	
gcc gga aaa tct cct aca ggg tta aag ctc aaa aac gac act gaa aat				856
Ala Gly Lys Ser Pro Thr Gly Leu Lys Leu Lys Asn Asp Thr Glu Asn				
199	204	209	214	
cat cag cct gcg tct ctt tct gac tta gaa ata caa gca tca gca ggc				904
His Gln Pro Ala Ser Leu Ser Asp Leu Glu Ile Gln Ala Ser Ala Gly				
215	220	225	230	
gtc ata tca aaa aag gcc aaa gta aaa gtt ccc cag aaa aca gca ggc				952
Val Ile Ser Lys Lys Ala Lys Val Lys Val Pro Gln Lys Thr Ala Gly				
231	236	241	246	

aaa gaa aat cat ttt gat atg cac aga gtg gga aaa tgg cac caa gat	1000
Lys Glu Asn His Phe Asp Met His Arg Val Gly Lys Trp His Gln Asp	
247 252 257 262	
ttt cca gtg aag aaa aga aag aaa ctt tca acc tgg aaa caa gag ctg	1048
Phe Pro Val Lys Lys Arg Lys Lys Leu Ser Thr Trp Lys Gln Glu Leu	
263 268 273 278	
ctc aaa ctt atg gat cgt cac aag aaa gat tgt gca aga gag aag cct	1096
Leu Lys Leu Met Asp Arg His Lys Lys Asp Cys Ala Arg Glu Lys Pro	
279 284 289 294	
ttt aaa tgt cag gaa tgt ggg aaa acc ttc aga gtt agc tct gac ctt	1144
Phe Lys Cys Gln Glu Cys Gly Lys Thr Phe Arg Val Ser Ser Asp Leu	
295 300 305 310	
att aag cac caa aga att cac act gaa gag aaa ccc tat aaa tgt caa	1192
Ile Lys His Gln Arg Ile His Thr Glu Glu Lys Pro Tyr Lys Cys Gln	
311 316 321 326	
cag tgt gat aag agg ttt aga tgg agt tca gat ctt aat aag cac tta	1240
Gln Cys Asp Lys Arg Phe Arg Trp Ser Ser Asp Leu Asn Lys His Leu	
327 332 337 342	
aca aca cac caa gga ata aaa cca tat aaa tgt tca tgg tgt ggg aaa	1288
Thr Thr His Gln Gly Ile Lys Pro Tyr Lys Cys Ser Trp Cys Gly Lys	
343 348 353 358	
agc ttc agt caa aat aca aat tta cat aca cac caa aga act cat aca	1336
Ser Phe Ser Gln Asn Thr Asn Leu His Thr His Gln Arg Thr His Thr	
359 364 369 374	
gga gaa aag ccc ttc aca tgt cat gaa tgt gga aaa aaa ttc agt cag	1384
Gly Glu Lys Pro Phe Thr Cys His Glu Cys Gly Lys Lys Phe Ser Gln	
375 380 385 390	
aac tcc cac ctt att aaa cac cgg aga acc cac aca ggt gag cag cca	1432
Asn Ser His Leu Ile Lys His Arg Arg Thr His Thr Gly Glu Gln Pro	
391 396 401 406	
tat act tgt agc ata tgc agg aga aac ttc agc agg cgg tca agc ctt	1480
Tyr Thr Cys Ser Ile Cys Arg Arg Asn Phe Ser Arg Arg Ser Ser Leu	
407 412 417 422	
ctt aga cac cag aaa ctc cac ctg tga agaga agcttgcca gtgtcctcat	1532
Leu Arg His Gln Lys Leu His Leu *	
423 428	
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agaaaggcag gatcctgggc cctgctacgt ttctggggcc atg gct ggt ctg ggc 235

Met Ala Gly Leu Gly

1

ccc ggc gta ggc gat tca gag ggg gga ccc cgg ccc ctg ttt tgc aga 283

Pro Gly Val Gly Asp Ser Glu Gly Gly Pro Arg Pro Leu Phe Cys Arg

6 11 16 21

aag ggg gct ctg agg cag aag gtg gtc cac gaa gtc aag agc cac aag 331

Lys Gly Ala Leu Arg Gln Lys Val Val His Glu Val Lys Ser His Lys

22 27 32 37

ttc acc gct cgc ttc ttc aag cag ccc acc ttc tgc agc cac tgc acc 379

Phe Thr Ala Arg Phe Phe Lys Gln Pro Thr Phe Cys Ser His Cys Thr

38 43 48 53

gac ttc atc tgg ggt atc gga aag cag ggc ctg caa tgt caa gtc tgc 427

Asp Phe Ile Trp Gly Ile Gly Lys Gln Gly Leu Gln Cys Gln Val Cys

54 59 64 69

agc ttt gtg gtt cat cga cga tgc cac gaa ttt gtg acc ttc gag tgt 475

Ser Phe Val Val His Arg Arg Cys His Glu Phe Val Thr Phe Glu Cys

70 75 80 85

cca ggc gct ggg aag ggc ccc cag acg gac gac ccc cgg aac aaa cac 523

Pro Gly Ala Gly Lys Gly Pro Gln Thr Asp Asp Pro Arg Asn Lys His

86 91 96 101

aag ttc cgc ctg cat agc tac agc agc ccc acc ttc tgc gac cac tgt 571

Lys Phe Arg Leu His Ser Tyr Ser Ser Pro Thr Phe Cys Asp His Cys

102 107 112 117

ggc tcc ctc ctc tac ggg ctt gtg cac cag ggc atg aaa tgc tcc tgc 619

Gly Ser Leu Leu Tyr Gly Leu Val His Gln Gly Met Lys Cys Ser Cys

118 123 128 133

tgc gag atg aac gtg cac cgg cgc tgt gtg cgt agc gtg ccc tcc ctg 667

Cys Glu Met Asn Val His Arg Arg Cys Val Arg Ser Val Pro Ser Leu

134 139 144 149

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Cys Gly Val Asp His Thr Glu Arg Arg Gly Arg Leu Gln Leu Glu Ile

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Arg Ala Pro Thr Ala Asp Glu Ile His Val Thr Val Gly Glu Ala Arg				
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aac cta att cct atg gac ccc aat ggt ctc tct gat ccc tat gtg aaa				811
Asn Leu Ile Pro Met Asp Pro Asn Gly Leu Ser Asp Pro Tyr Val Lys				
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ctg aag ctc atc cca gac cct cgg aac ctg acg aaa cag aag acc cga				859
Leu Lys Leu Ile Pro Asp Pro Arg Asn Leu Thr Lys Gln Lys Thr Arg				
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Thr Val Lys Ala Thr Leu Asn Pro Val Trp Asn Glu Thr Phe Val Phe				
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Asn Leu Lys Pro Gly Asp Val Glu Arg Arg Leu Ser Val Glu Val Trp				
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Asp Trp Asp Arg Thr Ser Arg Asn Asp Phe Met Gly Ala Met Ser Phe				
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Gly Val Ser Glu Leu Leu Lys Ala Pro Val Asp Gly Trp Tyr Lys Leu				
262	267	272	277	
ctg aac cag gag gag ggc gag tat tac aat gtg ccg gtg gcc gat gct				1099
Leu Asn Gln Glu Glu Gly Glu Tyr Tyr Asn Val Pro Val Ala Asp Ala				
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Asp Asn Cys Ser Leu Leu Gln Lys Phe Glu Ala Cys Asn Tyr Pro Leu				
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Ser Pro Ser Pro Ser Pro Thr Asp Pro Lys Arg Cys Phe Phe Gly Ala				
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Ser Pro Gly Arg Leu His Ile Ser Asp Phe Ser Phe Leu Met Val Leu				
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Gly Lys Gly Ser Phe Gly Lys Val Met Leu Ala Glu Arg Arg Gly Ser				
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gat gag ctc tac gcc atc aag atc ttg aaa aag gac gtg atc gtc cag				1387
Asp Glu Leu Tyr Ala Ile Lys Ile Leu Lys Lys Asp Val Ile Val Gln				
374	379	384	389	

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Asp Asp Asp Val Asp Cys Thr Leu Val Glu Lys Arg Val Leu Ala Leu	
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Gly Gly Arg Gly Pro Gly Gly Arg Pro His Phe Leu Thr Gln Leu His	
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Ser Thr Phe Gln Thr Pro Asp Arg Leu Tyr Phe Val Met Glu Tyr Val	
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Thr Gly Gly Asp Leu Met Tyr His Ile Gln Gln Leu Gly Lys Phe Lys	
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Glu Pro His Ala Ala Phe Tyr Ala Ala Glu Ile Ala Ile Gly Leu Phe	
454 459 464 469	
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Phe Leu His Asn Gln Gly Ile Ile Tyr Arg Asp Leu Lys Leu Asp Asn	
470 475 480 485	
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486 491 496 501	
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Cys Lys Glu Asn Val Phe Pro Gly Thr Thr Thr Arg Thr Phe Cys Gly	
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Val Pro Val Met *	
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Val	Trp	Pro	Met	Tyr	Leu	Lys	Tyr	Arg	Gln	Glu	Met	Gln	Asp	Ile	Thr	
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31 36 41 46
gac cag tac tgg cac gag gac tgc ctg agc tgc gac ctc tgt ggc tgc 854
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47 52 57 62

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Lys His Phe Cys Val Gly Asp Arg Tyr Leu Leu Ile Asn Ser Asp Ile	
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ccttacttaa agatctggaa agc      atg aag act ggg ctt ttt ttc cta tgt      350
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Leu Leu Gly Thr Ala Ala Ala Ile Pro Thr Asn Ala Arg Leu Leu Ser
 10                               15                               20                               25

gat cat tcc aaa cca act gct gaa acg gta gca cct gac aac act gca      446
Asp His Ser Lys Pro Thr Ala Glu Thr Val Ala Pro Asp Asn Thr Ala
 26                               31                               36                               41

atc ccc agt tta agg gct gaa gct gaa gaa aat gaa aaa gaa aca gca      494
Ile Pro Ser Leu Arg Ala Glu Ala Glu Glu Asn Glu Lys Glu Thr Ala
 42                               47                               52                               57

gta tcc aca gaa gac gat tcc cac cat aag gct gaa aaa tca tca gta      542
Val Ser Thr Glu Asp Asp Ser His His Lys Ala Glu Lys Ser Ser Val
 58                               63                               68                               73

cta aag tca aaa gag gaa agc cat gaa cag tca gca gaa cag ggc aag      590
Leu Lys Ser Lys Glu Glu Ser His Glu Gln Ser Ala Glu Gln Gly Lys
 74                               79                               84                               89

agt tct agc caa gag ctg gga ttg aag gat caa gag gac agt gat ggt      638
Ser Ser Ser Gln Glu Leu Gly Leu Lys Asp Gln Glu Asp Ser Asp Gly
 90                               95                               100                               105

cac tta agt gtg aat ttg gag tat gca cca act gaa ggt aca ttg gac      686
His Leu Ser Val Asn Leu Glu Tyr Ala Pro Thr Glu Gly Thr Leu Asp
106                               111                               116                               121

ata aaa gaa gat atg agt gag cct cag gag aaa aaa ctc tca gag aac      734

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Thr	Asp	Phe	Leu	Ala	Pro	Gly	Val	Ser	Ser	Phe	Thr	Asp	Ser	Asn	Gln		
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Gln	Glu	Ser	Ile	Thr	Lys	Arg	Glu	Glu	Asn	Gln	Glu	Gln	Pro	Arg	Asn		
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Gln	Glu	Gln	Glu	Asp	Asn	Ser	Asn	Ala	Glu	Met	Glu	Glu	Glu	Asn	Ala		
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Thr	Thr	Pro	Arg	Asn	His	Gly	Val	Asp	Asp	Asp	Gly	Asp	Asp	Asp	Gly		
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Gln Phe Pro Leu Arg Met Arg Asp Trp Leu Lys Asn Ile Leu Met Gln							
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Cys Phe Gly Ile Lys Glu Glu Asp Ile Asp Glu Asn Leu Leu Phe *	
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Ser Ala Glu Ala Arg Arg Ala Leu Arg Glu Ala Ala Gly Pro Val Gly	
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Pro Ala Leu Glu Pro Pro Thr Leu Pro Leu His Arg Ala Leu Thr Leu	
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Leu Arg Ala Pro Pro Pro Pro Ser Ser Pro Pro Pro Gly Gly Ala Pro	
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Asp Gly Ser Glu Pro Ser Pro Asp Phe Pro Ala Leu Leu Val Glu Lys	
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Val	Asp	Leu	Ile	Asn	His	Tyr	Arg	His	Glu	Ser	Leu	Ala	Gln	Tyr	Asn	
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Ala	Lys	Leu	Asp	Thr	Arg	Leu	Leu	Tyr	Pro	Val	Ser	Lys	Tyr	Gln	Gln	
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Thr	Ala	Ile	Glu	Ala	Phe	Asn	Glu	Thr	Ile	Lys	Ile	Phe	Glu	Glu	Gln	
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Arg	Leu	Lys	Ser	Arg	Ile	Ala	Glu	Ile	His	Glu	Ser	Arg	Thr	Lys	Leu	
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Glu	Gln	Gln	Leu	Arg	Ala	Gln	Ala	Ser	Asp	Asn	Arg	Glu	Ile	Asp	Lys	

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Ile Asn Glu Trp Leu Gly Ile Lys Asn Glu Thr Glu Asp Gln Tyr Ala				
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Leu Met Glu Asp Glu Asp Asp Leu Pro His His Glu Glu Arg Thr Trp				
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Tyr Arg Thr Ala Thr Gly Phe Gly Phe Ala Glu Pro Tyr Asn Leu Tyr				
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ggg tgc ctg aag gag ctg gtg ctg cac tac cag cac gcc tgc ctg gtg				3192
Gly Ser Leu Lys Glu Leu Val Leu His Tyr Gln His Ala Ser Leu Val				
687	692	697	702	
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Gln His Asn Asp Ala Leu Thr Val Thr Leu Ala His Pro Val Arg Ala				
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Pro Gly Pro Gly Pro Pro Pro Ala Ala Arg *				
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 aagctttact tacctggg atg gac tct gcc aga cac cat ata agc cac tct 291
 Met Asp Ser Ala Arg His His Ile Ser His Ser
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 act tct gca ggc ccc atc cct tcc cag aaa gaa gag gaa atg act gag 339
 Thr Ser Ala Gly Pro Ile Pro Ser Gln Lys Glu Glu Glu Met Thr Glu
 12 17 22 27
 tcc cag gga aca gta aca ttc aaa gat gtg gct atc gac ttc act cag 387
 Ser Gln Gly Thr Val Thr Phe Lys Asp Val Ala Ile Asp Phe Thr Gln
 28 33 38 43
 gag gag tgg aag aga ttg gat cct gct cag aga aaa ctg tac cgg aat 435
 Glu Glu Trp Lys Arg Leu Asp Pro Ala Gln Arg Lys Leu Tyr Arg Asn
 44 49 54 59
 gtg atg cta gaa aac tat aac aac tta atc aca gta ggc tat ccg ttc 483
 Val Met Leu Glu Asn Tyr Asn Asn Leu Ile Thr Val Gly Tyr Pro Phe
 60 65 70 75

acc aaa cct gat gtg att ttc aaa ttg gag caa gaa gaa gaa cca tgg	531
Thr Lys Pro Asp Val Ile Phe Lys Leu Glu Gln Glu Glu Glu Pro Trp	
76 81 86 91	
gtg atg gag gaa gaa gta tta agg aga cac tgg caa gga gaa ata tgg	579
Val Met Glu Glu Glu Val Leu Arg Arg His Trp Gln Gly Glu Ile Trp	
92 97 102 107	
gga gtt gat gag cat cag aaa aac cag gac aga ctt ttg aga caa gtt	627
Gly Val Asp Glu His Gln Lys Asn Gln Asp Arg Leu Leu Arg Gln Val	
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gaa gtt aaa ttc cag aaa aca ctg act gaa gaa aaa ggc aat gaa tgt	675
Glu Val Lys Phe Gln Lys Thr Leu Thr Glu Glu Lys Gly Asn Glu Cys	
124 129 134 139	
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Gln Lys Lys Phe Ala Asn Val Phe Pro Leu Asn Ser Asp Phe Phe Pro	
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tcc aga cac aat ctc tat gag tat gac tta ttt gga aag tgt tta gaa	771
Ser Arg His Asn Leu Tyr Glu Tyr Asp Leu Phe Gly Lys Cys Leu Glu	
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His Asn Phe Asp Cys His Asn Asn Val Lys Cys Leu Met Arg Lys Glu	
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cat tgt gaa tat aat gaa cct gtg aaa tca tat ggt aat agc tca tcc	867
His Cys Glu Tyr Asn Glu Pro Val Lys Ser Tyr Gly Asn Ser Ser Ser	
188 193 198 203	
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His Phe Val Ile Thr Pro Phe Lys Cys Asn His Cys Gly Lys Gly Phe	
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Asn Gln Thr Leu Asp Leu Ile Arg His Leu Arg Ile His Thr Gly Glu	
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Lys Leu Ile Lys His Tyr Lys Ile His Ser Arg Glu Gln Ser Tyr Lys	
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Cys Asn Glu Cys Gly Lys Ala Phe Ile Lys Met Ser Asn Leu Ile Arg	
268 273 278 283	
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Glu Lys Ser Phe Ser	Gln Lys Ser Asn Leu Ile Asp His Glu Lys Ile	
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396	401 406 411	
gga aaa gcc ttc tct caa agc tca gcc ctt act gta cat atg aga agt	1539	
Gly Lys Ala Phe Ser	Gln Ser Ser Ala Leu Thr Val His Met Arg Ser	
412	417 422 427	
cac act ggt gag aaa ccc tat gaa tgt aag gaa tgc aga aaa gcc ttc	1587	
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Cys Lys Glu Cys Gly	Lys Ala Phe Ser Gln Asn Ser Asn Leu Ile Ala	
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His Thr Gly Glu Lys Pro Tyr Asp Cys Asn Glu Cys Gly Lys Ala Phe	
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Ser Gln Ile Ala Ser Leu Thr Leu His Leu Arg Ser His Thr Gly Glu	
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Lys Pro Tyr Glu Cys Asp Lys Cys Gly Lys Ala Phe Ser Gln Cys Ser	
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Cys Asn Glu Cys Gly Lys Ala Phe Ser Gln Arg Thr Ser Leu Ile Val	
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668 673 678 683	
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 Val Ser Ile Asp Thr Ala Ser Tyr Lys Ile Phe Val Ser Gly Lys Ser
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 Pro Val Val His His Glu Thr Thr Gly Ile Gln Thr Thr Val Val Phe
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 gag ttc tgg gac tgt gga gag tct gca ctc aaa aag ttc gat cat atg 802
 Glu Phe Trp Asp Cys Gly Glu Ser Ala Leu Lys Lys Phe Asp His Met
 113 118 123 128
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 129 134 139 144

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Phe Thr Asp Arg Ala Ser Phe Glu Asp Leu Pro Gly Gln Leu Ala Arg	
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Ile Ala Gly Glu Ala Pro Gly Val Val Arg Met Val Ile Gly Ser Lys	
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Phe Asp Gln Tyr Met His Thr Asp Val Pro Glu Arg Asp Leu Thr Ala	
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Phe Arg Gln Ala Trp Glu Leu Pro Leu Leu Arg Val Lys Ser Val Pro	
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Gly Arg Arg Leu Ala Asp Gly Arg Thr Leu Asp Gly Arg Ala Gly Leu	
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Gln Asp Gln Val Ala Ala Gly Leu Leu Pro Asn Pro Pro Glu Ser Ala	
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Pro Glu *	
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Lys Gln Gln Leu Ala Leu Tyr Thr Glu Lys Phe Glu Glu Phe Gln Asn	
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Thr Leu Ser Lys Ser Ser Glu Val Phe Thr Thr Phe Lys Gln Glu Met	
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Ala Pro Ser Ser Pro Arg Val Thr Glu Ala Pro Cys Tyr Pro Gly Ala	
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Pro Ser Thr Glu Ala Ser Gly Gln Thr Gly Pro Gln Glu Pro Thr Ser	
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 atg ggg gac aag aaa gat gac aag gac tca ccc aag aag aac aag ggc 165
 Met Gly Asp Lys Lys Asp Asp Lys Asp Ser Pro Lys Lys Asn Lys Gly
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 aag gag cgc cgg gac ctg gat gac ctc aag aag gag gtg gct atg aca 213
 Lys Glu Arg Arg Asp Leu Asp Asp Leu Lys Lys Glu Val Ala Met Thr
 17 22 27 32
 gag cac aag atg tca gtg gaa gag gtc tgc cgg aaa tac aac aca gac 261
 Glu His Lys Met Ser Val Glu Glu Val Cys Arg Lys Tyr Asn Thr Asp
 33 38 43 48
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 Cys Val Gln Gly Leu Thr His Ser Lys Ala Gln Glu Ile Leu Ala Arg
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Gly Ala Ile Leu Cys Phe Leu Ala Tyr Gly Ile Gln Ala Gly Thr Glu	
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Asn Pro Leu Glu Thr Arg Asn Ile Thr Phe Phe Ser Thr Asn Cys Val	
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Pro Ile Ala Ile Glu Ile Glu His Phe Ile Gln Leu Ile Thr Gly Val	
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Tyr Thr Trp Leu Glu Ala Val Ile Phe Leu Ile Gly Ile Ile Val Ala	
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Asn Val Pro Glu Gly Leu Leu Ala Thr Val Thr Val Cys Leu Thr Leu	
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acc gcc aag cgc atg gcc cgg aag aac tgc ctg gtg aag aac ctg gag	1173
Thr Ala Lys Arg Met Ala Arg Lys Asn Cys Leu Val Lys Asn Leu Glu	
337 342 347 352	
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Ser Ile His Glu Thr Glu Asp Pro Asn Asp Asn Arg Tyr Leu Leu Val	
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Met Lys Gly Ala Pro Glu Arg Ile Leu Asp Arg Cys Ser Thr Ile Leu	
497 502 507 512	
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Phe	Cys	His	Tyr	Tyr	Leu	Pro	Glu	Glu	Gln	Phe	Pro	Lys	Gly	Phe	Ala		
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Phe	Asp	Cys	Asp	Asp	Val	Asn	Phe	Thr	Thr	Asp	Asn	Leu	Cys	Phe	Val		
561					566					571					576		
ggc	ctc	atg	tcc	atg	atc	gac	cca	ccc	cgg	gca	gcc	gtc	cct	gac	gcg	1893	
Gly	Leu	Met	Ser	Met	Ile	Asp	Pro	Pro	Arg	Ala	Ala	Val	Pro	Asp	Ala		
577					582					587					592		
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Val	Gly	Lys	Cys	Arg	Ser	Ala	Gly	Ile	Lys	Val	Ile	Met	Val	Thr	Gly		
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Asp	His	Pro	Ile	Thr	Ala	Lys	Ala	Ile	Ala	Lys	Gly	Val	Gly	Ile	Ile		
609					614					619					624		
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ccc	gtc	agc	cag	gtt	aac	ccc	cgg	gat	gcc	aag	gcc	tgc	gtg	atc	cac	2085	
Pro	Val	Ser	Gln	Val	Asn	Pro	Arg	Asp	Ala	Lys	Ala	Cys	Val	Ile	His		
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ggc	acc	gac	ctc	aag	gac	ttc	acc	tcc	gag	caa	atc	gac	gag	atc	ctg	2133	
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657					662					667					672		
cag	aat	cac	acc	gag	atc	gtc	ttc	gcc	cgc	aca	tcc	ccc	cag	cag	aag	2181	
Gln	Asn	His	Thr	Glu	Ile	Val	Phe	Ala	Arg	Thr	Ser	Pro	Gln	Gln	Lys		
673					678					683					688		
ctc	atc	att	gtg	gag	ggc	tgt	cag	aga	cag	ggg	gca	att	gtg	gct	gtg	2229	
Leu	Ile	Ile	Val	Glu	Gly	Cys	Gln	Arg	Gln	Gly	Ala	Ile	Val	Ala	Val		
689					694					699					704		
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705					710					715					720		
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Gly	Val	Ala	Met	Gly	Ile	Ala	Gly	Ser	Asp	Val	Ser	Lys	Gln	Ala	Ala		
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Asp	Met	Ile	Leu	Leu	Asp	Asp	Asn	Phe	Ala	Ser	Ile	Val	Thr	Gly	Val		

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753	758	763	768	
acc ctg acc agc aat atc ccg gag atc acg ccc ttc ctg ctg ttc atc				2469
Thr Leu Thr Ser Asn Ile Pro Glu Ile Thr Pro Phe Leu Leu Phe Ile				
769	774	779	784	
atg gcc aac atc ccg ctg ccc ctg ggc acc atc acc atc ctc tgc atc				2517
Met Ala Asn Ile Pro Leu Pro Leu Gly Thr Ile Thr Ile Leu Cys Ile				
785	790	795	800	
gat ctg ggc act gac atg gtc cct gcc atc tca ctg gcg tac gag gct				2565
Asp Leu Gly Thr Asp Met Val Pro Ala Ile Ser Leu Ala Tyr Glu Ala				
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gcc gaa agc gac atc atg aag aga cag ccc agg aac ccg cgg acg gac				2613
Ala Glu Ser Asp Ile Met Lys Arg Gln Pro Arg Asn Pro Arg Thr Asp				
817	822	827	832	
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Lys Leu Ala Glu Glu Pro Met Gly Arg Ser Tyr His Leu Trp Asp Tyr				
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Asp *				
849				
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Arg Arg Leu Gln Gly Ile Ser Phe Gly Met Tyr Ser Ala Glu Glu Leu	
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Lys Lys Leu Ser Val Lys Ser Ile Thr Asn Pro Arg Tyr Leu Asp Ser	
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Cys Ser Gly His Leu Gly His Ile Glu Leu Pro Leu Thr Val Tyr Asn	
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Pro Leu Leu Phe Asp Lys Leu Tyr Leu Leu Arg Gly Ser Cys Leu	
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Asn Cys His Met Leu Thr Cys Pro Arg Ala Val Ile His Leu Leu Leu	
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Cys Gln Leu Arg Val Leu Glu Val Gly Ala Leu Gln Ala Val Tyr Glu	
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186 191 196 201	
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Glu His Asn Ser Lys Leu Thr Ile Thr Phe Pro Ala Met Val His Arg	
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Phe Leu Asp Phe Leu Val Val Pro Pro Ser Arg Tyr Arg Pro Val Ser	
298 303 308 313	
cgc cta gga gac cag atg ttt act aat ggc cag acg gtg aac ttg cag	1131
Arg Leu Gly Asp Gln Met Phe Thr Asn Gly Gln Thr Val Asn Leu Gln	
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gct gtc atg aag gat gta gtt ctg att cga aaa ctt ctg gca ttg atg	1179
Ala Val Met Lys Asp Val Val Leu Ile Arg Lys Leu Leu Ala Leu Met	
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Ala Gln Glu Gln Lys Leu Pro Glu Glu Val Ala Thr Pro Thr Thr Asp	
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gag gaa aaa gac tct ttg att gct att gac cga tcc ttt ttg agt aca	1275
Glu Glu Lys Asp Ser Leu Ile Ala Ile Asp Arg Ser Phe Leu Ser Thr	
362 367 372 377	
ctt cca ggc cag tcc ctc ata gac aaa ctt tac aac att tgg att cgc	1323
Leu Pro Gly Gln Ser Leu Ile Asp Lys Leu Tyr Asn Ile Trp Ile Arg	
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ctt cag agc cac gtc aat att gtg ttt gat agc gag atg gac aaa cta	1371
Leu Gln Ser His Val Asn Ile Val Phe Asp Ser Glu Met Asp Lys Leu	
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atg atg gac aag tac cca ggc att agg cag atc ctg gag aag aaa gaa	1419
Met Met Asp Lys Tyr Pro Gly Ile Arg Gln Ile Leu Glu Lys Lys Glu	
410 415 420 425	
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Gly Leu Phe Arg Lys His Met Met Gly Lys Arg Val Asp Tyr Ala Ala	
426 431 436 441	
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Arg Ser Val Ile Cys Pro Asp Met Tyr Ile Asn Thr Asn Glu Ile Gly	
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Ile Pro Met Val Phe Ala Thr Lys Leu Thr Tyr Pro Gln Pro Val Thr	
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Pro Trp Asn Val Gln Glu Leu Arg Gln Ala Val Ile Asn Gly Pro Asn	
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Val His Pro Gly Ala Ser Met Val Ile Asn Glu Asp Gly Ser Arg Thr	
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Pro Thr Leu His Arg Pro Ser Ile Gln Ala His Arg Ala Arg Ile Leu	
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Pro Glu Glu Lys Val Leu Arg Leu His Tyr Ala Asn Cys Lys Ala Tyr	
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Gly Arg Val Lys Leu Leu Ser Pro Ser Ile Leu Lys Pro Phe Pro Leu	
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Glu	Asp	His	Ile	Pro	Leu	Asn	Leu	Ser	Gly	Lys	Ala	Lys	Ile	Thr	Gly		
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aaa	gcc	tgg	gtg	aag	gaa	act	cct	cga	tcc	gtt	cct	ggc	ttt	aac	cct	2331	
Lys	Ala	Trp	Val	Lys	Glu	Thr	Pro	Arg	Ser	Val	Pro	Gly	Phe	Asn	Pro		
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Asp	Ser	Met	Cys	Glu	Ser	Gln	Val	Ile	Ile	Arg	Glu	Gly	Glu	Leu	Leu		
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tgc	gga	gtg	ctg	gac	aag	gcg	cac	tat	ggg	agc	tcc	gcc	tac	ggc	ctg	2427	
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Val	His	Cys	Cys	Tyr	Glu	Ile	Tyr	Gly	Gly	Glu	Thr	Ser	Gly	Lys	Val		
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cta	acc	tgc	ctg	gcc	cgc	ctc	ttc	acc	gcc	tac	ctg	cag	ctc	tac	aga	2523	
Leu	Thr	Cys	Leu	Ala	Arg	Leu	Phe	Thr	Ala	Tyr	Leu	Gln	Leu	Tyr	Arg		
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Gly	Phe	Thr	Leu	Gly	Val	Glu	Asp	Ile	Leu	Val	Lys	Pro	Lys	Ala	Asp		
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Val	Lys	Arg	Gln	Arg	Ile	Ile	Glu	Glu	Ser	Thr	His	Cys	Gly	Pro	Gln		
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Ala	Val	Arg	Ala	Ala	Leu	Asn	Leu	Pro	Glu	Ala	Ala	Ser	Tyr	Asp	Glu		
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Val	Arg	Gly	Lys	Trp	Gln	Asp	Ala	His	Leu	Gly	Lys	Asp	Gln	Arg	Asp		
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Thr	Val	Asn	Thr	Met	Gln	Ile	Ser	Cys	Leu	Leu	Gly	Gln	Ile	Glu	Leu		

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Glu Gly Arg Ser Thr Pro Leu Met Ala Ser Gly Lys Ser Leu Pro Cys				
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Phe Glu Pro Tyr Glu Phe Thr Pro Arg Ala Gly Gly Phe Val Thr Gly				
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Arg Phe Leu Thr Gly Ile Lys Pro Pro Glu Phe Phe Phe His Cys Met				
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Ala Gly Arg Glu Gly Leu Val Asp Thr Ala Val Lys Thr Ser Arg Ser				
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Gly Tyr Leu Gln Arg Cys Ile Ile Lys His Leu Glu Gly Leu Val Val				
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Gln Tyr Asp Leu Thr Val Arg Asp Ser Asp Gly Ser Val Val Gln Phe				
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Leu Tyr Gly Glu Asp Gly Leu Asp Ile Pro Lys Thr Gln Phe Leu Gln				
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Thr Leu Leu Arg Arg Gly Ala Phe Leu Ser Tyr Ser Gln Lys Ile Gln				
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Arg Pro Trp Asp Ser Gly Arg Met Leu Arg Met Trp Tyr Glu Leu Asp				
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Glu Thr Phe Glu Thr Lys Val Asp Asp Tyr Ser Gln Glu Trp Ala Ala	
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Gln Thr Glu Lys Ser Tyr Glu Lys Ser Glu Leu Ser Leu Asp Arg Leu	
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Gln Met Thr Leu Asn Thr Phe His Phe Ala Gly Arg Gly Glu Met Asn	
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Ser Ile Lys Lys Lys Asn Asn Lys Ala Ser Ala Phe Arg Asn Val Asn	
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Ile Ser Ser Asp Asn Ser Asp Thr Thr Asp Ser His Ala Thr Ser Thr
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Ser Ala Ser Arg Cys Ser Lys Leu Pro Ser Ser Thr Lys Ser Gly Trp
26 31 36 41

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Ile Thr Ala Met Lys Ile Pro Asp Ser Tyr Gln Leu Ser Pro Asp Asp
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74 79 84 89

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Leu Lys Glu Met Glu Arg Pro Glu Leu Asp Glu Leu Thr Leu Glu Arg							
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Val Leu Glu Glu Leu Glu Thr Leu Cys His Gln Asn Met Ala Arg Ala							
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Ile Glu Thr Gln Glu Gly Leu Gly Ile Glu Tyr Asp Glu Asp Val Val							
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tgc gac gtg tgt cgc tct cct gag ggc gag gat ggc aac gag atg gtc							677
Cys Asp Val Cys Arg Ser Pro Glu Gly Glu Asp Gly Asn Glu Met Val							
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ttc tgt gac aag tgc aac gtc tgt gtg cat cag gca tgc tac ggg atc							725
Phe Cys Asp Lys Cys Asn Val Cys Val His Gln Ala Cys Tyr Gly Ile							
218		223		228		233	
ctc aag gtg ccc acg ggc agc tgg ctg tgc cgg acg tgt gcc ctg ggt							773
Leu Lys Val Pro Thr Gly Ser Trp Leu Cys Arg Thr Cys Ala Leu Gly							
234		239		244		249	
gtc cag cca aag tgc ctg ctc tgc ccc aag cga gga gga gcc ttg aag							821
Val Gln Pro Lys Cys Leu Leu Cys Pro Lys Arg Gly Gly Ala Leu Lys							
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ccc act aga agt ggg acc aag tgg gtg cat gtc agc tgt gcc cta tgg							869
Pro Thr Arg Ser Gly Thr Lys Trp Val His Val Ser Cys Ala Leu Trp							
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att cct gag gtc agc atc ggc tgc cca gag aag atg gag ccc atc acc							917
Ile Pro Glu Val Ser Ile Gly Cys Pro Glu Lys Met Glu Pro Ile Thr							
282		287		292		297	
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Lys Ile Ser His Ile Pro Ala Ser Arg Trp Ala Leu Ser Cys Ser Leu							
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tgc aag gaa tgc aca ggc acc tgc atc cag tgt tcc atg cct tcc tgc							1013
Cys Lys Glu Cys Thr Gly Thr Cys Ile Gln Cys Ser Met Pro Ser Cys							
314		319		324		329	
gtc aca gcg ttc cat gtc aca tgc gcc ttt gac cac ggc ctg gaa atg							1061
Val Thr Ala Phe His Val Thr Cys Ala Phe Asp His Gly Leu Glu Met							
330		335		340		345	

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Leu Leu Gln Asp Glu Glu Thr Leu Leu Ser Phe Met Arg Asp Pro Ser	
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Leu Arg Pro Gly Asp Pro Ala Arg Lys Ala Arg Gly Arg Thr Arg Leu	
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Ser Arg Thr Thr Pro Asp Lys Ala Pro Lys Lys Thr Trp Gly Gln Asp	
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Arg Arg Thr Ser Ser His Leu Pro Ser Ser Pro Ala Ala Gly Asp Cys	
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Pro Asp Glu Ala Ala Ser Val Ala Ala Asp Ser Asp Val Gln Val Pro	
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agaagctgta agccttctcc ttggggaaa atg tct ggg aag aag ctt ttc gtg 1013
Met Ser Gly Lys Lys Leu Phe Val
1 5

acc aat ggt gag cgg atg cct ttc tcc aaa gtg aag gct ctg tgt gct 1061
Thr Asn Gly Glu Arg Met Pro Phe Ser Lys Val Lys Ala Leu Cys Ala
9 14 19 24

ggg ctc cag gcc aca gtg gct gcc ccc aag aat gcc gag gag aat aag 1109
Gly Leu Gln Ala Thr Val Ala Ala Pro Lys Asn Ala Glu Glu Asn Lys
25 30 35 40

gcc atc cag gat gtg gcc aaa gac act gcc ttc ctg ggc atc aca gat 1157
Ala Ile Gln Asp Val Ala Lys Asp Thr Ala Phe Leu Gly Ile Thr Asp
41 46 51 56

gag gca act gaa ggc cag ttc atg tac ttg acg ggc ggg agg ctg acc 1205
Glu Ala Thr Glu Gly Gln Phe Met Tyr Leu Thr Gly Gly Arg Leu Thr
57 62 67 72

tac agc aac tgg aag aag gat gag cca aat gac cac ggc tca ggg gag 1253
Tyr Ser Asn Trp Lys Lys Asp Glu Pro Asn Asp His Gly Ser Gly Glu
73 78 83 88

gac tgc gtt att ctc ctg aac aat ggg ctc tgg aat ggc atc tcc tgc 1301
Asp Cys Val Ile Leu Leu Asn Asn Gly Leu Trp Asn Gly Ile Ser Cys
89 94 99 104

acc tcc tcc ttc att gcc atc tgt gag ttt cct gcc tga agaggcacgt 1350
Thr Ser Ser Phe Ile Ala Ile Cys Glu Phe Pro Ala *
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Ala Gln Glu Ser Leu Thr Leu Glu Asp Val Ala Val Asp Phe Thr Trp	
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Glu Glu Trp Gln Phe Leu Ser Pro Ala Gln Lys Asp Leu Tyr Arg Asp	
20 25 30 35	
gtg atg ttg gag aac tac agc aac ctt gtg tca gtg ggg tat caa gcc	441
Val Met Leu Glu Asn Tyr Ser Asn Leu Val Ser Val Gly Tyr Gln Ala	
36 41 46 51	
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Gly Lys Pro Asp Ala Leu Thr Lys Leu Glu Gln Gly Glu Pro Leu Trp	
52 57 62 67	
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Thr Leu Glu Asp Glu Ile His Ser Pro Ala His Pro Glu Ile Glu Lys	
68 73 78 83	
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Ala Asp Asp His Leu Gln Gln Pro Leu Gln Asn Gln Lys Ile Leu Lys	
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Arg Thr Gly Gln Arg Tyr Glu His Gly Arg Thr Leu Lys Ser Tyr Leu	
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Gly Leu Thr Asn Gln Ser Arg Arg Tyr Asn Arg Lys Glu Pro Ala Glu	
116 121 126 131	
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Phe Asn Gly Asp Gly Ala Phe Leu His Asp Asn His Glu Gln Met Pro	
132 137 142 147	
acg gaa att gaa ttc cct gaa agt aga aaa ccc atc agc acc aag tca	777
Thr Glu Ile Glu Phe Pro Glu Ser Arg Lys Pro Ile Ser Thr Lys Ser	
148 153 158 163	
caa ttc ctt aaa cat cag caa aca cac aac ata gag aaa gcc cat gaa	825
Gln Phe Leu Lys His Gln Gln Thr His Asn Ile Glu Lys Ala His Glu	
164 169 174 179	
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Cys Thr Asp Cys Gly Lys Ala Phe Leu Lys Lys Ser Gln Leu Thr Glu	
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His Lys Arg Ile His Thr Gly Lys Lys Pro His Val Cys Ser Leu Cys	
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Gly Lys Ala Phe Tyr Lys Lys Tyr Arg Leu Thr Glu His Glu Arg Ala	
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His Arg Gly Glu Lys Pro His Gly Cys Ser Leu Cys Gly Lys Ala Phe	
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Tyr Lys Arg Tyr Arg Leu Thr Glu His Glu Arg Ala His Lys Gly Glu	
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His Gln Arg Thr His Thr Gly Glu Lys Pro His Thr Cys Ser Glu Cys	
308 313 318 323	
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324 329 334 339	
cac act gga gag aaa cct tat gga tgc att gac tgt ggc aag gcc ttc	1353
His Thr Gly Glu Lys Pro Tyr Gly Cys Ile Asp Cys Gly Lys Ala Phe	
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agc cag aag tct tgc ctt gta gca cat cag aga tat cat aca gga aag	1401
Ser Gln Lys Ser Cys Leu Val Ala His Gln Arg Tyr His Thr Gly Lys	
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act ccc ttt gta tgt cct gaa tgt ggg caa ccc tgt tca cag aag tca	1449
Thr Pro Phe Val Cys Pro Glu Cys Gly Gln Pro Cys Ser Gln Lys Ser	
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Gly Leu Ile Arg His Gln Lys Ile His Ser Gly Glu Lys Pro Tyr Lys	
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Cys Ser Asp Cys Gly Lys Ala Phe Leu Thr Lys Thr Met Leu Ile Val	
404 409 414 419	
cat cac aga act cac acg gga gag aga ccc tat ggc tgt gat gag tgt	1593

His His Arg Thr His Thr Gly Glu Arg Pro Tyr Gly Cys Asp Glu Cys	
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gag aaa gct tac ttc tat atg tct tgc ctt gtt aaa cat aag aga ata	1641
Glu Lys Ala Tyr Phe Tyr Met Ser Cys Leu Val Lys His Lys Arg Ile	
436 441 446 451	
cac tca agg gag aaa cgg ggg gat tca gtg aag gtg gaa aat cct tcc	1689
His Ser Arg Glu Lys Arg Gly Asp Ser Val Lys Val Glu Asn Pro Ser	
452 457 462 467	
aca gca agt cac agc tta agt cct agt gaa cat gtg cag ggg aaa agc	1737
Thr Ala Ser His Ser Leu Ser Pro Ser Glu His Val Gln Gly Lys Ser	
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cct gtt aat atg gta act gtg gca atg gtg gca ggg cag tgt gag ttt	1785
Pro Val Asn Met Val Thr Val Ala Met Val Ala Gly Gln Cys Glu Phe	
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Ala His Ile Leu His Ser *	
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Lys Ile Ser Arg Asp Lys Ser Val Thr Ile Tyr Leu Gly Asn Arg Asp	
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Tyr Ile Asp His Val Ser Gln Val Gln Pro Val Asp Gly Val Val Leu	
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Cys Gly Val Asp Phe Glu Val Lys Ala Phe Ala Thr Asp Ser Thr Asp	
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Val Ser Leu Asn Lys Glu Ile Tyr Phe His Gly Glu Pro Ile Pro Val	

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Ala Phe Val Glu Gln Val Ala Asn Val Val Leu Tyr Ser Ser Asp Tyr				
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Tyr Val Lys Pro Val Ala Met Glu Glu Ala Gln Glu Lys Val Pro Pro				
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Asn Arg Glu Arg Arg Gly Ile Ala Leu Asp Gly Lys Ile Lys His Glu				
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Asp Thr Asn Leu Ala Ser Ser Thr Ile Ile Lys Glu Gly Ile Asp Arg				
307	312	317	322	
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Ser Tyr Gln Asp Ala Asn Leu Val Phe Glu Glu Phe Ala Arg His Asn				
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Val Gly His Cys His Pro Leu Val Val Gln Ala Ala His Glu Gln Asn
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cag gtg ctc aac acc aac agc cgg tac ctg cat gac aac atc gtg gac      531
Gln Val Leu Asn Thr Asn Ser Arg Tyr Leu His Asp Asn Ile Val Asp
 76                   81                   86                   91

tat gcg cag agg ctg tca gag acc ctg ccg gag cag ctc tgt gtg ttc      579
Tyr Ala Gln Arg Leu Ser Glu Thr Leu Pro Glu Gln Leu Cys Val Phe
 92                   97                   102                   107

tat ttc ctg aat tct ggg tca gaa gcc aat gac ctg gcc ctg agg ctg      627
Tyr Phe Leu Asn Ser Gly Ser Glu Ala Asn Asp Leu Ala Leu Arg Leu
108                   113                   118                   123

gct cgc cac tac acg gga cac cag gac gtg gtg gta tta gat cat gcg      675
Ala Arg His Tyr Thr Gly His Gln Asp Val Val Val Leu Asp His Ala
124                   129                   134                   139

tat cac ggc cac ctg agc tcc ctg att gac atc agt ccc tac aag ttc      723
Tyr His Gly His Leu Ser Ser Leu Ile Asp Ile Ser Pro Tyr Lys Phe
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364 369 374 379	

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Ile Gly Trp Leu Glu Glu Phe Thr Ser Gln Tyr Ser Arg Asp Gln Lys	
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Glu Pro Pro Ser His Gln Tyr Leu Ser Leu Thr Leu Leu His Leu Leu	
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Lys Ala Leu Ser Cys Gln Glu Val Thr Asp Asp Glu Val Leu His Ala	
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Val Lys Gln Lys Trp Ala Ser Arg Leu Leu Ala Lys Leu Arg Lys Asp	
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 <213> Homo sapiens

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 <222> (265) .. (2067)

<400> 94

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ctggccacct	gccatgccct	cagccggctc	caggacaccc	ccgtgggcga	ccccatggac	180
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tttgggaccc	aggtcttggc	agtg	atg aga ccc cca ctt tgg gag ccc cag			291
			Met Arg Pro Pro Leu Trp Glu Pro Gln			
			1 5			
ctg cag gca atg gag gag ccc ccg gtg cca gtc agc gtc ctc cac cgc						339
Leu Gln Ala Met Glu Glu Pro Pro Val Pro Val Ser Val Leu His Arg						
10 15 20 25						
ttc ccc ttc tct tgc gct ctg cag cgc atg agt gtg gtg gtg gcg tgg						387
Phe Pro Phe Ser Ser Ala Leu Gln Arg Met Ser Val Val Val Ala Trp						
26 31 36 41						
cca ggg gcc act cag ccc gag gcc tac gtc aaa ggc tcc ccg gag ctg						435
Pro Gly Ala Thr Gln Pro Glu Ala Tyr Val Lys Gly Ser Pro Glu Leu						
42 47 52 57						
gtg gca ggg ctc tgc aac ccc gag aca gtg ccc acc gac ttc gcc cag						483
Val Ala Gly Leu Cys Asn Pro Glu Thr Val Pro Thr Asp Phe Ala Gln						
58 63 68 73						
atg ctg cag agc tat aca gct gct ggc tac cgt gtc gtg gcc ctg gcc						531
Met Leu Gln Ser Tyr Thr Ala Ala Gly Tyr Arg Val Val Ala Leu Ala						
74 79 84 89						
agc aag cca ctg ccc act gtg ccc agc ctg gag gca gcc cag caa ctg						579
Ser Lys Pro Leu Pro Thr Val Pro Ser Leu Glu Ala Ala Gln Gln Leu						
90 95 100 105						
acg agg gac act gtg gaa gga gac ctg agc ctc ctg ggg ctg ctg gtc						627
Thr Arg Asp Thr Val Glu Gly Asp Leu Ser Leu Leu Gly Leu Leu Val						
106 111 116 121						
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Met Arg Asn Leu Leu Lys Pro Gln Thr Thr Pro Val Ile Gln Ala Leu						
122 127 132 137						
cga agg acc cgc atc cgc gcc gtc atg gtg aca ggg gac aac ctg cag						723
Arg Arg Thr Arg Ile Arg Ala Val Met Val Thr Gly Asp Asn Leu Gln						
138 143 148 153						
aca gcg gtg act gtg gcc cgg ggc tgt ggc atg gtg gcc ccc cag gag						771
Thr Ala Val Thr Val Ala Arg Gly Cys Gly Met Val Ala Pro Gln Glu						
154 159 164 169						
cat ctg atc atc gtc cac gcc acc cac cct gag cgg ggt cag cct gcc						819
His Leu Ile Ile Val His Ala Thr His Pro Glu Arg Gly Gln Pro Ala						
170 175 180 185						
tct ctc gag ttc ctg ccg atg gag tcc ccc aca gcc gtg aat ggc gtt						867

Ser	Leu	Glu	Phe	Leu	Pro	Met	Glu	Ser	Pro	Thr	Ala	Val	Asn	Gly	Val	
186					191					196					201	
aag	gat	cct	gac	cag	gct	gca	agc	tac	acc	gtg	gag	cca	gac	ccc	cga	915
Lys	Asp	Pro	Asp	Gln	Ala	Ala	Ser	Tyr	Thr	Val	Glu	Pro	Asp	Pro	Arg	
202					207					212					217	
tcc	agg	cac	ctg	gcc	ctc	agc	ggg	ccc	acc	ttt	ggg	atc	att	gtg	aag	963
Ser	Arg	His	Leu	Ala	Leu	Ser	Gly	Pro	Thr	Phe	Gly	Ile	Ile	Val	Lys	
218					223					228					233	
cac	ttc	ccc	aag	ctg	ctg	ccc	aag	gtc	ctg	gtc	cag	ggc	act	gtc	ttt	1011
His	Phe	Pro	Lys	Leu	Leu	Pro	Lys	Val	Leu	Val	Gln	Gly	Thr	Val	Phe	
234					239					244					249	
gcc	cgc	atg	gcc	cct	gag	cag	aag	aca	gag	ctg	gtg	tgc	gag	cta	cag	1059
Ala	Arg	Met	Ala	Pro	Glu	Gln	Lys	Thr	Glu	Leu	Val	Cys	Glu	Leu	Gln	
250					255					260					265	
aag	ctt	cag	tac	tgc	gtg	ggc	atg	tgc	gga	gac	ggg	gcc	aat	gac	tgt	1107
Lys	Leu	Gln	Tyr	Cys	Val	Gly	Met	Cys	Gly	Asp	Gly	Ala	Asn	Asp	Cys	
266					271					276					281	
ggg	gcc	ctg	aag	gcg	gct	gat	gtc	ggc	atc	tcg	ctg	tcc	cag	gca	gaa	1155
Gly	Ala	Leu	Lys	Ala	Ala	Asp	Val	Gly	Ile	Ser	Leu	Ser	Gln	Ala	Glu	
282					287					292					297	
gcc	tca	gtg	gtc	tca	ccc	ttc	acc	tcg	agc	atg	gcc	agt	att	gag	tgc	1203
Ala	Ser	Val	Val	Ser	Pro	Phe	Thr	Ser	Ser	Met	Ala	Ser	Ile	Glu	Cys	
298					303					308					313	
gtg	ccc	atg	gtc	atc	agg	gag	ggg	cgc	tgt	tcc	ctt	gac	act	tcg	ttc	1251
Val	Pro	Met	Val	Ile	Arg	Glu	Gly	Arg	Cys	Ser	Leu	Asp	Thr	Ser	Phe	
314					319					324					329	
agc	gtc	ttc	aag	tac	atg	gct	ctg	tac	agc	ctg	acc	cag	ttc	atc	tcc	1299
Ser	Val	Phe	Lys	Tyr	Met	Ala	Leu	Tyr	Ser	Leu	Thr	Gln	Phe	Ile	Ser	
330					335					340					345	
gtc	ctg	atc	ctc	tac	acg	atc	aac	acc	aac	ctg	ggg	gac	ctg	cag	ttc	1347
Val	Leu	Ile	Leu	Tyr	Thr	Ile	Asn	Thr	Asn	Leu	Gly	Asp	Leu	Gln	Phe	
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ctg	gcc	atc	gac	ctg	gtc	atc	acc	acc	aca	gtg	gca	gtg	ctc	atg	agc	1395
Leu	Ala	Ile	Asp	Leu	Val	Ile	Thr	Thr	Thr	Val	Ala	Val	Leu	Met	Ser	
362					367					372					377	
cgc	acg	ggg	cca	gcg	ctg	gtc	ctg	gga	cgg	gtg	cgg	cca	ccg	ggg	gcg	1443
Arg	Thr	Gly	Pro	Ala	Leu	Val	Leu	Gly	Arg	Val	Arg	Pro	Pro	Gly	Ala	
378					383					388					393	
ctg	ctc	agc	gtg	ccc	gtg	ctc	agc	agc	ctg	ctg	ctg	cag	atg	gtc	ctg	1491
Leu	Leu	Ser	Val	Pro	Val	Leu	Ser	Ser	Leu	Leu	Leu	Gln	Met	Val	Leu	
394					399					404					409	
gtg	acc	ggc	gtg	cag	cta	ggg	ggc	tac	ttc	ctg	acc	ctg	gcc	cag	cca	1539
Val	Thr	Gly	Val	Gln	Leu	Gly	Gly	Tyr	Phe	Leu	Thr	Leu	Ala	Gln	Pro	

410	415	420	425	
tgg ttc gtg cct ctg aac agg aca gtg gcc gca cca gac aac ctg ccc				1587
Trp Phe Val Pro Leu Asn Arg Thr Val Ala Ala Pro Asp Asn Leu Pro				
426	431	436	441	
aac tac gag aac acc gtg gtc ttc tct ctg tcc agc ttc cag tac ctc				1635
Asn Tyr Glu Asn Thr Val Val Phe Ser Leu Ser Ser Phe Gln Tyr Leu				
442	447	452	457	
atc ctg gct gca gcc gtg tcc aag ggg gcg ccc ttc cgc cgg ccg ctc				1683
Ile Leu Ala Ala Ala Val Ser Lys Gly Ala Pro Phe Arg Arg Pro Leu				
458	463	468	473	
tac acc aat gag cgt gct aga cca gtg cct ccc cgc ctg cct gcg ccg				1731
Tyr Thr Asn Glu Arg Ala Arg Pro Val Pro Pro Arg Leu Pro Ala Pro				
474	479	484	489	
cct ccg gcc caa gcg ggc ctc caa gaa gcg ctt caa gca gct gga acg				1779
Pro Pro Ala Gln Ala Gly Leu Gln Glu Ala Leu Gln Ala Ala Gly Thr				
490	495	500	505	
aga gct ggc cga gca gcc ctg gcc gcc gct gcc cgc cgg ccc cct gag				1827
Arg Ala Gly Arg Ala Ala Leu Ala Ala Ala Ala Arg Arg Pro Pro Glu				
506	511	516	521	
gta gtg cag gcc cac ggg cac ccc aga cac tgg aac tcc ctg cct ctg				1875
Val Val Gln Ala His Gly His Pro Arg His Trp Asn Ser Leu Pro Leu				
522	527	532	537	
agc cac caa ctg gac ccc tct cca gca aca cca ccg cca cca cct ccc				1923
Ser His Gln Leu Asp Pro Ser Pro Ala Thr Pro Pro Pro Pro Pro				
538	543	548	553	
aca tcc ctg agg ttg gcg act gtc tac act cct ccc ccg aga cca ccc				1971
Thr Ser Leu Arg Leu Ala Thr Val Tyr Thr Pro Pro Pro Arg Pro Pro				
554	559	564	569	
cca ccc tgg gga agc gtt gac tac tgt ccc cta cct tgg acc atc ccg				2019
Pro Pro Trp Gly Ser Val Asp Tyr Cys Pro Leu Pro Trp Thr Ile Pro				
570	575	580	585	
cgt agg ggt ggc agc ccc cag ctc ccc tca gtg ctg ctg tca gtg tag				2067
Arg Arg Gly Gly Ser Pro Gln Leu Pro Ser Val Leu Leu Ser Val *				
586	591	596	601	
caaataaagt catgatattt tcctggcaaa aaaaaaaaaa				2106

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ccctgcatct ggagccaccc acctggagga actcatcggg cttcctctgt agacgggaaa      180
aaacaaacgc accacaaacc gacaatcaaa gccatggcgg atgcggggcc gccaccagtt      240
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gcaggtgaga agacaccccc acaaaacccc aaaactagcc ttaggctgtt tttccccaac      420
acaacgcacc tccacacccc acaccgccag cagcccacct gggtagccaa agtgagctgc      480
caggggggttc cgaggaccct gcctggtgcc ttccagctca taaggagagg ccaagagcca      540
tggggaggaa gccacacggc ccagcgtca gggcttgtca tccaagagtg agagaagtgg      600
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aggtgcttgt gggattctgc tggctggagc caggaggtaa gtgtgaacag ggaggccaaa      720
gatgaaagtt atctgaaaga gcccgtaccc cctataaaca cggcagagga atgtcttaag      780
agccaccaac agtaattccc tttccgg      atg tta aca ggt tat ttg tat ctt      831
                                Met Leu Thr Gly Tyr Leu Tyr Leu
                                1                               5

atg tgg cgt cgt aaa gca ttc tgg agt ggc aca caa cgt cat ccc ctt      879
Met Trp Arg Arg Lys Ala Phe Trp Ser Gly Thr Gln Arg His Pro Leu
  9                14                19                24

ccc ggt ggt ctg aag agg agg agg aga cca ggg agg ggt cct tgg cca      927
Pro Gly Gly Leu Lys Arg Arg Arg Arg Pro Gly Arg Gly Pro Trp Pro
  25                30                35                40

gcc cct ggc ggc caa ggg gtg ggt cct tct gct cta tag aaggcaggaa      976
Ala Pro Gly Gly Gln Gly Val Gly Pro Ser Ala Leu *
  41                46                51

gcccgccagc taaccgcccg ggtcaggggg agcaggcctg atctctccca agcctgtgac      1036
cgaggtcctg cctgatgtcc aaggggcccc tgtgccagta ccccaacttc ccacgcccc      1096
cagccttcct cacctccaga atcagccgcc caggtgcagc actatctcct ttctttttct      1156

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aaa ggc ctt ggc ctc ctc cag ctg ggt ctg ctc ctt cct ttg aac ccc	96
Lys Gly Leu Gly Leu Leu Gln Leu Gly Leu Leu Leu Pro Leu Asn Pro	
17 22 27 32	
atc ggt acc tat gcc cac acc ttt cag agc ttt cct gat cag tgt caa	144
Ile Gly Thr Tyr Ala His Thr Phe Gln Ser Phe Pro Asp Gln Cys Gln	
33 38 43 48	
cat gct gct ctt cct ctt aca aaa tgt acc atc aat aca gcc cag gca	192
His Ala Ala Leu Pro Leu Thr Lys Cys Thr Ile Asn Thr Ala Gln Ala	
49 54 59 64	
cat ggc tcc cac aaa gct agc cac tta tat agt atg ggt cac atc aaa	240
His Gly Ser His Lys Ala Ser His Leu Tyr Ser Met Gly His Ile Lys	
65 70 75 80	
aat gac tcc agc aca atc att cat aca gac ttc tct cac act aaa cct	288
Asn Asp Ser Ser Thr Ile Ile His Thr Asp Phe Ser His Thr Lys Pro	
81 86 91 96	
tta aac aag caa ggt tca gta gct aca gaa ctc tcc atc atc atc atc	336
Leu Asn Lys Gln Gly Ser Val Ala Thr Glu Leu Ser Ile Ile Ile Ile	
97 102 107 112	
atc atc atc tgg ttg ctt ttg gca agg ttc agt agc tac aga act ctc	384
Ile Ile Ile Trp Leu Leu Leu Ala Arg Phe Ser Ser Tyr Arg Thr Leu	

113		118		123		128	
ctt cat cat cat cat cat ctg gtt gct ttt ggc aag caa ggt tca gta	432						
Leu His His His His His Leu Val Ala Phe Gly Lys Gln Gly Ser Val							
129		134		139		144	
gct aca gaa ctc tcc tcc tcc tcc tcc tcc tcc tca tca tca tca tca	480						
Ala Thr Glu Leu Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser							
145		150		155		160	
tct ggt tgc ttt cag caa ggt tca gta gct aca gaa ctc tcc atc atc	528						
Ser Gly Cys Phe Gln Gln Gly Ser Val Ala Thr Glu Leu Ser Ile Ile							
161		166		171		176	
atc atc atc atc atc atc atc atc atc atc atc atc tgg ttg ctt ttg gca	576						
Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Trp Leu Leu Leu Ala							
177		182		187		192	
agg ttc agt agc tac aga act ctc ctc ctc ctc ctc ctc ctc ctc ctc	624						
Arg Phe Ser Ser Tyr Arg Thr Leu Leu Leu Leu Leu Leu Leu Leu Leu							
193		198		203		208	
ctc ctc atc atc atc atc atc atc atc tgg ttg ctt tta gca agg ttc agt	672						
Leu Leu Ile Ile Ile Ile Ile Ile Ile Trp Leu Leu Leu Ala Arg Phe Ser							
209		214		219		224	
agc tac aga act ctc ctc ctc ctc ctc ctc ctc ctc atc atc atc atc	720						
Ser Tyr Arg Thr Leu Leu Leu Leu Leu Leu Leu Leu Leu Ile Ile Ile Ile							
225		230		235		240	
atc tgg ttg ctt tca gca agg ttc agt agc tac aga act ctc ctt cat	768						
Ile Trp Leu Leu Ser Ala Arg Phe Ser Ser Tyr Arg Thr Leu Leu His							
241		246		251		256	
cat cat caa cat cat cat ctg gtt gct ttt ggc aag caa ggt tca gta	816						
His His Gln His His His Leu Val Ala Phe Gly Lys Gln Gly Ser Val							
257		262		267		272	
gct aca gaa ctc tcc tcc tcc tcc tcc tcc tcc tca tca tca tca tca	864						
Ala Thr Glu Leu Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser							
273		278		283		288	
tct ggt tgc ttt cag caa ggt tca gta gct aca gaa ctc tcc atc atc	912						
Ser Gly Cys Phe Gln Gln Gly Ser Val Ala Thr Glu Leu Ser Ile Ile							
289		294		299		304	
atc atc atc atc atc atc atc atc atc atc atc atc tgg ttg ctt ttg gca	960						
Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Trp Leu Leu Leu Ala							
305		310		315		320	
agg ttc agt agc tac aga act ctc ctt cat cat cat cat cat cat cat	1008						
Arg Phe Ser Ser Tyr Arg Thr Leu Leu His His His His His His His							
321		326		331		336	
ctg gtt gct ttt ggc aag caa ggt tca gta gct aca gaa ctc tcc atc	1056						
Leu Val Ala Phe Gly Lys Gln Gly Ser Val Ala Thr Glu Leu Ser Ile							
337		342		347		352	

atc atc atc atc atc atc atc atc atc atc atc atc tgg ttg ctt ttg	1104
Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Trp Leu Leu Leu	
353 358 363 368	
gca agg ttc agt agc tac aga act ctc ctt cat cat cat cat cat cat	1152
Ala Arg Phe Ser Ser Tyr Arg Thr Leu Leu His His His His His His	
369 374 379 384	
cat ctg gtt gct ttt ggc aag gcc ctg gca aga att att tgg ctt tac	1200
His Leu Val Ala Phe Gly Lys Ala Leu Ala Arg Ile Ile Trp Leu Tyr	
385 390 395 400	
cga aac acc tat tcc ata ggt aac caa ttc cag tca aaa atg cca gag	1248
Arg Asn Thr Tyr Ser Ile Gly Asn Gln Phe Gln Ser Lys Met Pro Glu	
401 406 411 416	
tat tac tcc tca acc caa tgc cct atc tcc tta gtg gat tat aaa ctt	1296
Tyr Tyr Ser Ser Thr Gln Cys Pro Ile Ser Leu Val Asp Tyr Lys Leu	
417 422 427 432	
act acg aca acc tgt ctt ctt tgg atc caa tcc ccg ccc aag tct gag	1344
Thr Thr Thr Thr Cys Leu Leu Trp Ile Gln Ser Pro Pro Lys Ser Glu	
433 438 443 448	
tct tct ctc cca ggc tac aag ccc cca agt cct ggc agc tct atg ctt	1392
Ser Ser Leu Pro Gly Tyr Lys Pro Pro Ser Pro Gly Ser Ser Met Leu	
449 454 459 464	
gac agc tcg ctg acc tcc acc tca tca gac cat tgg gtc gcc ctt ctc	1440
Asp Ser Ser Leu Thr Ser Thr Ser Ser Asp His Trp Val Ala Leu Leu	
465 470 475 480	
gcc gtc ctc cag cct tct tcc cgc tca gac act cat cca ctg tcc ggg	1488
Ala Val Leu Gln Pro Ser Ser Arg Ser Asp Thr His Pro Leu Ser Gly	
481 486 491 496	
gag cct cga ccc ctc cta tac ccc ctc ccc gat ccc gca gtc ccc ttc	1536
Glu Pro Arg Pro Leu Leu Tyr Pro Leu Pro Asp Pro Ala Val Pro Phe	
497 502 507 512	
tgg acc ttg cgg acc cct ctc agc ccc cgt acc ccc tac cgc ctc ttc	1584
Trp Thr Leu Arg Thr Pro Leu Ser Pro Arg Thr Pro Tyr Arg Leu Phe	
513 518 523 528	
ctc ctc cac tcc cac aac tcc gcc cga gct cca ctg cgc ctg tgc ggc	1632
Leu Leu His Ser His Asn Ser Ala Arg Ala Pro Leu Arg Leu Cys Gly	
529 534 539 544	
caa cga ggc cgc gcg cag gcg atc ggg gca gaa gag ctt ccg gtt cct	1680
Gln Arg Gly Arg Ala Gln Ala Ile Gly Ala Glu Glu Leu Pro Val Pro	
545 550 555 560	
gct gtc aat aag acg tgg acc tgc gag ccg ggg caa aag ggc ttc cgg	1728
Ala Val Asn Lys Thr Trp Thr Cys Glu Pro Gly Gln Lys Gly Phe Arg	
561 566 571 576	

tct gcg gga aac tgg agg cta gcg gtg ggc gtg gac cgt cga ggt gac	1776
Ser Ala Gly Asn Trp Arg Leu Ala Val Gly Val Asp Arg Arg Gly Asp	
577 582 587 592	
tggt cgg ttg tct gat ctg ctg ttg ttt gct gac cag gca gcc gta ggt	1824
Trp Arg Leu Ser Asp Leu Leu Leu Phe Ala Asp Gln Ala Ala Val Gly	
593 598 603 608	
aat gac gga tgc cca gac cct gtg ggc gga gta aag gaa tca tgc act	1872
Asn Asp Gly Cys Pro Asp Pro Val Gly Gly Val Lys Glu Ser Cys Thr	
609 614 619 624	
gat aca cgc aca ctc acc gag ggg cgc gtc cgt ctg cgt gcc cct cat	1920
Asp Thr Arg Thr Leu Thr Glu Gly Arg Val Arg Leu Arg Ala Pro His	
625 630 635 640	
ctc gta gcc gaa agg agc gcg ttc cgg ggc agg cct ccg ggt act tcc	1968
Leu Val Ala Glu Arg Ser Ala Phe Arg Gly Arg Pro Pro Gly Thr Ser	
641 646 651 656	
cgc aga gga ccg ggc ttt ata ctc ttt gct cct ttt cct ccc cta aaa	2016
Arg Arg Gly Pro Gly Phe Ile Leu Phe Ala Pro Phe Pro Pro Leu Lys	
657 662 667 672	
gct gtg ctt gac ttc ttg gtg tac atg gat aaa ggc tac aat gaa gga	2064
Ala Val Leu Asp Phe Leu Val Tyr Met Asp Lys Gly Tyr Asn Glu Gly	
673 678 683 688	
aac att tta gaa ata ctc gcc tac ctg gta gtc cac aga tct tta gat	2112
Asn Ile Leu Glu Ile Leu Ala Tyr Leu Val Val His Arg Ser Leu Asp	
689 694 699 704	
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Phe Ile Gly Gln Gln Asn Leu Lys Gly Arg Glu Arg Glu Asn Lys Arg	
705 710 715 720	
gac cat cat atg gaa gac aaa ttt gat gcc atc act tca aaa tga	2205
Asp His His Met Glu Asp Lys Phe Asp Ala Ile Thr Ser Lys *	
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gcctgaggag	atg agc tgg ccg cca tgc ggg gag att gcc agc cca cca	169				
	Met Ser Trp Pro Pro Ser Gly Glu Ile Ala Ser Pro Pro					
	1 5 10					
gag ctg cca agc agc cca cct cct ggg ctt ccc gaa gtg gcc cca gat	217					
Glu Leu Pro Ser Ser Pro Pro Pro Gly Leu Pro Glu Val Ala Pro Asp						
14 19 24 29						
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Ala Thr Ser Thr Gly Leu Pro Asp Thr Pro Ala Ala Pro Glu Thr Ser						
30 35 40 45						
acc aac tac cca gtg gag tgc acc gag ggg tct gca ggc ccc cag tct	313					
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46 51 56 61						
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 Tyr His Pro Phe Leu Pro His Arg Ala Pro Asp Phe Ala Met Ser Ala
 17 22 27 32

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 Val Leu Gly His Gln Pro Pro Phe Phe Pro Ala Leu Thr Leu Pro Pro
 33 38 43 48

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 49 54 59 64

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 Met Asp Gln Leu Val Gly Ala Ala Glu Thr Gly Ile Pro Phe Ser Ser
 65 70 75 80

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gaa gag gtg gag gac gac ccc aag gtg cac ctg gag gct aaa gaa ctt 336
 Glu Glu Val Glu Asp Asp Pro Lys Val His Leu Glu Ala Lys Glu Leu
 97 102 107 112

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 Trp Asp Gln Phe His Lys Arg Gly Thr Glu Met Val Ile Thr Lys Ser
 113 118 123 128

gga agg cga atg ttt cct cca ttt aaa gtg aga tgt tct ggg ctg gat 432
 Gly Arg Arg Met Phe Pro Pro Phe Lys Val Arg Cys Ser Gly Leu Asp
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Cys Arg Tyr Lys Phe His Asn Ser Arg Trp Met Val Ala Gly Lys Ala	
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Asp Pro Glu Met Pro Lys Arg Met Tyr Ile His Pro Asp Ser Pro Ala	
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Arg Arg Gln Thr Ser Gly Pro Leu Tyr Leu Ala Val Trp Asp Lys Ala
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Gln Cys Thr Ala Asp Leu Gly Ala Gln Tyr Ile Thr Cys Thr Pro His
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Tyr Ala Lys Lys His Gln Arg Phe Tyr Asp Glu Leu Leu Ala Tyr Gly
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Val	Thr	Asn	Ala	Ala	Ala	Asn	Cys	Pro	Gly	Gln	Met	Thr	Leu	His	His	
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Tyr Ile *				
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Arg Ser Gly Pro Phe Ala Pro Val Leu Ser Ala Thr Pro Glu Gln Pro	
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Val Leu Asp Leu Lys Arg Pro Phe Leu Ser Arg Glu Ser Leu Ser Gly	
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cag gcc gtg cgc cgg cct ttg gtc gcc tcc gtg ggc ctc aat gtc cct	256
Gln Ala Val Arg Arg Pro Leu Val Ala Ser Val Gly Leu Asn Val Pro	
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Ala Ser Val Cys Tyr Ser His Thr Asp Ile Lys Val Pro Asp Phe Ser	
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Glu Tyr Arg Arg Leu Glu Val Leu Asp Ser Thr Lys Ser Ser Arg Glu	
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Ser Ser Glu Ala Arg Lys Gly Phe Ser Tyr Leu Val Thr Gly Val Thr	
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Thr Val Gly Val Ala Tyr Ala Ala Lys Asn Ala Val Thr Gln Phe Val	
103 108 113 118	
tcc agc atg agt gct tct gct gat gtg ttg gcc ctg gcg aaa atc gaa	496
Ser Ser Met Ser Ala Ser Ala Asp Val Leu Ala Leu Ala Lys Ile Glu	
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Ile Lys Leu Ser Asp Ile Pro Glu Gly Lys Asn Met Ala Phe Lys Trp	
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Arg Gly Lys Pro Leu Phe Val Arg His Arg Thr Gln Lys Glu Ile Glu	
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Gln Glu Ala Ala Val Glu Leu Ser Gln Leu Arg Asp Pro Gln His Asp	
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Thr His Leu Gly Cys Val Pro Ile Ala Asn Ala Gly Asp Phe Gly Gly	
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Tyr Tyr Cys Pro Cys His Gly Ser His Tyr Asp Ala Ser Gly Arg Ile	
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Arg Leu Gly Pro Ala Pro Leu Asn Leu Glu Val Pro Thr Tyr Glu Phe	
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Thr Ser Asp Asp Met Val Ile Val Gly *	
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tcg act gcg gcc ttg ccc gaa gcc ctt ttg tgc agc tcc gcg ccc gca      151
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gcc cga cgc ccc agc ttg tgc ggg gcc acg gga ggg tca tgc gcg gat      199
Ala Arg Arg Pro Ser Leu Cys Gly Ala Thr Gly Gly Ser Cys Ala Asp
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ttc gac tcg ggt gtg gat ttc gtc cgt aga gag agc agc ggt ctg tgg      247
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Gly Pro Gln Pro Pro Leu Ser Pro Val Lys Asn Tyr Thr Glu Met Phe
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cag gac cca gtg gct ttt aag gat gtg gct gtg aac ttc acc cag gag      343
Gln Asp Pro Val Ala Phe Lys Asp Val Ala Val Asn Phe Thr Gln Glu
  82                               87                               92                               97

gag tgg gct ttg ctg gat att tcc cag aag aat ctc tac agg gaa gtg      391
Glu Trp Ala Leu Leu Asp Ile Ser Gln Lys Asn Leu Tyr Arg Glu Val
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atg ctg gaa act ttc tgg aac ctg acc tct ata gga aaa aag tgg aaa      439
Met Leu Glu Thr Phe Trp Asn Leu Thr Ser Ile Gly Lys Lys Trp Lys
  114                               119                               124                               129

gac cag aac att gaa tat gag tac caa aac ccc agg aga aac ttc agg      487
Asp Gln Asn Ile Glu Tyr Glu Tyr Gln Asn Pro Arg Arg Asn Phe Arg
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agt gtc aca gaa gag aaa gtc aat gaa att aaa gaa gac agt cat tgt      535
Ser Val Thr Glu Glu Lys Val Asn Glu Ile Lys Glu Asp Ser His Cys
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Gly Glu Thr Phe Thr Pro Val Pro Asp Asp Arg Leu Asn Phe Gln Lys	
162 167 172 177	
aag aaa gct tct cct gaa gta aaa tca tgt gac agc ttt gtg tgt gaa	631
Lys Lys Ala Ser Pro Glu Val Lys Ser Cys Asp Ser Phe Val Cys Glu	
178 183 188 193	
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Val Gly Leu Gly Asn Ser Ser Ser Asn Met Asn Ile Arg Gly Asp Thr	
194 199 204 209	
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Gly His Lys Ala Cys Glu Cys Gln Glu Tyr Gly Pro Lys Pro Trp Lys	
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242 247 252 257	
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Gly Lys Asn Ile Ile Tyr His Ser Ser Ile Gln Arg His Met Val Val	
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His Cys Leu Ser Leu Tyr Leu Ile His Glu Arg Thr His Thr Gly Glu	
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Lys Pro Tyr Glu Cys Lys Gln Cys Gly Lys Ser Phe Ser Tyr Ser Ala	
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acc cat cga ata cat gaa aga act cac att gga gaa aag cct tat gaa	1063
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Cys	Lys	Gln	Cys	Gly	Lys	Ala	Phe	Thr	Arg	Ser	Gly	Ser	Phe	Arg	Tyr	
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			Met Leu Leu	
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Val Phe Leu Ala Thr Cys Phe Asn Ala Leu Leu Pro Ala Val Arg Glu	
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Lys Leu Gln Lys Val Leu Ser Leu Gly His Ile Ser Thr Asp Tyr Pro	
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Leu Glu Thr Phe Asn Ala Gly Ser Asp Val Gly Ser Asp Ser Glu Tyr	
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Ala Lys Leu Ala Val Thr Val Ser Ala Met Ile Pro Leu Gly Ile Gly	
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Val Phe Leu Lys Trp *	
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Cys Asp Thr Glu Ile His Ile Val Asn Ala Thr Ile Ser Asp Thr Asp		
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Cys Met Lys Ser Ala Met Val Val Ala Leu Ser Lys Arg Ser Gln Glu		
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Arg	Val	Gln	Gln	Gly	Gln	His	Asp	Pro	Lys	Thr	Asp	Asn	Gln	Asn	Thr		
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Gln	Gln	Lys	Ala	Gly	Phe	Lys	Glu	Gly	Trp	Leu	Ala	Glu	Ala	Ser	Glu		
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Ser	Gly	Gln	Pro	Arg	Arg	Asp	Leu	His	Thr	Ser	Trp	Lys	Arg	Asn	Pro		
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Leu 381	Leu	Ala	Ser	Pro	Glu 386	Glu	Asp	Pro	Ser	Glu 391	Asp	Asp	Ser	Ile	Lys 396	
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Glu Pro Phe Ile Lys Met Lys Gln Phe Leu Ser Asp Glu Gln Asn Val				
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Arg Ile Arg Thr Pro Glu Thr Gly Ser Asp Asp Ala Ile Lys Ser Ile				
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Leu Glu Gln Ala Lys Lys Glu Ile Glu Ser Gln Lys Gly Gly Glu Pro				
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Lys Thr Ser Val Ala Pro Leu Ser Ile Ala Asn Gly Thr Thr Pro Ala				
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Ser Thr Ser Glu Asp Ala Ile Lys Ser Ile Leu Glu Gln Ala Arg Arg				
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Arg Gly Arg Ser Val Pro Pro Ser Pro Pro Glu Arg Pro Ser Leu Ala				
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Thr Ala Ser Gln Asn Gly Ala Pro Ala Leu Val Lys Gln Glu Glu Gly				
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Pro Tyr Ala Ser Val Ser Pro Ser Leu Ser Ser Ser Ser Ser Gly				
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Ala Arg Leu Pro Tyr Tyr Pro Ala Tyr Val Pro Arg Thr Leu Lys Pro	
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catgaccact	gaagcttagt	aaccagcgcc	aaaaaagtag	attcatcaaa	ctagagaccc	5506
cagctccctt	tctcgccatc	ttctttctca	agttgaccgt	gggtgctgtt	ctggaaggca	5566
tctgcaactc	caagtccatg	cagaactctg	gaaggccaag	ttcatcgcag	catgttcacc	5626
attatcccag	cctccaaatc	tatcctccta	ccttccaacg	catgacctgt	tggggagcag	5686
agacttaacc	cccaactcag	aggaaccctt	cctccagcgt	ctttggcatg	gtttctaggg	5746
tgagagtccc	caatttggat	agaacggcca	ccatattggt	tactgaatct	ctctcccttg	5806
tttttattac	gtttcctttt	tcaaactgtc	catgggaagg	ctgaattgag	tgactcccca	5866
gaatgaagat	gagaaggtga	atataatcaa	tgccaatgta	atgccagcgg	gtgagatggc	5926
cgatggaggt	ttcaaagatg	tagctagcat	tttgaaacca	tatgggcaaa	accgggcaac	5986
cagaagggga	cagataagga	ccgttccaga	aatcccaact	ctcacacca	gcccaggctg	6046
cagtctccac	accaaacagt	caacaaaaca	caaaccctga	aggaaaacct	tttccataca	6106

Lys	Gln	His	Leu	Gly	Glu	Lys	His	Phe	Ile	Ser	Asn	Val	Gly	Arg	Ala		
59					64					69					74		
ttg	ttt	gtg	aag	acc	tgc	aca	ttc	cat	gtg	tca	ggg	gag	cct	tcc	acc		531
Leu	Phe	Val	Lys	Thr	Cys	Thr	Phe	His	Val	Ser	Gly	Glu	Pro	Ser	Thr		
75					80					85					90		
tgc	aga	gaa	ttt	ggg	aag	gac	ttc	ctg	gcc	aag	ttg	gga	ttt	ctc	cat		579
Cys	Arg	Glu	Phe	Gly	Lys	Asp	Phe	Leu	Ala	Lys	Leu	Gly	Phe	Leu	His		
91					96					101					106		
caa	cag	gct	gct	cac	act	ggg	gag	caa	tcc	aat	agc	aaa	agc	gac	ggc		627
Gln	Gln	Ala	Ala	His	Thr	Gly	Glu	Gln	Ser	Asn	Ser	Lys	Ser	Asp	Gly		
107					112					117					122		
ggg	gcc	atc	agt	cac	aga	gga	aaa	act	cat	tac	aac	tgt	gga	gaa	cac		675
Gly	Ala	Ile	Ser	His	Arg	Gly	Lys	Thr	His	Tyr	Asn	Cys	Gly	Glu	His		
123					128					133					138		
aca	aaa	gca	ttc	agc	ggc	aaa	cac	aca	ctt	gtt	cag	cag	cag	aga	acc		723
Thr	Lys	Ala	Phe	Ser	Gly	Lys	His	Thr	Leu	Val	Gln	Gln	Gln	Arg	Thr		
139					144					149					154		
ctc	act	aca	gaa	aga	tgt	tac	ata	tgc	agt	gaa	tgt	ggg	aaa	tcc	ttt		771
Leu	Thr	Thr	Glu	Arg	Cys	Tyr	Ile	Cys	Ser	Glu	Cys	Gly	Lys	Ser	Phe		
155					160					165					170		
agc	aaa	agc	tac	agt	ctc	aat	gac	cat	tgg	aga	ctt	cac	act	gga	gaa		819
Ser	Lys	Ser	Tyr	Ser	Leu	Asn	Asp	His	Trp	Arg	Leu	His	Thr	Gly	Glu		
171					176					181					186		
aag	cct	tat	gaa	tgt	cga	gag	tgt	ggg	aag	tcc	ttt	agg	caa	agc	tct		867
Lys	Pro	Tyr	Glu	Cys	Arg	Glu	Cys	Gly	Lys	Ser	Phe	Arg	Gln	Ser	Ser		
187					192					197					202		
agt	ctc	att	caa	cac	cgg	aga	ggc	cac	act	gca	gta	cga	cct	cat	gag		915
Ser	Leu	Ile	Gln	His	Arg	Arg	Gly	His	Thr	Ala	Val	Arg	Pro	His	Glu		
203					208					213					218		
ggg	gat	gaa	tgt	gga	aaa	tta	ttt	agc	aac	ccg	tct	aac	ctc	att	aaa		963
Gly	Asp	Glu	Cys	Gly	Lys	Leu	Phe	Ser	Asn	Pro	Ser	Asn	Leu	Ile	Lys		
219					224					229					234		
cat	cgg	aga	gtt	cac	act	ggg	gaa	agg	cca	tat	gag	tgc	agc	gaa	tgt		1011
His	Arg	Arg	Val	His	Thr	Gly	Glu	Arg	Pro	Tyr	Glu	Cys	Ser	Glu	Cys		
235					240					245					250		
ggg	aaa	tcc	ttt	aac	caa	agg	tct	gca	ctc	ctt	caa	cat	cgg	gga	ggc		1059
Gly	Lys	Ser	Phe	Asn	Gln	Arg	Ser	Ala	Leu	Leu	Gln	His	Arg	Gly	Gly		
251					256					261					266		
cac	act	ggg	gag	agg	cct	tat	gag	tgc	agt	gaa	tgt	ggg	aag	ttt	ttt		1107
His	Thr	Gly	Glu	Arg	Pro	Tyr	Glu	Cys	Ser	Glu	Cys	Gly	Lys	Phe	Phe		
267					272					277					282		
ccc	tac	agc	tcc	agt	ctc	cga	aaa	cac	cag	aga	gtt	cac	act	gga	tca		1155
Pro	Tyr	Ser	Ser	Ser	Leu	Arg	Lys	His	Gln	Arg	Val	His	Thr	Gly	Ser		

283	288	293	298	
aga ccc tat gag tgc agt gaa tgt ggg aaa tcc ttt act caa aat tcc				1203
Arg Pro Tyr Glu Cys Ser Glu Cys Gly Lys Ser Phe Thr Gln Asn Ser				
299	304	309	314	
ggc ctc att aag cac agg agg gtt cac act ggg gag aag cct tat gag				1251
Gly Leu Ile Lys His Arg Arg Val His Thr Gly Glu Lys Pro Tyr Glu				
315	320	325	330	
tgc acg gaa tgt ggg aaa tcc ttt agc cat aac tcc agc ctt att aaa				1299
Cys Thr Glu Cys Gly Lys Ser Phe Ser His Asn Ser Ser Leu Ile Lys				
331	336	341	346	
cat cag aga att cat agt cga taa aaggcttatg agtggcaaat gtggaaaatc				1353
His Gln Arg Ile His Ser Arg *				
347	352			
tgttagcacc ctggagaaag tccttgagta cacagtgaat gtcagaaagc ttcagctgaa				1413
ggccatatct cattgagtgc cacacaggtc acaagggaaa gacacttt				1461

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<220>
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 <222> (206)..(1009)

<400> 107

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gtgcatctgc caggagaccc agctccagca cgtggaggac tacagccgga ttctgtgtcc	180
atcttcctct cctcattgac tctgc atg aag ggg att tct ggt gga gta agg	232
Met Lys Gly Ile Ser Gly Gly Val Arg	
1 5	
gta gca gct ctt gcc gca cgt gca gag aga gag gaa ctt cca gtg ccc	280
Val Ala Ala Leu Ala Ala Arg Ala Glu Arg Glu Glu Leu Pro Val Pro	
10 15 20 25	
gct atg gag cca cag ccc aca gca tgg gga agt ccc cat cca gag gca	328
Ala Met Glu Pro Gln Pro Thr Ala Trp Gly Ser Pro His Pro Glu Ala	
26 31 36 41	
gtg ctg cag cta gag gta gct cca gag tcc tcc ggg ccc tgc acc gat	376
Val Leu Gln Leu Glu Val Ala Pro Glu Ser Ser Gly Pro Cys Thr Asp	
42 47 52 57	

aca gcc aaa gac cag caa agc gac aag ctg cca gac ctc atg cca cct	424
Thr Ala Lys Asp Gln Gln Ser Asp Lys Leu Pro Asp Leu Met Pro Pro	
58 63 68 73	
gct gta gcc act ggg ctc agc cct gga gct gag agc atc gct gga gat	472
Ala Val Ala Thr Gly Leu Ser Pro Gly Ala Glu Ser Ile Ala Gly Asp	
74 79 84 89	
aga cgt ggc aga gaa gag gtt gcg agc atg gcc cca gcc agc agc tcc	520
Arg Arg Gly Arg Glu Glu Val Ala Ser Met Ala Pro Ala Ser Ser Ser	
90 95 100 105	
cac gct gcc cct agt cct ggg cat gga gcg agc ctt ggt gtc aga gac	568
His Ala Ala Pro Ser Pro Gly His Gly Ala Ser Leu Gly Val Arg Asp	
106 111 116 121	
cag ggt gtg cag tct gag ctc ctc tac ctt act aaa gag agg cct ctt	616
Gln Gly Val Gln Ser Glu Leu Leu Tyr Leu Thr Lys Glu Arg Pro Leu	
122 127 132 137	
tta ttt acc aga gcc aca gcc ctg ctg cct cag gac ctt ttc att ctg	664
Leu Phe Thr Arg Ala Thr Ala Leu Leu Pro Gln Asp Leu Phe Ile Leu	
138 143 148 153	
ccg gtg ctg ggg ctg tct atc tgc aag ctg gag gtg ttg aga gca gga	712
Pro Val Leu Gly Leu Ser Ile Cys Lys Leu Glu Val Leu Arg Ala Gly	
154 159 164 169	
aaa gga ggc tgt gag gaa ggg ttc ggg cag ctc ctc ctg ctc tca gag	760
Lys Gly Gly Cys Glu Glu Gly Phe Gly Gln Leu Leu Leu Leu Ser Glu	
170 175 180 185	
gtg gcc tcc tcc tcc agg cat gga ggt ctg tcc act act ggg ctt ctg	808
Val Ala Ser Ser Ser Arg His Gly Gly Leu Ser Thr Thr Gly Leu Leu	
186 191 196 201	
ggc tat ttg ccc ctg att tgc tcc ctg gta cgg gct ctt gtt aac agg	856
Gly Tyr Leu Pro Leu Ile Cys Ser Leu Val Arg Ala Leu Val Asn Arg	
202 207 212 217	
cag gca agg ggt gcg ggg acc agg caa ggg ctt caa agg gta cag tac	904
Gln Ala Arg Gly Ala Gly Thr Arg Gln Gly Leu Gln Arg Val Gln Tyr	
218 223 228 233	
caa atc ttc caa act cag cac ttg tgc cct ggg gtc tcc aaa ctg tct	952
Gln Ile Phe Gln Thr Gln His Leu Cys Pro Gly Val Ser Lys Leu Ser	
234 239 244 249	
tct gcc cta gga ttt att cat act gtt aaa tta cca gtt tat gca aat	1000
Ser Ala Leu Gly Phe Ile His Thr Val Lys Leu Pro Val Tyr Ala Asn	
250 255 260 265	
gat atg taa ataaagctca attttttgaa aaaaaa	1035
Asp Met *	
266	

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 <222> (49) .. (756)

<400> 108

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 Met Pro Trp

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gct ctg ctc ctc ctg acc ctc ctc act cac tct gca gtg tca gtg gtc 105
 Ala Leu Leu Leu Leu Thr Leu Leu Thr His Ser Ala Val Ser Val Val
 4 9 14 19

cag gca ggg ctg act cag cca ccc tcg gtg tcc aag ggc ttg aga cag 153
 Gln Ala Gly Leu Thr Gln Pro Pro Ser Val Ser Lys Gly Leu Arg Gln
 20 25 30 35

acc gcc aca ctc acc tgc act ggg aac agc aac aat gtt ggc gac caa 201
 Thr Ala Thr Leu Thr Cys Thr Gly Asn Ser Asn Asn Val Gly Asp Gln
 36 41 46 51

gga gca tct tgg ctg cag cag cac cag ggc cac cct ccc aaa ctc ctc 249
 Gly Ala Ser Trp Leu Gln Gln His Gln Gly His Pro Pro Lys Leu Leu
 52 57 62 67

tcc tac agg aat aac aac cgg ccc tca ggg atc tca gag aga tta tct 297
 Ser Tyr Arg Asn Asn Asn Arg Pro Ser Gly Ile Ser Glu Arg Leu Ser
 68 73 78 83

gca tcc agg tca gga aac aca gcc tcc ctg acc att act gga ctc cag 345
 Ala Ser Arg Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Leu Gln
 84 89 94 99

cct gag gac gag gct gac tat tac tgc tca gca tgg gac agc agc ctc 393
 Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ala Trp Asp Ser Ser Leu
 100 105 110 115

agt gct tgg gtg ttc ggc gga ggg acc aag ctg acc gtc cta ggt cag 441
 Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
 116 121 126 131

ccc aag gct gcc ccc tcg gtc act ctg ttc ccg ccc tcc tct gag gag 489
 Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
 132 137 142 147

ctt caa gcc aac aag gcc aca ctg gtg tgt ctc ata agt gac ttc tac 537
 Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
 148 153 158 163

ccg gga gcc gtg aca gtg gcc tgg aag gca gat agc agc ccc gtc aag 585
 Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
 164 169 174 179

gcg gga gtg gag acc acc aca ccc tcc aaa caa agc aac aac aag tac 633
 Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
 180 185 190 195

gcg gcc agc agc tac ctg agc ctg acg cct gag cag tgg aag tcc cac 681
 Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
 196 201 206 211

aga agc tac agc tgc cag gtc acg cat gaa ggg agc acc gtg gag aag 729
 Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
 212 217 222 227

aca gtg gcc cct aca gaa tgt tca tag gttct caaccctcac cccaccacg 781
 Thr Val Ala Pro Thr Glu Cys Ser *
 228 233

ggagactaga gctgcaggat cccaggggag ggggtctctcc tcccacccca aggcataag 841

cccttctccc tgcactcaat aaaccctcaa taaatattct cattgtcaat caaaaaaaaa 901

aaaaa 906

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 <213> Homo sapiens

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 <222> (203)..(1588)

<400> 109

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ctctgcttgc tccagaggcc tcgtcctaata ccacctcggc tgacggcgcg ggatccctgg 180

ctccgcgagc ctcagcctca cc atg tgt gtc agg agc tgt ttc cag tcc ccc 232
 Met Cys Val Arg Ser Cys Phe Gln Ser Pro
 1 5

cgt ctc cag tgg gtg tgg aga aca gcc ttc ctg aaa cac acc cag cgc 280
 Arg Leu Gln Trp Val Trp Arg Thr Ala Phe Leu Lys His Thr Gln Arg
 11 16 21 26

agg cac cag ggg tcc cac cga tgg aca cac ctt gga ggc agc acc tac 328
 Arg His Gln Gly Ser His Arg Trp Thr His Leu Gly Gly Ser Thr Tyr
 27 32 37 42

aga gcg gtg att ttc gac atg ggc gga gtt ctc att cct tct cca ggg	376
Arg Ala Val Ile Phe Asp Met Gly Gly Val Leu Ile Pro Ser Pro Gly	
43 48 53 58	
aga gtc gct gca gaa tgg gag gta cag aat cgt atc cct tct gga act	424
Arg Val Ala Ala Glu Trp Glu Val Gln Asn Arg Ile Pro Ser Gly Thr	
59 64 69 74	
ata tta aag gcc ttg atg gaa ggt ggt gaa aat ggg ccc tgg atg aga	472
Ile Leu Lys Ala Leu Met Glu Gly Gly Glu Asn Gly Pro Trp Met Arg	
75 80 85 90	
ttt atg aga gca gaa ata aca gca gag ggt ttt tta cga gaa ttt ggg	520
Phe Met Arg Ala Glu Ile Thr Ala Glu Gly Phe Leu Arg Glu Phe Gly	
91 96 101 106	
aga ctt tgc tct gaa atg tta aag acc tcc gtg cct gtg gac tca ttt	568
Arg Leu Cys Ser Glu Met Leu Lys Thr Ser Val Pro Val Asp Ser Phe	
107 112 117 122	
ttc tct ctg ttg acc agt gag cga gtg gca aag cag ttc cca gtg atg	616
Phe Ser Leu Leu Thr Ser Glu Arg Val Ala Lys Gln Phe Pro Val Met	
123 128 133 138	
act gag gcc ata act caa att cgg gca aaa ggt ctt cag act gca gtc	664
Thr Glu Ala Ile Thr Gln Ile Arg Ala Lys Gly Leu Gln Thr Ala Val	
139 144 149 154	
ttg agc aat aat ttt tat ctt ccc aac cag aaa agc ttt ttg ccc ctg	712
Leu Ser Asn Asn Phe Tyr Leu Pro Asn Gln Lys Ser Phe Leu Pro Leu	
155 160 165 170	
gac cgg aaa cag ttt gat gtg att gtg gag tcc tgc atg gaa ggg atc	760
Asp Arg Lys Gln Phe Asp Val Ile Val Glu Ser Cys Met Glu Gly Ile	
171 176 181 186	
tgt aag cca gac cct agg atc tac aag ctg tgc ttg gag cag ctc ggc	808
Cys Lys Pro Asp Pro Arg Ile Tyr Lys Leu Cys Leu Glu Gln Leu Gly	
187 192 197 202	
ctg cag ccc tct gag tcc atc ttt ctt gat gac ctt gga aca aat cta	856
Leu Gln Pro Ser Glu Ser Ile Phe Leu Asp Asp Leu Gly Thr Asn Leu	
203 208 213 218	
aaa gaa gct gcc aga ctt ggt att cac acc att aag gtt aat gac cca	904
Lys Glu Ala Ala Arg Leu Gly Ile His Thr Ile Lys Val Asn Asp Pro	
219 224 229 234	
gag act gca gta aag gaa tta gaa gct ctc ttg ggt ttt aca ttg aga	952
Glu Thr Ala Val Lys Glu Leu Glu Ala Leu Leu Gly Phe Thr Leu Arg	
235 240 245 250	
gta ggt gtt cca aac act cgg cct gtg aaa aag acg atg gaa att ccg	1000
Val Gly Val Pro Asn Thr Arg Pro Val Lys Lys Thr Met Glu Ile Pro	
251 256 261 266	
aaa gat tcc ttg cag aag tac ctc aaa gac tta ctg ggt atc cag acc	1048

Lys Asp Ser Leu Gln	Lys Tyr Leu Lys Asp	Leu Leu Gly Ile Gln Thr	
267	272	277	282
aca ggc cca ttg gaa cta ctt cag ttt gat cac ggg cag tca aat cca			1096
Thr Gly Pro Leu Glu	Leu Leu Gln Phe Asp	His Gly Gln Ser Asn Pro	
283	288	293	298
act tac tac atc agg ctg gct aat cgt gat cta gtt ctg agg aag aag			1144
Thr Tyr Tyr Ile Arg	Leu Ala Asn Arg Asp	Leu Val Leu Arg Lys Lys	
299	304	309	314
ccc cca ggg aca ctc ctt cca tct gcc cat gcc ata gag agg gag ttc			1192
Pro Pro Gly Thr Leu	Leu Pro Ser Ala His	Ala Ile Glu Arg Glu Phe	
315	320	325	330
agg att atg aaa gcc ctt gca aat gct gga gta cct gtc cct aac gtt			1240
Arg Ile Met Lys Ala	Leu Ala Asn Ala Gly	Val Pro Val Pro Asn Val	
331	336	341	346
ctt gat ctc tgt gaa gat tca agt gtc att ggc acc ccc ttc tat gtg			1288
Leu Asp Leu Cys Glu	Asp Ser Ser Val Ile	Gly Thr Pro Phe Tyr Val	
347	352	357	362
atg gag tac tgc cca ggt ctc atc tac aaa gac cct tcc ctg cca ggc			1336
Met Glu Tyr Cys Pro	Gly Leu Ile Tyr Lys	Asp Pro Ser Leu Pro Gly	
363	368	373	378
ttg gag ccc agc cac aga cga gcc ata tac act gcc atg aac aca gtc			1384
Leu Glu Pro Ser His	Arg Arg Ala Ile Tyr	Thr Ala Met Asn Thr Val	
379	384	389	394
ctg tgc aaa att cac agt gtg gat ctg cag gct gtg gga ctt gaa gac			1432
Leu Cys Lys Ile His	Ser Val Asp Leu Gln	Ala Val Gly Leu Glu Asp	
395	400	405	410
tat ggg aag caa ggc tcg aca acc tgg tgt ttc atc cag aag agc cag			1480
Tyr Gly Lys Gln Gly	Ser Thr Thr Trp Cys	Phe Ile Gln Lys Ser Gln	
411	416	421	426
agg tgc ttg ctg tcc ttg act ggg aac ttt cta cct tgg gcg acc ccc			1528
Arg Cys Leu Leu Ser	Leu Thr Gly Asn Phe	Leu Pro Trp Ala Thr Pro	
427	432	437	442
ttg ctg atg tgg cct aca gct gcc tgg ctc att acc tgc cat cca gtt			1576
Leu Leu Met Trp Pro	Thr Ala Ala Trp Leu	Ile Thr Cys His Pro Val	
443	448	453	458
ttc ccg tgc tga gag gtattaatga ctgtgacttg acacagctgg gaatccctgc			1631
Phe Pro Cys *			
459			
tgcagaggag tatttcagga tgtactgtct ccaaattgggg ctccctccca ctgagaactg			1691
gaacttctat atggcttttt cctttttccg tgtggctgca atcctacagg gagtctacaa			1751
gcgatcactc acaggtaatg ggatggctgc cctgaagagc cactgcgggc attctgccga			1811

ctg cag ccg ttc aag gag ctc tgc acg cac ctc atg gag gag aac atg	619
Leu Gln Pro Phe Lys Glu Leu Cys Thr His Leu Met Glu Glu Asn Met	
119 124 129 134	
atc gtg tat gtg gaa aag aaa gtg cta gaa gac cct gcc atc gcc agc	667
Ile Val Tyr Val Glu Lys Lys Val Leu Glu Asp Pro Ala Ile Ala Ser	
135 140 145 150	
gat gaa agc ttt ggg gca gtg aag aag aaa ttc tgt acc ttt cga gaa	715
Asp Glu Ser Phe Gly Ala Val Lys Lys Lys Phe Cys Thr Phe Arg Glu	
151 156 161 166	
gat tat gat gac att tcc aat cag ata gac ttc atc atc tgc ctg ggg	763
Asp Tyr Asp Asp Ile Ser Asn Gln Ile Asp Phe Ile Ile Cys Leu Gly	
167 172 177 182	
gga gac ggg acg ctg ctg tac gct tcc tcg ctt ttc cag gga acg cag	811
Gly Asp Gly Thr Leu Leu Tyr Ala Ser Ser Leu Phe Gln Gly Thr Gln	
183 188 193 198	
ctg ttg ttc tcc gga gtc ggc tga aggtcagggt ggtgaaggag ctccggggga	865
Leu Leu Phe Ser Gly Val Gly *	
199 204	
agaagacggc cgtgcacaat gggctgggtg agaaaggctc gcaggctgca ggcctggaca	925
tggatgtcgg gaagcaggcc atgcagtacc aggtcctgaa tgagggtggtg attgacagag	985
gcccctcctc ctacctgtcc aatgtggatg tctacctgga cggacacctc atcaccacgg	1045
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gctta	1110

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 <222> (602) .. (2251)

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ttatgggtct ttcaactctc gtatatatatt aaatgcaatt ggagccccgc aggggaatacc	180
agatcaattt aaagcttgaa atcaaatagt tacaggactg aagtcaatat tttggtagat	240
gacagtcaat aaaaatgtaa attagataca ctacatctat tacaaccaac agcaacgagc	300

ttttcatgag ttaaaaagaa aaactcatgt cggccccgagc cctgggggcta cctgacctga	360
caaaactctt tacactccat gtgtcaaaaa gagaaaaaat ggcagttgga gttttaaccc	420
agactgtggg gccctggcca aggccagtgg cctatctctc aaaacaacta gatggggttc	480
caaaggctgg ccactatgtc taaggaccct ggcagcaaca gccctgttag cacaagaagc	540
agataaacta acccttgggc aaaacctgaa tataaaggcc ccccatgctg tggttaacttt	600
g atg act acc gaa gga cat cat tgg cta aca aat gct aga tta acc	646
Met Thr Thr Glu Gly His His Trp Leu Thr Asn Ala Arg Leu Thr	
1 5 10	
aag tac caa agc ttg cca tgt gaa aat ccc cac ata act att gaa gtc	694
Lys Tyr Gln Ser Leu Pro Cys Glu Asn Pro His Ile Thr Ile Glu Val	
16 21 26 31	
tgt aac acc cta aat ccc acc acc ctg ctc cca gta tca gag agc ccg	742
Cys Asn Thr Leu Asn Pro Thr Thr Leu Leu Pro Val Ser Glu Ser Pro	
32 37 42 47	
ggc gag cat aac tgt gta gag gtg ttg gac tca gtc tat tct agc aga	790
Gly Glu His Asn Cys Val Glu Val Leu Asp Ser Val Tyr Ser Ser Arg	
48 53 58 63	
cct gac ctt cgg gac cag cca tgg gca tca tca gta gac tgg gag tta	838
Pro Asp Leu Arg Asp Gln Pro Trp Ala Ser Ser Val Asp Trp Glu Leu	
64 69 74 79	
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Tyr Met Asp Gly Ser Ser Phe Ile Asn Ser Gln Gly Glu Arg Cys Ala	
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Gly Tyr Ala Val Val Thr Leu Asp Ala Val Ile Lys Ala Lys Leu Trp	
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Ala Val Glu Leu Ser Glu Gly Gln Glu Ser Leu Glu Glu Leu Leu Gly	
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Arg Tyr Phe Tyr Val Ser His Leu Pro Ala Phe Ala Lys Ala Val Ala	
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Gln Leu Cys Ile Thr Cys Arg Gln His Asn Ala Arg Gln Ser Pro Thr	
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Val Ser Pro His Ile Gln Ala Tyr Gly Ala Ala Pro Phe Glu Asp Leu	
176 181 186 191	

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Gln Val Asp Phe Thr Glu Met Pro Lys Cys Gly Gly Asn Lys Tyr Leu	
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Leu Val Leu Thr Cys Thr Tyr Ser Gly Trp Val Glu Ala Tyr Pro Thr	
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Arg Thr Glu Lys Ala Tyr Glu Val Thr Arg Val Leu Leu Arg Asp Leu	
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Ile Pro Arg Phe Gly Leu Pro Leu Arg Ile Gly Ser His Asn Gly Pro	
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Val Phe Val Ala Asp Leu Asp Cys Val Glu Ile Asn Val Asp Thr Gly	
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Asn Ile Leu Val Arg Gly Glu Val Tyr Lys Cys Ser Leu Glu Pro Val	
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Phe Gln Thr Phe Tyr Asp Glu Leu Asn Val Pro Ile Thr Glu Phe Pro	
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Val Ile Gly Thr Ile Lys Pro Ser Phe Phe Leu Leu Ser Ile Lys Thr	
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Tyr Lys Lys Leu Lys Gln *	
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 atg agt tgg cga gga aga tca aca tat agg cct agg cca aga aga agt 287
 Met Ser Trp Arg Gly Arg Ser Thr Tyr Arg Pro Arg Pro Arg Arg Ser
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 Leu Gln Pro Pro Glu Leu Ile Gly Ala Met Leu Glu Pro Thr Asp Glu
 17 22 27 32
 gag cct aaa gaa gag aaa cca ccc act aaa agt cgg aat cct aca cct 383
 Glu Pro Lys Glu Glu Lys Pro Pro Thr Lys Ser Arg Asn Pro Thr Pro
 33 38 43 48
 gat cag aag aga gaa gat gat cag ggt gca gct gag att caa gtg cct 431
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 Asp Leu Glu Ala Asp Leu Gln Glu Leu Cys Gln Thr Lys Thr Gly Asp
 65 70 75 80
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 Gly Cys Glu Gly Gly Thr Asp Val Lys Gly Lys Ile Leu Pro Lys Ala

81	86	91	96	
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Glu His Phe Lys Met Pro Glu Ala Gly Glu Gly Lys Ser Gln Val *				
97	102	107	112	
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Ser	Arg	Thr	Ser	Trp	Gly	Pro	His	Arg	Ser	Cys	Tyr	Pro	Ser	Cys	Pro	
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gcc	cgt	gag	tcc	aac	cgg	cgc	ctc	tgg	cca	aga	aag	gcg	agc	tga	acc	912
Ala	Arg	Glu	Ser	Asn	Arg	Arg	Leu	Trp	Pro	Arg	Lys	Ala	Ser	*		
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		1		5	10											
tat aaa atg	aaa act gac	cac ttc tcc	tta cgt tat	ctt cac agt	agc											338
Tyr Lys Met	Lys Thr Asp	His Phe Ser	Leu Arg Tyr	Leu His Ser	Ser											
13		18		23	28											
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Cys Ala Glu	Asp Asn Lys	Ser Ser Val	Asp Ser Ser	Gly Gln Ala	Ala											
29		34		39	44											
cac ccc agc	aaa ggg aag	ttc ttc ccc	cat ggg acc	cac tgg ggg	acc											434
His Pro Ser	Lys Gly Lys	Phe Phe Pro	His Gly Thr	His Trp Gly	Thr											
45		50		55	60											
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Gln Cys Arg	Gly His Ile	Ser Val Leu	Gly Trp Gln	Cys Ser Cys	Pro											
61		66		71	76											
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Ser	Thr	Gly	Cys	Arg	Val	Gly	Leu	Gly	Leu	Ala	Met	Cys	Gln	Thr	His	
77					82					87					92	
gca tac ata cac aca cac aca cac aca cac aca cac acc cca ccc gat																578
Ala	Tyr	Ile	His	Thr	His	Thr	His	Thr	His	Thr	His	Thr	Pro	Pro	Asp	
93					98					103					108	
tat gga gca cat cac acc gat ccc ttg cag agg tgg ggg ctg ggg ccc																626
Tyr	Gly	Ala	His	His	Thr	Asp	Pro	Leu	Gln	Arg	Trp	Gly	Leu	Gly	Pro	
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Arg	Thr	Ile	Arg	Ser	Arg	Ala	Pro	Pro	Pro	Ala	Val	Ser	Arg	Pro	Lys	
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Pro	Ser	Arg	Ala	Ser	Glu	Pro	Trp	Gly	Ile	Thr	Gln	Lys	Arg	Trp	Ala	
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Arg	Gln	Gly	Arg	Ser	Phe	Thr	Pro	Asp	Gln	Ala	Asp	*				
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gta tct gcc gct ctt cag ttt tca tta tct tgc att ttt ctg agg gaa      151
Val Ser Ala Ala Leu Gln Phe Ser Leu Ser Cys Ile Phe Leu Arg Glu
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gga aaa gcc aca gat gaa gac atg caa agt ttg gct agt ttg atg agt      199
Gly Lys Ala Thr Asp Glu Asp Met Gln Ser Leu Ala Ser Leu Met Ser
  35                               40                               45                               50

atg aag cag gct gac att ggc aat tta gat gac ttc gaa gaa gat aat      247
Met Lys Gln Ala Asp Ile Gly Asn Leu Asp Asp Phe Glu Glu Asp Asn
  51                               56                               61                               66

gaa gat gat gat gag aac aga gtg aac caa gaa gaa aag gca gct aaa      295
Glu Asp Asp Asp Glu Asn Arg Val Asn Gln Glu Glu Lys Ala Ala Lys
  67                               72                               77                               82

att aca gag ctt atc aac aaa ctt aac ttt ttg gat gaa gca gaa aag      343
Ile Thr Glu Leu Ile Asn Lys Leu Asn Phe Leu Asp Glu Ala Glu Lys
  83                               88                               93                               98

gac ttg gcc acc gtg aat tca aat cca ttt gat gat cct gat gct gca      391
Asp Leu Ala Thr Val Asn Ser Asn Pro Phe Asp Asp Pro Asp Ala Ala
  99                               104                               109                               114

gaa tta aat cca ttt gga gat cct gac tca gaa gaa cct atc act gaa      439
Glu Leu Asn Pro Phe Gly Asp Pro Asp Ser Glu Glu Pro Ile Thr Glu
  115                               120                               125                               130

aca gct tca cct aga aaa aca gaa gac tct ttt tat aat aac agc tat      487
Thr Ala Ser Pro Arg Lys Thr Glu Asp Ser Phe Tyr Asn Asn Ser Tyr
  131                               136                               141                               146

aat ccc ttt aaa gag gtg cag act cca cag tat ttg aac cca ttc gat      535
Asn Pro Phe Lys Glu Val Gln Thr Pro Gln Tyr Leu Asn Pro Phe Asp
  147                               152                               157                               162

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Glu Pro Glu Ala Phe Val Thr Ile Lys Asp Ser Pro Pro Gln Ser Thr

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Asp Ser Ser Lys Thr	Glu Glu Glu Glu Leu	Asp Glu Ser Asn Pro	Phe	
195	200	205	210	
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211	216	221	226	
caa gaa cta gaa act	gaa agg cga gtg aaa	aga aag gcc ccg gct	cca	775
Gln Glu Leu Glu Thr	Glu Arg Arg Val Lys	Arg Lys Ala Pro Ala	Pro	
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Ala Gly Lys Asp Leu	Ser Thr Ser Pro Lys	Pro Ser Pro Ile Pro	Ser	
259	264	269	274	
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Pro Val Leu Gly Arg	Lys Pro Asn Ala Ser	Gln Ser Leu Leu Val	Trp	
275	280	285	290	
tgt aaa gaa gtt aca	aag aac tac cga gga	gta aaa atc acc aat	ttt	967
Cys Lys Glu Val Thr	Lys Asn Tyr Arg Gly	Val Lys Ile Thr Asn	Phe	
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Thr Thr Ser Trp Arg	Asn Gly Leu Ser Phe	Cys Ala Ile Leu His	His	
307	312	317	322	
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Phe Arg Pro Asp Leu	Ile Asp Tyr Lys Ser	Leu Asn Pro Gln Asp	Ile	
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aaa ctg act gtt atg	act tat ctc tat caa	ata agg gca cat ttc	agt	1207
Lys Leu Thr Val Met	Thr Tyr Leu Tyr Gln	Ile Arg Ala His Phe	Ser	
371	376	381	386	
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Gln Glu Lys Phe Tyr Ala Glu Leu Ser Asp Leu Lys Arg Glu Pro Glu	
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aatattttct tcttttagcat agcactgtca ttttttgtga aaatggttat gtttatttat	4081
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Arg Arg Thr Ala Leu Ile Leu Gly Ser Gly Leu Leu Ser Phe Val Ala
  2                               7                               12                               17

ttc tgg aac tca gtg aca tgg cat ctt cag aga ttt tgg ggt gct tct      152
Phe Trp Asn Ser Val Thr Trp His Leu Gln Arg Phe Trp Gly Ala Ser
 18                               23                               28                               33

ggc tac ttt tgg caa gcc cag tgg gag agg ctg ctg act aca ttt gaa      200
Gly Tyr Phe Trp Gln Ala Gln Trp Glu Arg Leu Leu Thr Thr Phe Glu
 34                               39                               44                               49

ggg aag gag tgg atc ctc ttc ttt ata ggt gcc atc caa gtg cct tgt      248
Gly Lys Glu Trp Ile Leu Phe Phe Ile Gly Ala Ile Gln Val Pro Cys
 50                               55                               60                               65

ctc ttc ttc tgg agc ttc aat ggg ctt cta ttg gtg gtt gac aca aca      296
Leu Phe Phe Trp Ser Phe Asn Gly Leu Leu Leu Val Val Asp Thr Thr
 66                               71                               76                               81

gga aaa cct aac ttc atc tct cgc tac cga att cag gtc ggc aag aat      344
Gly Lys Pro Asn Phe Ile Ser Arg Tyr Arg Ile Gln Val Gly Lys Asn
 82                               87                               92                               97

gaa cct gtg gat cct gtg aaa ctg cac cag tgc atg ata tct ttc ccc      392
Glu Pro Val Asp Pro Val Lys Leu His Gln Cys Met Ile Ser Phe Pro
 98                               103                               108                               113

atg gtg gtc ttc ctc tat ccc ttc ctc aaa tgg tgg aga gac ccc tgc      440
Met Val Val Phe Leu Tyr Pro Phe Leu Lys Trp Trp Arg Asp Pro Cys
114                               119                               124                               129

cgc cgt gag cta ccc acc ttc cac tgg ttc ctc ctg gag ctg gcc atc      488
Arg Arg Glu Leu Pro Thr Phe His Trp Phe Leu Leu Glu Leu Ala Ile
130                               135                               140                               145

ttc acg ctg atc gag gaa gtc ttg ttc tac tat tca cac cgg ctc ctt      536
Phe Thr Leu Ile Glu Glu Val Leu Phe Tyr Tyr Ser His Arg Leu Leu
146                               151                               156                               161

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His His Pro Thr Phe Tyr Lys Lys Ile His Lys Lys His His Glu Trp	
162 167 172 177	
aca gct ccc att ggc gtg atc tct ctc tat gcc cac cct ata gag cat	632
Thr Ala Pro Ile Gly Val Ile Ser Leu Tyr Ala His Pro Ile Glu His	
178 183 188 193	
gca gtc tcc aac atg cta ccg gtg ata gtg ggc cca tta gta atg ggc	680
Ala Val Ser Asn Met Leu Pro Val Ile Val Gly Pro Leu Val Met Gly	
194 199 204 209	
tcc cac ttg tcc tcc atc acc atg tgg ttt tcc ttg gcc ctc atc atc	728
Ser His Leu Ser Ser Ile Thr Met Trp Phe Ser Leu Ala Leu Ile Ile	
210 215 220 225	
acc acc atc tcc cac tgt ggc tac cac ctt ccc ttc ctg cct tcg cct	776
Thr Thr Ile Ser His Cys Gly Tyr His Leu Pro Phe Leu Pro Ser Pro	
226 231 236 241	
gaa ttc cac gac tac cac cat ctc aag ttc aac cag tgc tat ggg gtg	824
Glu Phe His Asp Tyr His His Leu Lys Phe Asn Gln Cys Tyr Gly Val	
242 247 252 257	
ctg ggt gtg ctg gac cac ctc cat ggg act gac acc atg ttc aag cag	872
Leu Gly Val Leu Asp His Leu His Gly Thr Asp Thr Met Phe Lys Gln	
258 263 268 273	
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Thr Lys Ala Tyr Glu Arg His Val Leu Leu Leu Gly Phe Thr Pro Leu	
274 279 284 289	
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Ser Glu Ser Ile Pro Asp Ser Pro Lys Arg Met Glu *	
290 295 300	
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aaggcgccg	gacccggagg	aaccggaaaa	aacagaactc	agcgaaagag	agctggcagt	180
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tgataatctc	cccagtgc	cc atg tat	gag cgc agt	tac atg cat	aga gat	352
		Met Tyr Glu Arg Ser Tyr Met His Arg Asp				
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Val Ile Thr His	Val Val Cys Thr	Lys Thr Asp Phe	Ile Ile Thr Ala			
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agt cat gat gga	cat gtc aag ttc	tggtggaaa	ata gaa gag gga	att		448
Ser His Asp Gly	His Val Lys Phe	Trp Lys Lys Ile	Glu Glu Gly Ile			
27	32	37	42			
gaa ttt gtt aaa	cat ttt cgt agt	cac ctg gga gtt	att gag agt att			496
Glu Phe Val Lys	His Phe Arg Ser	His Leu Gly Val	Ile Glu Ser Ile			
43	48	53	58			
gca gtt agc tct	gag gga gca ttg	ttc tgt tct gtc	ggg gat gat aaa			544
Ala Val Ser Ser	Glu Gly Ala Leu	Phe Cys Ser Val	Gly Asp Asp Lys			
59	64	69	74			
gca atg aag gtg	ttt gat gta gtg	aac ttt gac atg	atc aac atg ctg			592
Ala Met Lys Val	Phe Asp Val Val	Asn Phe Asp Met	Ile Asn Met Leu			
75	80	85	90			
aaa ctt ggc tat	ttt cct gga cag	tgt gag tgg atc	tat tgc cca ggg			640
Lys Leu Gly Tyr	Phe Pro Gly Gln	Cys Glu Trp Ile	Tyr Cys Pro Gly			
91	96	101	106			
gat gca att tct	tca gtt gct gct	tcc gaa aag agt	aca gga aaa att			688
Asp Ala Ile Ser	Ser Val Ala Ala	Ser Glu Lys Ser	Thr Gly Lys Ile			
107	112	117	122			
ttc att tat gat	ggc cga gga gat	aac cag cca ctt	cat att ttt gac			736
Phe Ile Tyr Asp	Gly Arg Gly Asp	Asn Gln Pro Leu	His Ile Phe Asp			
123	128	133	138			
aaa ctc cat aca	tca cct ctt act	cag ata cgg cta	aac cca gtt tac			784
Lys Leu His Thr	Ser Pro Leu Thr	Gln Ile Arg Leu	Asn Pro Val Tyr			
139	144	149	154			

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155 160 165 170	
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Gly Pro Pro His Glu Tyr Lys Phe Pro Lys Asn Val Asn Trp Glu Tyr	
171 176 181 186	
aaa act gac act gat tta tat gaa ttt gcc aag tgt aag gct tat cca	928
Lys Thr Asp Thr Asp Leu Tyr Glu Phe Ala Lys Cys Lys Ala Tyr Pro	
187 192 197 202	
acc agc gta tgt ttt tca cca gat ggg aag aaa ata gct act att ggt	976
Thr Ser Val Cys Phe Ser Pro Asp Gly Lys Lys Ile Ala Thr Ile Gly	
203 208 213 218	
tct gat aga aaa gtt aga att ttc aga ttt gta act gga aaa ctc atg	1024
Ser Asp Arg Lys Val Arg Ile Phe Arg Phe Val Thr Gly Lys Leu Met	
219 224 229 234	
aga gtc ttt gat gaa tca cta agc atg ttt act gaa ctg caa cag atg	1072
Arg Val Phe Asp Glu Ser Leu Ser Met Phe Thr Glu Leu Gln Gln Met	
235 240 245 250	
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Arg Gln Gln Leu Pro Asp Met Glu Phe Gly Arg Arg Met Ala Val Glu	
251 256 261 266	
cgt gag ttg gag aag gtt gat gct gta aga tta att aat ata gtt ttt	1168
Arg Glu Leu Glu Lys Val Asp Ala Val Arg Leu Ile Asn Ile Val Phe	
267 272 277 282	
gat gaa act gga cac ttc gtg ctg tat gga aca atg ctg ggc att aaa	1216
Asp Glu Thr Gly His Phe Val Leu Tyr Gly Thr Met Leu Gly Ile Lys	
283 288 293 298	
gtt ata aat gta gag aca aac cgg tgt gtg cgg att tta ggc aaa caa	1264
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Glu Asn Ile Arg Val Met Gln Leu Ala Leu Phe Gln Gly Ile Ala Lys	
315 320 325 330	
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Lys His Arg Ala Ala Thr Thr Ile Glu Met Lys Ala Ser Glu Asn Pro	
331 336 341 346	
gtt ctt cag aat att caa gct gac cca aca ata gtc tgt aca tca ttc	1408
Val Leu Gln Asn Ile Gln Ala Asp Pro Thr Ile Val Cys Thr Ser Phe	
347 352 357 362	
aaa aag aat aga ttt tat atg ttt acc aaa cga gaa cca gaa gat acg	1456
Lys Lys Asn Arg Phe Tyr Met Phe Thr Lys Arg Glu Pro Glu Asp Thr	
363 368 373 378	
aaa agt gca gat tct gat cga gat gtt ttt aat gag aaa cct tct aaa	1504

Lys Ser Ala Asp Ser Asp Arg Asp Val Phe Asn Glu Lys Pro Ser Lys	
379 384 389 394	
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Glu Glu Val Met Ala Ala Thr Gln Ala Glu Gly Pro Lys Arg Val Ser	
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Asp Ser Ala Ile Ile His Thr Ser Met Gly Asp Ile His Thr Lys Leu	
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Phe Pro Val Glu Cys Pro Lys Thr Val Glu Asn Phe Cys Val His Ser	
427 432 437 442	
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Arg Asn Gly Tyr Tyr Asn Gly His Thr Phe His Arg Ile Ile Lys Gly	
443 448 453 458	
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Phe Met Ile Gln Thr Gly Asp Pro Thr Gly Thr Gly Met Gly Gly Glu	
459 464 469 474	
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Ser Ile Trp Gly Gly Glu Phe Glu Asp Glu Phe His Ser Thr Leu Arg	
475 480 485 490	
cat gac agg cca tac aca ctc agc atg gct aac gcg gga tca aat act	1840
His Asp Arg Pro Tyr Thr Leu Ser Met Ala Asn Ala Gly Ser Asn Thr	
491 496 501 506	
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Asn Gly Ser Gln Phe Phe Ile Thr Val Val Pro Thr Pro Trp Leu Asp	
507 512 517 522	
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Asn Lys His Thr Val Phe Gly Arg Val Thr Lys Gly Met Glu Val Val	
523 528 533 538	
cag agg atc tcc aac gtc aaa gtc aat ccc aaa aca gat aag ccc tat	1984
Gln Arg Ile Ser Asn Val Lys Val Asn Pro Lys Thr Asp Lys Pro Tyr	
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Glu Asp Val Ser Ile Ile Asn Ile Thr Val Lys *	
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      Met Ala Ala Ser Arg Lys Pro Pro Arg Val Arg Val
              1              5              10

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Asn His Gln Asp Phe Gln Leu Arg Asn Leu Arg Ile Ile Glu Pro Asn
      13              18              23              28

gag gtg aca cac tca gga gac aca ggt gtg gaa aca gac ggc aga atg      207
Glu Val Thr His Ser Gly Asp Thr Gly Val Glu Thr Asp Gly Arg Met
      29              34              39              44

cct cca aag gtg act tca gag ctg ctt cgg cag ctg aga caa gcc atg      255
Pro Pro Lys Val Thr Ser Glu Leu Leu Arg Gln Leu Arg Gln Ala Met
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agg aac tct gag tat gtg acc gaa ccg atc cag gcc tac atc atc cca      303
Arg Asn Ser Glu Tyr Val Thr Glu Pro Ile Gln Ala Tyr Ile Ile Pro
      61              66              71              76

tcg gga gat gct cat cag agt gag tat att gct cca tgt gac tgt cgg      351
Ser Gly Asp Ala His Gln Ser Glu Tyr Ile Ala Pro Cys Asp Cys Arg
      77              82              87              92

cgg gct ttt gtc tct gga ttc gat ggc tct gcg ggc aca gcc atc atc      399
Arg Ala Phe Val Ser Gly Phe Asp Gly Ser Ala Gly Thr Ala Ile Ile
      93              98              103              108

aca gaa gag cat gca gcc atg tgg act gac ggg cgc tac ttt ctg cag      447
Thr Glu Glu His Ala Ala Met Trp Thr Asp Gly Arg Tyr Phe Leu Gln
      109              114              119              124

gct gcc aag caa atg gac agc aac tgg aca ctt atg aag atg ggt ctg      495
Ala Ala Lys Gln Met Asp Ser Asn Trp Thr Leu Met Lys Met Gly Leu
      125              130              135              140

aag gac aca cca act cag gaa gac tgg ctg gtg agt gtg ctt cct gaa      543
Lys Asp Thr Pro Thr Gln Glu Asp Trp Leu Val Ser Val Leu Pro Glu
      141              146              151              156

gga tcc agg gtt ggt gtg gac ccc ttg atc att cct aca gat tat tgg      591

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Gly	Ser	Arg	Val	Gly	Val	Asp	Pro	Leu	Ile	Ile	Pro	Thr	Asp	Tyr	Trp	
157					162					167					172	
aag	aaa	atg	gcc	aaa	gtt	ctg	aga	agt	gcc	ggc	cat	cac	ctc	att	cct	639
Lys	Lys	Met	Ala	Lys	Val	Leu	Arg	Ser	Ala	Gly	His	His	Leu	Ile	Pro	
173					178					183					188	
gtc	aag	gag	aac	ctc	gtt	gac	aaa	atc	tgg	aca	gac	cgt	cct	gag	cgc	687
Val	Lys	Glu	Asn	Leu	Val	Asp	Lys	Ile	Trp	Thr	Asp	Arg	Pro	Glu	Arg	
189					194					199					204	
cct	tgc	aag	cct	ctc	ctc	aca	ctg	ggc	ctg	gat	tac	aca	ggc	atc	tcc	735
Pro	Cys	Lys	Pro	Leu	Leu	Thr	Leu	Gly	Leu	Asp	Tyr	Thr	Gly	Ile	Ser	
205					210					215					220	
tgg	aag	gac	aag	gtt	gca	gac	ctt	cgg	ttg	aaa	atg	gct	gag	agg	aac	783
Trp	Lys	Asp	Lys	Val	Ala	Asp	Leu	Arg	Leu	Lys	Met	Ala	Glu	Arg	Asn	
221					226					231					236	
gtc	atg	tgg	ttt	gtg	gtc	act	gcc	ttg	gat	gag	att	gcg	tgg	cta	ttt	831
Val	Met	Trp	Phe	Val	Val	Thr	Ala	Leu	Asp	Glu	Ile	Ala	Trp	Leu	Phe	
237					242					247					252	
aat	ctc	cga	gga	tca	gat	gtg	gag	cac	aat	cca	gta	ttt	ttc	tcc	tac	879
Asn	Leu	Arg	Gly	Ser	Asp	Val	Glu	His	Asn	Pro	Val	Phe	Phe	Ser	Tyr	
253					258					263					268	
gca	atc	ata	gga	cta	gag	acg	atc	atg	ctc	ttc	att	gat	ggc	gac	cgc	927
Ala	Ile	Ile	Gly	Leu	Glu	Thr	Ile	Met	Leu	Phe	Ile	Asp	Gly	Asp	Arg	
269					274					279					284	
ata	gac	gcc	ccc	agt	gtg	aag	gag	cac	ctg	ctt	ctt	gac	ttg	ggc	ctg	975
Ile	Asp	Ala	Pro	Ser	Val	Lys	Glu	His	Leu	Leu	Leu	Asp	Leu	Gly	Leu	
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Glu	Ala	Glu	Tyr	Arg	Ile	Gln	Val	His	Pro	Tyr	Lys	Ser	Ile	Leu	Ser	
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333					338					343					348	
cac	cgc	tgc	tgt	atg	cct	tac	acc	ccc	atc	tgc	atc	gcc	aaa	gct	gtg	1167
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Lys	Asn	Ser	Ala	Glu	Ser	Glu	Gly	Met	Arg	Arg	Ala	His	Ile	Lys	Asp	
365					370					375					380	
gct	gtt	gct	ctc	tgt	gaa	ctc	ttt	aac	tgg	ctg	gag	aaa	gag	gtt	ccc	1263
Ala	Val	Ala	Leu	Cys	Glu	Leu	Phe	Asn	Trp	Leu	Glu	Lys	Glu	Val	Pro	

381	386	391	396	
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Lys Gly Gly Val Thr Glu Ile Ser Ala Ala Asp Lys Ala Glu Glu Phe				
397	402	407	412	
cgc agg caa cag gca gag ttt gtg gac ctg agc ttc cca aca att tcc				1359
Arg Arg Gln Gln Ala Asp Phe Val Asp Leu Ser Phe Pro Thr Ile Ser				
413	418	423	428	
agt acg gga ccc aac ggc gcc atc att cac tac gcg cca gtc cct gag				1407
Ser Thr Gly Pro Asn Gly Ala Ile Ile His Tyr Ala Pro Val Pro Glu				
429	434	439	444	
acg aat agg acc ttg tcc ctg gat gag gtg tac ctt att gac tcg ggt				1455
Thr Asn Arg Thr Leu Ser Leu Asp Glu Val Tyr Leu Ile Asp Ser Gly				
445	450	455	460	
gct caa tac aag gat ggc acc aca gat gtg acg cgg aca atg cat ttt				1503
Ala Gln Tyr Lys Asp Gly Thr Thr Asp Val Thr Arg Thr Met His Phe				
461	466	471	476	
ggg acc cct aca gcc tac gag aag gaa tgc ttc aca tat gtc ctc aag				1551
Gly Thr Pro Thr Ala Tyr Glu Lys Glu Cys Phe Thr Tyr Val Leu Lys				
477	482	487	492	
ggc cac ata gct gtg agt gca gcc gtt ttc ccg act gga acc aaa ggt				1599
Gly His Ile Ala Val Ser Ala Ala Val Phe Pro Thr Gly Thr Lys Gly				
493	498	503	508	
cac ctt ctt gac tcc ttt gcc cgt tca gct tta tgg gat tca ggc cta				1647
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509	514	519	524	
gat tac ttg cac ggg act gga cat ggt gtt ggg tct ttt ttg aat gtc				1695
Asp Tyr Leu His Gly Thr Gly His Gly Val Gly Ser Phe Leu Asn Val				
525	530	535	540	
cat gag ggt cct tgc ggc atc agt tac aaa aca ttc tct gat gag ccc				1743
His Glu Gly Pro Cys Gly Ile Ser Tyr Lys Thr Phe Ser Asp Glu Pro				
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Leu Glu Ala Gly Met Ile Val Thr Asp Glu Pro Gly Tyr Tyr Glu Asp				
557	562	567	572	
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Gly Ala Phe Gly Ile Arg Ile Glu Asn Val Val Leu Val Val Pro Val				
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Lys Thr Lys Tyr Asn Phe Asn Asn Arg Gly Ser Leu Thr Phe Glu Pro				
589	594	599	604	
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Leu Thr Leu Val Pro Ile Gln Thr Lys Met Ile Asp Val Asp Ser Leu				
605	610	615	620	

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637 642 647 652	
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Leu Gln Glu Lys Gly Asp Thr Ser Gln Asn Glu Lys Leu Ser Met Phe	
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Tyr Glu Thr Leu Lys Ser Pro Leu Phe Asn Gln Ile Leu Thr Leu Gln	
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Gln Ser Ile Lys Gln Leu Lys Gly Gln Leu Asn His Ile Pro Ser Asp	
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Cys Ser Ala Asn Phe Asp Phe Ser Arg Lys Gly Leu Leu Val Phe Thr	
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Asp Gly Ser Ile Thr Asn Gly Asn Val His Arg Pro Ser Asn Asn Ser	
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Asp Gln Ile Leu Ala Ile Asn His Thr Pro Leu Asp Gln Asn Ile Ser	
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His Gln Gln Ala Ile Ala Leu Leu Gln Gln Thr Thr Gly Ser Leu Arg	
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Leu Ile Val Ala Arg Glu Pro Val His Thr Lys Ser Ser Thr Ser Ser	
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Ser Leu Asn Asp Thr Thr Leu Pro Glu Thr Val Cys Trp Gly His Val	
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Val Gly Gly Lys Thr Ser Gly Val Val Val Arg Thr Ile Val Pro Gly	
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Gly Leu Ala Asp Arg Asp Gly Arg Leu Gln Thr Gly Asp His Ile Leu	
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Tyr His Asn Gly His Ile Gln Val Asn Asp Lys Ile Val Ala Val Asp	
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att cct atc atg tat agg aat tta cct gaa tat aaa gaa cta tta cag Ile Pro Ile Met Tyr Arg Asn Leu Pro Glu Tyr Lys Glu Leu Leu Gln 162 167 172 177	1003
ttt aaa aag tta aag aag cag aaa ctt cag caa atg caa gct gaa agt Phe Lys Lys Leu Lys Lys Gln Lys Leu Gln Gln Met Gln Ala Glu Ser 178 183 188 193	1051
gga ttt gtg caa cat gtg ggc ttt aag tgt gat aac tgt ggc ata gaa Gly Phe Val Gln His Val Gly Phe Lys Cys Asp Asn Cys Gly Ile Glu 194 199 204 209	1099

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Pro Ile Gln Gly Val Arg Trp His Cys Gln Asp Cys Pro Pro Glu Met	
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Ser Leu Asp Phe Cys Asp Ser Cys Ser Asp Cys Leu His Glu Thr Asp	
226 231 236 241	
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Ile His Lys Glu Asp His Gln Leu Glu Pro Ile Tyr Arg Ser Glu Thr	
242 247 252 257	
ttc tta gac aga gac tac tgt gtg tct cag ggc acc agt tac aat tac	1291
Phe Leu Asp Arg Asp Tyr Cys Val Ser Gln Gly Thr Ser Tyr Asn Tyr	
258 263 268 273	
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2470

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ccttgaaagt ttaggcaggc accagagaga agcactgaaa aatcccattg gatttgtgga      240
aaaactccag aagaaggctg atattgggct tccatatcca cagagagttg ttcaattgcc      300
tgagatcgta tgggaccaat atacccatag ccttgggaat tttgaaagag aatttaaaaa      360
tcgtaaaaga catactagaa gagttaagct agtttttgat aaagtaggtt tacctgctag      420
accaaaaaagt ccttttagatc ctaagaagga tggagagtcc ctttcatatt ct      atg      475
                                     Met
                                     1

ttg cct ttg agt gat ggt cca gaa ggc tca agc agt cgt cct cag atg      523
Leu Pro Leu Ser Asp Gly Pro Glu Gly Ser Ser Ser Arg Pro Gln Met
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Ile Arg Gly Arg Leu Cys Asp Asp Thr Lys Pro Glu Thr Phe Asn Gln
 18              23              28              33

ttg tgg act gtt gaa gaa cag aaa aag ctg gaa cag cta ctc atc aaa      619
Leu Trp Thr Val Glu Glu Gln Lys Lys Leu Glu Gln Leu Leu Ile Lys
 34              39              44              49

tac cct cct gaa gaa gta gaa tct cga cgc tgg cag aag ata gca gat      667
Tyr Pro Pro Glu Glu Val Glu Ser Arg Arg Trp Gln Lys Ile Ala Asp
 50              55              60              65

gaa ttg ggc aac agg aca gca aaa cag tct tca aca agc aga cga cag      715
Glu Leu Gly Asn Arg Thr Ala Lys Gln Ser Ser Thr Ser Arg Arg Gln
 66              71              76              81

cac cct ctt aat aag cat ctc ttt aag cct tcc act ttc atg act tca      763
His Pro Leu Asn Lys His Leu Phe Lys Pro Ser Thr Phe Met Thr Ser
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His Ser His Met Asn Thr Ala Val Glu Asp Ala Ser Asp Asp Glu Ser	
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Ile Pro Ile Met Tyr Arg Asn Leu Pro Glu Tyr Lys Glu Leu Leu Gln	
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Phe Lys Lys Leu Lys Lys Gln Lys Leu Gln Gln Met Gln Ala Glu Ser	
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Pro Ile Gln Gly Val Arg Trp His Cys Gln Asp Cys Pro Pro Glu Met	
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Ser Leu Asp Phe Cys Asp Ser Cys Ser Asp Cys Leu His Glu Thr Asp	
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 Tyr Thr Tyr Pro Glu Asn Trp Arg Ala Phe Lys Ala Leu Ile Ala Ala
 13 18 23 28
 cag tac agc ggg gct cat gtc cgc gtg ctc tcc gca cca ccc cac ttc 144
 Gln Tyr Ser Gly Ala His Val Arg Val Leu Ser Ala Pro Pro His Phe
 29 34 39 44
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 His Phe Gly Gln Thr Asn Arg Thr Pro Glu Phe Leu Arg Lys Phe Pro
 45 50 55 60
 gcc ggc aag gtc cca gca ttt gag ggt gat gat gga ttc tgt gtg ttt 240
 Ala Gly Lys Val Pro Ala Phe Glu Gly Asp Asp Gly Phe Cys Val Phe
 61 66 71 76
 gag agc aac gcc att gcc tac tat gtg agc aat gag gag ctg cgg gga 288
 Glu Ser Asn Ala Ile Ala Tyr Tyr Val Ser Asn Glu Glu Leu Arg Gly
 77 82 87 92

agc act cca gag gca gca gcc cag gtg gtg cag tgg gtg agc ttt gct	336
Ser Thr Pro Glu Ala Ala Ala Gln Val Val Gln Trp Val Ser Phe Ala	
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Asp Ser Asp Ile Val Pro Pro Ala Ser Thr Trp Val Phe Pro Thr Leu	
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Gly Ile Met His His Asn Lys Gln Ala Thr Glu Asn Ala Lys Glu Glu	
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Val Arg Arg Ile Leu Gly Leu Leu Asp Ala Tyr Leu Lys Thr Arg Thr	
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Phe Leu Val Gly Glu Arg Val Thr Leu Ala Asp Ile Thr Val Val Cys	
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Thr Leu Leu Trp Leu Tyr Lys Gln Val Leu Glu Pro Ser Phe Arg Gln	
173 178 183 188	
gcc ttt ccc aat acc aac cgc tgg ttc ctc acc tgc att aac cag ccc	624
Ala Phe Pro Asn Thr Asn Arg Trp Phe Leu Thr Cys Ile Asn Gln Pro	
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Gln Phe Arg Ala Val Leu Gly Glu Val Lys Leu Cys Glu Lys Met Ala	
205 210 215 220	
cag ttt gat gct aaa aag ttt gca gag acc caa cct aaa aag gac aca	720
Gln Phe Asp Ala Lys Lys Phe Ala Glu Thr Gln Pro Lys Lys Asp Thr	
221 226 231 236	
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237 242 247 252	
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Glu Arg Lys Glu Glu Lys Lys Ala Ala Ala Pro Ala Pro Glu Glu Glu	
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Met Asp Glu Cys Glu Gln Ala Leu Ala Ala Glu Pro Lys Ala Lys Asp	
269 274 279 284	
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Pro Phe Ala His Leu Pro Lys Ser Thr Phe Val Leu Asp Glu Phe Lys	
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Arg Lys Tyr Ser Asn Glu Asp Thr Leu Ser Val Ala Leu Pro Tyr Phe	
301 306 311 316	

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Trp Glu His Phe Asp Lys Asp Gly Trp Ser Leu Trp Tyr Ser Glu Tyr	
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349 354 359 364	
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Ser Val Ile Leu Phe Gly Thr Asn Asn Ser Ser Ser Ile Ser Gly Val	
365 370 375 380	
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cag gtg gac tac gag tca tac aca tgg cgg aaa ctg gat cct ggc agc	1248
Gln Val Asp Tyr Glu Ser Tyr Thr Trp Arg Lys Leu Asp Pro Gly Ser	
397 402 407 412	
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413 418 423 428	
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Leu Lys Glu Ile Arg Lys Phe Ala Met Lys Glu Met Gly Thr Pro Asp						
46 51 56 61						
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Val Arg Ile Asp Thr Arg Leu Asn Lys Ala Val Trp Ala Lys Gly Ile						
62 67 72 77						
agg aat gtg cca tac cga atc cgt gtg cgg ctg tcc aga aaa cgt aat	528					
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78 83 88 93						
gag gat gaa gat tca cca aat aag cta tat act ttg gtt acc tat gta	576					
Glu Asp Glu Asp Ser Pro Asn Lys Leu Tyr Thr Leu Val Thr Tyr Val						
94 99 104 109						
cct gtt acc act ttc aaa aat cta cag aca gtc aat gtg gat gag aac	624					
Pro Val Thr Thr Phe Lys Asn Leu Gln Thr Val Asn Val Asp Glu Asn						
110 115 120 125						
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*						
126						
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Met Asp Leu Lys Gly Glu Pro Gly Pro Pro Gly Lys Pro Gly Pro Trp		
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Gly Pro Pro Gly Pro Pro Gly Phe Pro Gly Lys Pro Gly His Gly Lys		
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Pro Gly Leu His Gly Gln Pro Gly Pro Ala Gly Pro Pro Gly Phe Ser		
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Arg Met Gly Lys Ala Gly Pro Pro Gly Leu Pro Gly Asn Val Gly Pro		
56 61 66 71		
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Pro Gly Gln Pro Gly Leu Arg Gly Glu Pro Gly Ile Arg Gly Asp Gln		
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Gly Leu Arg Gly Pro Pro Gly Pro Pro Gly Leu Pro Gly Pro Ser Gly		
88 93 98 103		
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Ile Thr Ile Pro Gly Lys Pro Gly Ala Gln Gly Val Pro Gly Pro Pro		
104 109 114 119		
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136 141 146 151		
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Pro Ala Gly Leu Gly Lys Pro Gly Leu Asp Gly Leu Pro Gly Ala Pro		
168 173 178 183		
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Gly 184	Asp	Lys	Gly	Glu	Ser 189	Gly	Pro	Pro	Gly	Val 194	Pro	Gly	Pro	Arg	Gly 199	
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Pro 264	Ala	Gly	Val	Pro	Gly 269	Leu	Leu	Gly	Asp	Arg 274	Gly	Glu	Pro	Gly	Glu 279	
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Asp 280	Gly	Glu	Pro	Gly	Glu 285	Gln	Gly	Pro	Gln	Gly 290	Leu	Gly	Gly	Pro	Pro 295	
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Gly 296	Leu	Pro	Gly	Ser	Ala 301	Gly	Leu	Pro	Gly	Arg 306	Arg	Gly	Pro	Pro	Gly 311	
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Pro 312	Lys	Gly	Glu	Ala	Gly 317	Pro	Gly	Gly	Pro	Pro 322	Gly	Val	Pro	Gly	Ile 327	
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Ala 376	Gly	Ala	Leu	Gly	Gln 381	Lys	Gly	Asp	Leu	Gly 386	Leu	Pro	Gly	Gln	Pro 391	
ggc	ctg	agg	ggt	ccc	tca	gga	atc	cca	gga	ctc	cag	ggt	cca	gct	ggc	1251
Gly 392	Leu	Arg	Gly	Pro	Ser 397	Gly	Ile	Pro	Gly	Leu 402	Gln	Gly	Pro	Ala	Gly 407	
cct	att	ggc	ccc	caa	ggc	ctg	ccg	ggc	ctg	aag	ggg	gaa	cca	ggc	ctg	1299
Pro	Ile	Gly	Pro	Gln	Gly	Leu	Pro	Gly	Leu	Lys	Gly	Glu	Pro	Gly	Leu	

408	413	418	423	
cca ggg ccc cct gga gag ggg aga gca ggg gaa cct ggc acg gct ggc				1347
Pro Gly Pro Pro Gly Glu Gly Arg Ala Gly Glu Pro Gly Thr Ala Gly				
424	429	434	439	
cca cgg ggg ccc cca ggg gtc cct ggc tcc cct gga atc acg ggg cct				1395
Pro Arg Gly Pro Pro Gly Val Pro Gly Ser Pro Gly Ile Thr Gly Pro				
440	445	450	455	
ccg ggg ctc ccg gga ccc cct ggt gcc cct ggg gcc ttc gat gag act				1443
Pro Gly Leu Pro Gly Pro Pro Gly Ala Pro Gly Ala Phe Asp Glu Thr				
456	461	466	471	
ggc atc gca ggc ttg cac ctg ccc aac ggc ggt gtg gag ggt gcc gtg				1491
Gly Ile Ala Gly Leu His Leu Pro Asn Gly Gly Val Glu Gly Ala Val				
472	477	482	487	
ctg ggc aag ggg ggc aag cca cag ttt ggg ctg ggc gag ctg tct gcc				1539
Leu Gly Lys Gly Gly Lys Pro Gln Phe Gly Leu Gly Glu Leu Ser Ala				
488	493	498	503	
cat gcc aca ccg gcc ttc act gcg gtg ctc acc tcg ccc tta ccc gcc				1587
His Ala Thr Pro Ala Phe Thr Ala Val Leu Thr Ser Pro Leu Pro Ala				
504	509	514	519	
tcg ggc atg ccc gtg aaa ttt gac cgg act ctc tac aat ggc cac agc				1635
Ser Gly Met Pro Val Lys Phe Asp Arg Thr Leu Tyr Asn Gly His Ser				
520	525	530	535	
ggc tac aac cca gcc act ggc atc ttc acc tgc cct gtg ggc ggc gtc				1683
Gly Tyr Asn Pro Ala Thr Gly Ile Phe Thr Cys Pro Val Gly Gly Val				
536	541	546	551	
tac tac ttt gct tac cat gtg cac gtc aag ggc acc aac gtg tgg gtg				1731
Tyr Tyr Phe Ala Tyr His Val His Val Lys Gly Thr Asn Val Trp Val				
552	557	562	567	
gcc ctg tac aag aac aac gtg ccg gcc acc tat acc tac gat gag tac				1779
Ala Leu Tyr Lys Asn Asn Val Pro Ala Thr Tyr Thr Tyr Asp Glu Tyr				
568	573	578	583	
aag aag ggc tac ctg gac cag gca tct ggt ggg gcc gtg ctc cag ctg				1827
Lys Lys Gly Tyr Leu Asp Gln Ala Ser Gly Gly Ala Val Leu Gln Leu				
584	589	594	599	
cgg ccc aac gac cag gtc tgg gtg cag atg ccg tcg gac cag gcc aac				1875
Arg Pro Asn Asp Gln Val Trp Val Gln Met Pro Ser Asp Gln Ala Asn				
600	605	610	615	
ggc ctc tac tcc acg gag tac atc cac tcc tcc ttt tca gga ttc ttg				1923
Gly Leu Tyr Ser Thr Glu Tyr Ile His Ser Ser Phe Ser Gly Phe Leu				
616	621	626	631	
ctc tgc ccc aca taa cccgcggggg gtgtcctgct gccctggcct cctccccctt				1978
Leu Cys Pro Thr *				
632				

agtggtagag cgaccttttc aattacaaag aacctcctgg aaaaaaaaaac aaaagctgaa 2038
 cagaggcggc cgtggccttg gcccaggag actaacttgc tttctccctg catgcaggct 2098
 gagattgttt ctggaagggg ctggcctgag tttctttccc ccaaattgtct gtgcagtgtc 2158
 agggctgcac cccataggcc ctgaggcaca cagcccagcc ccttgtgagt cctggcctct 2218
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 ggaggaggga gggcgccccc cgacccttaa ccagagcgag gttgttgctt tgtgtccaca 180
 gggaccagga gcgaaccatg atgccaggta ggaggggctg actggggcct gcgagcgcgt 240
 gcctttcctg ctgggcagag gccctccaca tggggccacg cgggcccggc acaggagggc 300
 agtcagatgg gcagggcctg agagcctccc tctctcctt aggtccctaa tc atg 355
 Met
 1

gac tcc cca aga gct ggc acc cac cag ggc ccc ctc gat gca gag aca 403
 Asp Ser Pro Arg Ala Gly Thr His Gln Gly Pro Leu Asp Ala Glu Thr
 2 7 12 17

gag gtc ggt gct gac cgc tgc acg tcg act gcc tac cag gag cag agg 451
 Glu Val Gly Ala Asp Arg Cys Thr Ser Thr Ala Tyr Gln Glu Gln Arg
 18 23 28 33

ccc cag gtg gag caa gtt ggc aaa cag gct cct ctc tcc cca ggg ctg 499
 Pro Gln Val Glu Gln Val Gly Lys Gln Ala Pro Leu Ser Pro Gly Leu
 34 39 44 49

ccg gca atg ggg ggg cct ggc ccc ggc ccc tgt gag gac ccc gcg ggt 547
 Pro Ala Met Gly Gly Pro Gly Pro Gly Pro Cys Glu Asp Pro Ala Gly
 50 55 60 65

gct ggg gga gca ggt gca ggg ggc tcc gag ccc ctg gtg act gtc acc 595

Ala	Gly	Gly	Ala	Gly	Ala	Gly	Gly	Ser	Glu	Pro	Leu	Val	Thr	Val	Thr		
66					71					76					81		
gtg	cag	tgc	gcc	ttc	aca	gtg	gcc	ctg	agg	gca	cga	aga	gga	gcc	gac	643	
Val	Gln	Cys	Ala	Phe	Thr	Val	Ala	Leu	Arg	Ala	Arg	Arg	Gly	Ala	Asp		
82					87					92					97		
ctg	tcc	agc	ctg	cgg	gca	ctg	ctg	ggc	caa	gcc	ctc	cct	cac	cag	gcc	691	
Leu	Ser	Ser	Leu	Arg	Ala	Leu	Leu	Gly	Gln	Ala	Leu	Pro	His	Gln	Ala		
98					103					108					113		
cag	ctt	ggg	caa	ctc	agt	tac	cta	gcc	cca	ggt	gag	gac	ggg	cac	tgg	739	
Gln	Leu	Gly	Gln	Leu	Ser	Tyr	Leu	Ala	Pro	Gly	Glu	Asp	Gly	His	Trp		
114					119					124					129		
gtc	ccc	atc	ccc	gag	gag	gag	tcg	ctg	cag	agg	gcc	tgg	cag	gac	gca	787	
Val	Pro	Ile	Pro	Glu	Glu	Glu	Ser	Leu	Gln	Arg	Ala	Trp	Gln	Asp	Ala		
130					135					140					145		
gct	gcc	tgc	ccc	agg	ggg	ctg	cag	ctg	cag	tgc	agg	gga	gcc	ggg	ggt	835	
Ala	Ala	Cys	Pro	Arg	Gly	Leu	Gln	Leu	Gln	Cys	Arg	Gly	Ala	Gly	Gly		
146					151					156					161		
cgg	ccg	gtc	ctc	tac	cag	gtg	gtg	gcc	cag	cac	agc	tac	tcc	gcc	cag	883	
Arg	Pro	Val	Leu	Tyr	Gln	Val	Val	Ala	Gln	His	Ser	Tyr	Ser	Ala	Gln		
162					167					172					177		
ggg	cca	gag	gac	ctg	ggc	ttc	cga	cag	ggg	gac	acg	gtg	gac	gtc	ctg	931	
Gly	Pro	Glu	Asp	Leu	Gly	Phe	Arg	Gln	Gly	Asp	Thr	Val	Asp	Val	Leu		
178					183					188					193		
tgt	gaa	gtg	gac	cag	gca	tgg	ctg	gag	ggc	cac	tgt	gac	ggc	cgc	atc	979	
Cys	Glu	Val	Asp	Gln	Ala	Trp	Leu	Glu	Gly	His	Cys	Asp	Gly	Arg	Ile		
194					199					204					209		
ggc	atc	ttc	ccc	aag	tgc	ttc	gtg	gtc	ccc	gcc	ggc	cct	cgg	atg	tca	1027	
Gly	Ile	Phe	Pro	Lys	Cys	Phe	Val	Val	Pro	Ala	Gly	Pro	Arg	Met	Ser		
210					215					220					225		
gga	gcc	ccc	ggc	cgc	ctg	ccc	cga	tcc	cag	cag	gga	gat	cag	ccc	taa	1075	
Gly	Ala	Pro	Gly	Arg	Leu	Pro	Arg	Ser	Gln	Gln	Gly	Asp	Gln	Pro	*		
226					231					236					241		
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 <222> (694)..(1779)

<400> 127

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gcggatgcac acaaatgaaa ccctcacttc aacctgaaga cattcgcaca tgagttacgt	180
agaggggacct gcaggaagcg gtagagaaaa cataaggctt atgcgtttta tttccacacc	240
aatttcagga tctttgtcac tgacagcagc actaagactt gttaacttta tatagttaag	300
aagaacaagg ctgagcgcg tgactcacgc ctgtaagcct agaacttttg gagggcaaag	360
caggcagact gcttgagccc aggagttcca gaccagcctg ggcaacatgg caacacccca	420
tctctacaaa aaaatacaag aatcagctgg gcgtggtgat gtgttcctgt aatctcagct	480
actcgggagg cagaggcagg aggattgctt gaaccocggga ggagagggtt gtagttagcc	540
gagatctcgc cactgcactc cagtctggac gacagagtga gactcagtct caaataaata	600
aataaatata taaatataag gaaaaaaata aagctgcttt ctctcttcc tctcttttg	660
tctcatctgg ctctgctcca ggcactgccc aca atg tgg gtg ctt aca cct gct	714
Met Trp Val Leu Thr Pro Ala	
1 5	
gct ttt gct ggg aag ctc ttg agt gtg ttc agg caa cct ctg agc tct	762
Ala Phe Ala Gly Lys Leu Leu Ser Val Phe Arg Gln Pro Leu Ser Ser	
8 13 18 23	
ctg tgg agg agc ctg gtc ccg ctg ttc tgc tgg ctg agg gca acc ttc	810
Leu Trp Arg Ser Leu Val Pro Leu Phe Cys Trp Leu Arg Ala Thr Phe	
24 29 34 39	
tgg ctg cta gct acc aag agg aga aag cag cag ctg gtc ctg aga ggg	858
Trp Leu Leu Ala Thr Lys Arg Arg Lys Gln Gln Leu Val Leu Arg Gly	
40 45 50 55	
cca gat gag acc aaa gag gag gaa gag gac cct cct ctg ccc acc acc	906
Pro Asp Glu Thr Lys Glu Glu Glu Glu Asp Pro Pro Leu Pro Thr Thr	
56 61 66 71	
cca acc agc gtc aac tat cac ttc act cgc cag tgc aac tac aaa tgc	954
Pro Thr Ser Val Asn Tyr His Phe Thr Arg Gln Cys Asn Tyr Lys Cys	
72 77 82 87	
ggc ttc tgt ttc cac aca gcc aaa aca tcc ttt gtg ctg ccc ctt gag	1002
Gly Phe Cys Phe His Thr Ala Lys Thr Ser Phe Val Leu Pro Leu Glu	
88 93 98 103	
gaa gca aag aga gga ttg ctt ttg ctt aag gaa gct ggt atg gag aag	1050
Glu Ala Lys Arg Gly Leu Leu Leu Leu Lys Glu Ala Gly Met Glu Lys	
104 109 114 119	
atc aac ttt tca ggt gga gag cca ttt ctt caa gac cgg gga gaa tac	1098
Ile Asn Phe Ser Gly Gly Glu Pro Phe Leu Gln Asp Arg Gly Glu Tyr	

120	125	130	135	
ctg ggc aag ttg gtg agg ttc tgc aaa gta gag ttg cgg ctg ccc agc				1146
Leu Gly Lys Leu Val Arg Phe Cys Lys Val Glu Leu Arg Leu Pro Ser				
136	141	146	151	
gtg acg atc gtg agc aat gga agc ctg atc cgg gag agg tgg ttc cag				1194
Val Thr Ile Val Ser Asn Gly Ser Leu Ile Arg Glu Arg Trp Phe Gln				
152	157	162	167	
aat tat ggt gag tat ttg gac att ctc gct atc tcc tgt gac agc ttt				1242
Asn Tyr Gly Glu Tyr Leu Asp Ile Leu Ala Ile Ser Cys Asp Ser Phe				
168	173	178	183	
gac gag gaa gtc aat gtc ctt att ggc cgt ggc caa gga aag aag aac				1290
Asp Glu Glu Val Asn Val Leu Ile Gly Arg Gly Gln Gly Lys Lys Asn				
184	189	194	199	
cat gtg gaa aac ctt caa aag ctg agg agg tgg tgt agg gat tat aga				1338
His Val Glu Asn Leu Gln Lys Leu Arg Arg Trp Cys Arg Asp Tyr Arg				
200	205	210	215	
gtc gct ttc aag ata aat tct gtc att aat cgt ttc aac gtg gaa gag				1386
Val Ala Phe Lys Ile Asn Ser Val Ile Asn Arg Phe Asn Val Glu Glu				
216	221	226	231	
gac atg acg gaa cag atc aaa gca cta aac cct gtc cgc tgg aaa gtg				1434
Asp Met Thr Glu Gln Ile Lys Ala Leu Asn Pro Val Arg Trp Lys Val				
232	237	242	247	
ttc cag tgc ctc tta att gag ggt gag aat tgt gga gaa gat gct cta				1482
Phe Gln Cys Leu Leu Ile Glu Gly Glu Asn Cys Gly Glu Asp Ala Leu				
248	253	258	263	
aga gaa gca gaa aga ttt gtt att ggt gat gaa gaa ttt gaa aga ttc				1530
Arg Glu Ala Glu Arg Phe Val Ile Gly Asp Glu Glu Phe Glu Arg Phe				
264	269	274	279	
ttg gag cgc cac aaa gaa gtg tcc tgc ttg gtg cct gaa tct aac cag				1578
Leu Glu Arg His Lys Glu Val Ser Cys Leu Val Pro Glu Ser Asn Gln				
280	285	290	295	
aag atg aaa gac tcc tac ctt att ctg gat gaa tat atg cgc ttt ctg				1626
Lys Met Lys Asp Ser Tyr Leu Ile Leu Asp Glu Tyr Met Arg Phe Leu				
296	301	306	311	
aac tgt aga aag gga cgg aag gac cct tcc aag tcc atc ctg gat gtt				1674
Asn Cys Arg Lys Gly Arg Lys Asp Pro Ser Lys Ser Ile Leu Asp Val				
312	317	322	327	
ggt gta gaa gaa gct ata aaa ttc agt gga ttt gat gaa aag atg ttt				1722
Gly Val Glu Glu Ala Ile Lys Phe Ser Gly Phe Asp Glu Lys Met Phe				
328	333	338	343	
ctg aag cga gga gga aaa tac ata tgg agt aag gct gat ctg aag ctg				1770
Leu Lys Arg Gly Gly Lys Tyr Ile Trp Ser Lys Ala Asp Leu Lys Leu				
344	349	354	359	

gat tgg tag agcggaa agtggaaacga gacttcaaca caccagtggg aaaactccta	1826
Asp Trp *	
360	
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attttctgct gcacgtggca tctgattacc tgtggtcact gaacacacga ataacttgga	1946
tagcaaatcc tgagacaatg gaaaaccatt aactttaactt cattggctta taaccttggt	2006
gttattgaaa cagcacttct gtttttgagt ttgttttagc taaaaagaag gaatacacac	2066
aggaataatg accccaaaaa tgcttagata agggccctat acacaggacc tgacatttag	2126
ctcaatgatg cgtttgtaag aaataagctc tagtgatata tgtgggggca atatttaatt	2186
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<213> Homo sapiens

<220>

<221> CDS

<222> (480) .. (3572)

<400> 128

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tgcccc	ctgt	cccccc	cccc	tggtcccc	ca	ctgcttt	acc	tcttgctt	tg	cagcctt	180
tcctcac	agc	cttcct	gtgg	ctgtgtt	ttt	ggccct	gata	gccccat	ggc	acaact	240
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ctcacct	atg	tcagcc	aggt	gagcac	atac	gttgct	gaca	ggaggc	ggag	cttgca	479
atg	ggc	ttt	gac	ctg	cag	aac	gtc	tgg	aga	gtc	527
Met	Gly	Phe	Asp	Leu	Gln	Asn	Val	Trp	Arg	Val	
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aac	tac	aaa	ttg	tgc	ccc	agt	tac	ccc	cag	aag	575
Asn	Tyr	Lys	Leu	Cys	Pro	Ser	Tyr	Pro	Gln	Lys	
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tgg	atc	act	gac	aaa	gag	ctg	gag	aac	gtg	gct	623
Trp	Ile	Thr	Asp	Lys	Glu	Leu	Glu	Asn	Val	Ala	
33					38				43		48
aag	cgg	att	ccc	gtg	gtt	gtg	tat	aga	cac	ttg	671
Lys	Arg	Ile	Pro	Val	Val	Val	Tyr	Arg	His	Leu	
49					54				59		64
atc	gcc	cgc	tgc	agc	cag	cca	gag	atc	agc	tgg	719
Ile	Ala	Arg	Cys	Ser	Gln	Pro	Glu	Ile	Ser	Trp	
65					70				75		80
gct	gat	gat	gag	tac	ctg	gtc	acg	tcc	att	gct	767
Ala	Asp	Asp	Glu	Tyr	Leu	Val	Thr	Ser	Ile	Ala	
81					86				91		96
gac	ccg	ggg	aca	agg	gcc	act	ggg	ggc	tcc	ctc	815
Asp	Pro	Gly	Thr	Arg	Ala	Thr	Gly	Gly	Ser	Leu	
97					102				107		112
gat	acc	agc	gag	gcg	tgt	gat	gct	gac	ttt	gat	863
Asp	Thr	Ser	Glu	Ala	Cys	Asp	Ala	Asp	Phe	Asp	
113					118				123		128
tgc	tct	gga	gtg	gag	agc	aca	gca	gct	cct	caa	911
Cys	Ser	Gly	Val	Glu	Ser	Thr	Ala	Ala	Pro	Gln	
129					134				139		144

gat gcg cga tcc tac acg gca gca gtg gcc aac cgg gcc aag ggt gga	959
Asp Ala Arg Ser Tyr Thr Ala Ala Val Ala Asn Arg Ala Lys Gly Gly	
145 150 155 160	
ggc tgt gaa tgt gaa gag tac tat ccc aac tgt gag gtc gtg ttc atg	1007
Gly Cys Glu Cys Glu Glu Tyr Tyr Pro Asn Cys Glu Val Val Phe Met	
161 166 171 176	
gga atg gcc aac atc cat gcc atc cgg aac agc ttt cag tac ctc cgg	1055
Gly Met Ala Asn Ile His Ala Ile Arg Asn Ser Phe Gln Tyr Leu Arg	
177 182 187 192	
gct gtg tgt agc cag atg ccg gat cct agc aac tgg ttg tcg gca ctg	1103
Ala Val Cys Ser Gln Met Pro Asp Pro Ser Asn Trp Leu Ser Ala Leu	
193 198 203 208	
gag agt acc aaa tgg ctg cag cac ttg tcg gtg atg cta aaa gca gct	1151
Glu Ser Thr Lys Trp Leu Gln His Leu Ser Val Met Leu Lys Ala Ala	
209 214 219 224	
gtg ctg gtg gct aat aca gta gac cgg gaa ggc cgg cct gtg ctg gta	1199
Val Leu Val Ala Asn Thr Val Asp Arg Glu Gly Arg Pro Val Leu Val	
225 230 235 240	
cac tgc tca gat ggc tgg gac cgc aca ccg cag atc gta gcc ctg gcc	1247
His Cys Ser Asp Gly Trp Asp Arg Thr Pro Gln Ile Val Ala Leu Ala	
241 246 251 256	
aaa ata tta ctg gac cca tat tac agg acg ttg gag ggc ttc caa gtg	1295
Lys Ile Leu Leu Asp Pro Tyr Tyr Arg Thr Leu Glu Gly Phe Gln Val	
257 262 267 272	
tta gtg gag tct gac tgg ctg gat ttt ggg cac aag ttt gga gat cgc	1343
Leu Val Glu Ser Asp Trp Leu Asp Phe Gly His Lys Phe Gly Asp Arg	
273 278 283 288	
tgt ggc cac caa gag aat gtg gag gac caa aac gaa caa tgc cct gtg	1391
Cys Gly His Gln Glu Asn Val Glu Asp Gln Asn Glu Gln Cys Pro Val	
289 294 299 304	
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Phe Leu Gln Trp Leu Asp Ser Val His Gln Leu Leu Lys Gln Phe Pro	
305 310 315 320	
tgc atg ttt gaa ttt aat gaa gca ttc ctg gta aaa ctg gtg caa cac	1487
Cys Met Phe Glu Phe Asn Glu Ala Phe Leu Val Lys Leu Val Gln His	
321 326 331 336	
aca tac tcc tgc ctc tac ggc acc ttc ctg gcc aac aac ccc tgt gag	1535
Thr Tyr Ser Cys Leu Tyr Gly Thr Phe Leu Ala Asn Asn Pro Cys Glu	
337 342 347 352	
cga gag aag cgc aac atc tac aag cgg acc tgc tct gtg tgg gcg ctc	1583
Arg Glu Lys Arg Asn Ile Tyr Lys Arg Thr Cys Ser Val Trp Ala Leu	
353 358 363 368	

ctt cga gct ggc aat aaa aac ttt cat aac ttc ctc tac aca ccc agc	1631
Leu Arg Ala Gly Asn Lys Asn Phe His Asn Phe Leu Tyr Thr Pro Ser	
369 374 379 384	
tca gac atg gtc ctg cat cct gtt tgt cat gtc cgg gcc ctg cac ctc	1679
Ser Asp Met Val Leu His Pro Val Cys His Val Arg Ala Leu His Leu	
385 390 395 400	
tgg aca gct gtt tat ctg cca gca tca tct cca tgc aca ctt ggg gaa	1727
Trp Thr Ala Val Tyr Leu Pro Ala Ser Ser Pro Cys Thr Leu Gly Glu	
401 406 411 416	
gaa aac atg gat ctt tac ctt tcc cca gtg gcc cag agc cag gag ttc	1775
Glu Asn Met Asp Leu Tyr Leu Ser Pro Val Ala Gln Ser Gln Glu Phe	
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Pro	Gln	Gln	Ala	Gln	Pro	Asp	Ser	Met	Leu	Gly	Val	Pro	Ser	Lys	Cys		
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Ala Gly Tyr Lys Gln Glu Val Glu Gln Leu Arg Arg Gln Val Arg Glu				
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Ile Thr Thr Pro Lys Asn Phe Lys Gly Lys Glu Asp Lys Ile Leu Thr				
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Gly Pro Ser Thr Asn Thr Gln Ser Gly Leu Phe Asn Thr Pro Pro Pro	
223 228 233 238	
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Thr Pro Pro Asp Leu Asn Gln Asp Phe Ser Gly Phe Gln Leu Leu Val	
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gat gtt gca ctc aaa cgg gct gca gag atg gag ctt cag gca aaa ctt	1118
Asp Val Ala Leu Lys Arg Ala Ala Glu Met Glu Leu Gln Ala Lys Leu	
255 260 265 270	
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Thr Ala *	
271	
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cgggcacctg cgcgggcgccg ggtgaaggcg agagcctcgg cgagccctct gcagcggagc      180
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Ser Arg Pro Leu Ser Arg Leu Pro Gly Lys Thr Leu Ser Ala Cys Asp
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Arg Glu Asn Gly Ala Arg Arg Pro Leu Leu Leu Gly Ser Thr Ser Phe
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atc ccg att ggc cgt cgg act tat gcc agt gcg gcg gag ccg gtt ggc      558
Ile Pro Ile Gly Arg Arg Thr Tyr Ala Ser Ala Ala Glu Pro Val Gly
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agc aaa gct gtc ctg gtc aca ggc tgt gac tct gga ttt ggg ttc tca      606
Ser Lys Ala Val Leu Val Thr Gly Cys Asp Ser Gly Phe Gly Phe Ser
  55                60                65                70

ttg gcc aag cat ctg cat tca aaa ggc ttc ctt gtg ttt gct ggc tgc      654
Leu Ala Lys His Leu His Ser Lys Gly Phe Leu Val Phe Ala Gly Cys
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ttg atg aag gac aaa ggc cat gat ggg gtc aag gag ctg gac agc cta      702
Leu Met Lys Asp Lys Gly His Asp Gly Val Lys Glu Leu Asp Ser Leu
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aac agt gac cga ttg aga acc gtc cag ctc aat gtc tgc agc agc gaa      750
Asn Ser Asp Arg Leu Arg Thr Val Gln Leu Asn Val Cys Ser Ser Glu
 103                108                113                118

gag gtg gag aaa gtg gtg gag att gtc cgc tcg agc ctg aag gac cct      798
Glu Val Glu Lys Val Val Glu Ile Val Arg Ser Ser Leu Lys Asp Pro
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Gly Glu Val Glu Phe Thr Ser Leu Glu Thr Tyr Lys Gln Val Ala Glu	
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Val Asn Leu Trp Gly Thr Val Arg Met Thr Lys Ser Phe Leu Pro Leu	
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Ile Arg Arg Ala Lys Gly Arg Val Val Asn Ile Ser Ser Met Leu Gly	
183 188 193 198	
cgc atg gcc aac ccg gcc cgc tcc ccg tac tgc atc acc aag ttc ggg	1038
Arg Met Ala Asn Pro Ala Arg Ser Pro Tyr Cys Ile Thr Lys Phe Gly	
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Val Glu Ala Phe Ser Asp Cys Leu Arg Tyr Glu Met Tyr Pro Leu Gly	
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Val Lys Val Ser Val Val Glu Pro Gly Asn Phe Ile Ala Ala Thr Ser	
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Leu Tyr Ser Pro Glu Ser Ile Gln Ala Ile Ala Lys Lys Met Trp Glu	
247 252 257 262	
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Glu Leu Pro Glu Val Val Arg Lys Asp Tyr Gly Lys Lys Tyr Phe Asp	
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Glu Lys Ile Ala Lys Met Glu Thr Tyr Cys Ser Ser Gly Ser Thr Asp	
279 284 289 294	
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Thr Ser Pro Val Ile Asp Ala Val Thr His Ala Leu Thr Ala Thr Thr	
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Pro Tyr Thr Arg Tyr His Pro Met Asp Tyr Tyr Trp Trp Leu Arg Met	
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Gln Ile Met Thr His Leu Pro Gly Ala Ile Ser Asp Met Ile Tyr Ile	
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Arg *	
343	

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 ccgggcccga gagcacggcg gcgggagcgc ggccttagga ggccggccga gcgggtggga 180
 cagctcggcg cggagcgtcc tgtcaggcgg cgcccgaggg cgtcgaggac tctccccgcg 240
 atg atg ccg atg ata tta act gtt ttc ttg agc aac aat gaa cag att 288
 Met Met Pro Met Ile Leu Thr Val Phe Leu Ser Asn Asn Glu Gln Ile
 1 5 10 15
 tta aca gaa gtt cct ata aca ccg gaa aca acc tgt cga gat gtt gta 336
 Leu Thr Glu Val Pro Ile Thr Pro Glu Thr Thr Cys Arg Asp Val Val
 17 22 27 32
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 Glu Phe Cys Lys Glu Pro Gly Glu Gly Ser Cys His Leu Ala Glu Val
 33 38 43 48
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 Trp Arg Gly Asn Glu Arg Pro Ile Pro Phe Asp His Met Met Tyr Glu
 49 54 59 64
 cat ctt cag aaa tgg ggt cca cgg agg gaa gaa gtg aaa ttt ttc ctt 480
 His Leu Gln Lys Trp Gly Pro Arg Arg Glu Glu Val Lys Phe Phe Leu
 65 70 75 80
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 Arg His Glu Asp Ser Pro Thr Glu Asn Ser Glu Gln Gly Gly Arg Gln
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 acc caa gag caa cga act cag aga aat gta ata aat gta cct gga gaa 576
 Thr Gln Glu Gln Arg Thr Gln Arg Asn Val Ile Asn Val Pro Gly Glu

97	102	107	112	
aaa cgt act gaa aat ggg gtt ggg aat cca cgt gtt gaa ctt acc ctc				624
Lys Arg Thr Glu Asn Gly Val Gly Asn Pro Arg Val Glu Leu Thr Leu				
113	118	123	128	
tca gag ctc caa gat atg gca gct agg caa cag cag cag att gaa aat				672
Ser Glu Leu Gln Asp Met Ala Ala Arg Gln Gln Gln Gln Ile Glu Asn				
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Gln Gln Gln Met Leu Val Ala Lys Glu Gln Arg Leu His Phe Leu Lys				
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Gln Gln Glu Arg Arg Gln Gln Gln Ser Ile Ser Glu Asn Glu Lys Leu				
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cag aaa ttg aaa gaa cga gtt gaa gcc cag gag aac aag ctg aag aaa				816
Gln Lys Leu Lys Glu Arg Val Glu Ala Gln Glu Asn Lys Leu Lys Lys				
177	182	187	192	
att cgt gca atg aga gga caa gtc gac tac agc aaa atc atg aac ggc				864
Ile Arg Ala Met Arg Gly Gln Val Asp Tyr Ser Lys Ile Met Asn Gly				
193	198	203	208	
aat ctg tct gct gaa ata gaa agg ttc agt gcc atg ttc cag gaa aag				912
Asn Leu Ser Ala Glu Ile Glu Arg Phe Ser Ala Met Phe Gln Glu Lys				
209	214	219	224	
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Lys Gln Glu Val Gln Thr Ala Ile Leu Arg Val Asp Gln Leu Ser Gln				
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257	262	267	272	
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Gln Pro Val Pro Phe Ser Ala Leu Gly Pro Thr Glu Lys Pro Gly Ile	
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Glu Ile Gly Lys Val Pro Pro Pro Ile Pro Gly Val Gly Lys Gln Leu	
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Pro Pro Ser Tyr Gly Thr Tyr Pro Ser Pro Thr Pro Leu Gly Pro Gly	
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Ser Thr Ser Ser Leu Glu Arg Arg Lys Glu Gly Ser Leu Pro Arg Pro	
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Ser Ala Gly Leu Pro Ser Arg Gln Arg Pro Thr Leu Leu Pro Ala Thr	
497 502 507 512	
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Gly Ser Thr Pro Gln Pro Gly Ser Ser Gln Gln Ile Gln Gln Arg Ile	
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Pro Ala Gly Asp Ser Lys Pro Glu Leu Pro Leu Thr Val Ala Ile Arg	
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Pro Phe Leu Ala Asp Lys Gly Ser Arg Pro Gln Ser Pro Arg Lys Gly	
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Glu	Leu	Pro	Ser	Pro	Glu	Pro	Glu	Glu	Leu	Ile	Cys	Pro	Gln	Thr	Thr		
801					806					811					816		
cac	caa	act	gcc	gag	ccg	gca	gag	gac	aat	aac	aac	aac	gtg	gcc	acg	2736	
His	Gln	Thr	Ala	Glu	Pro	Ala	Glu	Asp	Asn	Asn	Asn	Asn	Val	Ala	Thr		
817					822					827					832		
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Val	Pro	Thr	Thr	Glu	Gln	Ile	Pro	Ser	Pro	Val	Ala	Glu	Ala	Pro	Ser		
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Pro	Gly	Glu	Glu	Gln	Val	Pro	Pro	Ala	Pro	Leu	Pro	Pro	Ala	Ser	His		
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Pro	Pro	Ala	Thr	Ser	Thr	Asn	Lys	Arg	Thr	Asn	Leu	Lys	Lys	Pro	Asn		
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Thr	Pro	Leu	His	Asn	Ala	Val	Cys	Ala	Gly	His	His	His	Ile	Val	Lys		
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Ile	Gln	Cys	Ser	Gln	Phe	Leu	Tyr	Gly	Val	Gln	Glu	Lys	Leu	Gly	Val		

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Met His Val
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gat atg gat tgc ttc ttt gta tca gtg ggt ata cga aat aga cca gat 163
Asp Met Asp Cys Phe Phe Val Ser Val Gly Ile Arg Asn Arg Pro Asp
4 9 14 19
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Leu Lys Gly Lys Pro Val Ala Val Thr Ser Asn Arg Gly Thr Gly Arg
20 25 30 35
gca cct tta cgt cct ggc gct aac ccc cag ctg gag tgg cag tat tac 259
Ala Pro Leu Arg Pro Gly Ala Asn Pro Gln Leu Glu Trp Gln Tyr Tyr
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Gln Asn Lys Ile Leu Lys Gly Lys Ala Asp Ile Pro Asp Ser Ser Leu
52 57 62 67
tgg gag aat cca gat tct gcg caa gca aat gga att gat tct gtt ttg 355
Trp Glu Asn Pro Asp Ser Ala Gln Ala Asn Gly Ile Asp Ser Val Leu
68 73 78 83
tca agg gct gaa att gca tct tgt agt tat gag gcc agg caa ctt ggc 403
Ser Arg Ala Glu Ile Ala Ser Cys Ser Tyr Glu Ala Arg Gln Leu Gly
84 89 94 99
att aag aac gga atg ttt ttt ggg cat gct aaa caa cta tgt cct aat 451

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Thr	Leu	Tyr	Glu	Thr	Leu	Ala	Ser	Tyr	Thr	His	Asn	Ile	Glu	Ala	Val		
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Ser	Cys	Asp	Glu	Ala	Leu	Val	Asp	Ile	Thr	Glu	Ile	Leu	Ala	Glu	Thr		
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Lys	Leu	Thr	Pro	Asp	Glu	Phe	Ala	Asn	Ala	Val	Arg	Met	Glu	Ile	Lys		
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Leu	Ala	Arg	Met	Ala	Thr	Arg	Lys	Ala	Lys	Pro	Asp	Gly	Gln	Tyr	His		
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cta	aaa	cca	gaa	gaa	gta	gat	gat	ttt	atc	aga	ggc	cag	cta	gtg	acc	787	
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Gln	Lys	Glu	Phe	Gly	Pro	Lys	Thr	Gly	Gln	Met	Leu	Tyr	Arg	Phe	Cys		
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Arg	Gly	Leu	Asp	Asp	Arg	Pro	Val	Arg	Thr	Glu	Lys	Glu	Arg	Lys	Ser		
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Val	Ser	Ala	Glu	Ile	Asn	Tyr	Gly	Ile	Arg	Phe	Thr	Gln	Pro	Lys	Glu		
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gca	gaa	gct	ttt	ctt	ctg	agt	ctt	tca	gaa	gaa	att	caa	aga	aga	cta	1075	
Ala	Glu	Ala	Phe	Leu	Leu	Ser	Leu	Ser	Glu	Glu	Ile	Gln	Arg	Arg	Leu		
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gaa	gcc	act	ggc	atg	aag	ggg	aaa	cgt	cta	act	ctc	aaa	atc	atg	gta	1123	
Glu	Ala	Thr	Gly	Met	Lys	Gly	Lys	Arg	Leu	Thr	Leu	Lys	Ile	Met	Val		

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cga aag cct ggg gct cct gta gaa act gca aaa ttt gga ggc cat gga				1171
Arg Lys Pro Gly Ala Pro Val Glu Thr Ala Lys Phe Gly Gly His Gly				
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att tgt gat aac att gcc agg act gta act ctt gac cag gca aca gat				1219
Ile Cys Asp Asn Ile Ala Arg Thr Val Thr Leu Asp Gln Ala Thr Asp				
356	361	366	371	
aat gca aaa ata att gga aag gcg atg cta aac atg ttt cat aca atg				1267
Asn Ala Lys Ile Ile Gly Lys Ala Met Leu Asn Met Phe His Thr Met				
372	377	382	387	
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Lys Leu Asn Ile Ser Asp Met Arg Gly Val Gly Ile His Val Asn Gln				
388	393	398	403	
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Leu Val Pro Thr Asn Leu Asn Pro Ser Thr Cys Pro Ser Arg Pro Ser				
404	409	414	419	
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Val Gln Ser Ser His Phe Pro Ser Gly Ser Tyr Ser Val Arg Asp Val				
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Phe Gln Val Gln Lys Ala Lys Lys Ser Thr Glu Glu Glu His Lys Glu				
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gta ttt cgg gct gct gtg gat ctg gaa ata tca tct gct tct aga act				1507
Val Phe Arg Ala Ala Val Asp Leu Glu Ile Ser Ser Ala Ser Arg Thr				
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tgc act ttc ttg cca cct ttt cct gca cat ctg ccg acc agt cct gat				1555
Cys Thr Phe Leu Pro Pro Phe Pro Ala His Leu Pro Thr Ser Pro Asp				
468	473	478	483	
act aac aag gct gag tct tca ggg aaa tgg aat ggt cta cat act cct				1603
Thr Asn Lys Ala Glu Ser Ser Gly Lys Trp Asn Gly Leu His Thr Pro				
484	489	494	499	
gtc agt gtg cag tcg aga ctt aac ctg agt ata gag gtc ccg tca cct				1651
Val Ser Val Gln Ser Arg Leu Asn Leu Ser Ile Glu Val Pro Ser Pro				
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tcc cag ctg gat cag tct gtt tta gaa gca ctt cca cct gat ctg ccg				1699
Ser Gln Leu Asp Gln Ser Val Leu Glu Ala Leu Pro Pro Asp Leu Arg				
516	521	526	531	
gaa caa gta gag caa gtc tgt gct gtc cag caa gca gag tca cat ggc				1747
Glu Gln Val Glu Gln Val Cys Ala Val Gln Gln Ala Glu Ser His Gly				
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Asp Lys Lys Lys Glu Pro Val Asn Gly Cys Asn Thr Gly Ile Leu Pro				
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Gln Pro Val Gly Thr Val Leu Leu Gln Ile Pro Glu Pro Gln Glu Ser	
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Asn Ser Asp Ala Gly Ile Asn Leu Ile Ala Leu Pro Ala Phe Ser Gln	
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Val Asp Pro Glu Val Phe Ala Ala Leu Pro Ala Glu Leu Gln Arg Glu	
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Leu Lys Ala Ala Tyr Asp Gln Arg Gln Arg Gln Gly Glu Asn Ser Thr	
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His Gln Gln Ser Ala Ser Ala Ser Val Pro Lys Asn Pro Leu Leu His	
628 633 638 643	
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Ile Gly Ser Pro Lys Arg Ile Gln Ser Pro Leu Asn Asn Lys Leu Leu	
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aac agt cct gca aaa act ctg cca ggg gcc tgt ggc agt ccc cag aag	2179
Asn Ser Pro Ala Lys Thr Leu Pro Gly Ala Cys Gly Ser Pro Gln Lys	
676 681 686 691	
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Leu Ile Asp Gly Phe Leu Lys His Glu Gly Pro Pro Ala Glu Lys Pro	
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Leu Glu Glu Leu Ser Ala Ser Thr Ser Gly Val Pro Gly Leu Ser Ser	
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Leu Gln Ser Asp Pro Ala Gly Cys Val Arg Pro Pro Ala Pro Asn Leu	
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gct gga gct gtt gaa ttc aat gat gtg aag acc ttg ctc aga gaa tgg	2371
Ala Gly Ala Val Glu Phe Asn Asp Val Lys Thr Leu Leu Arg Glu Trp	
740 745 750 755	
ata act aca att tca gat cca atg gaa gaa gac att ctc caa gtt gtg	2419
Ile Thr Thr Ile Ser Asp Pro Met Glu Glu Asp Ile Leu Gln Val Val	
756 761 766 771	
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Lys Tyr Cys Thr Asp Leu Ile Glu Glu Lys Asp Leu Glu Lys Leu Asp	
772 777 782 787	

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Lys His Asp Glu Trp Leu Ser Cys Ala Pro Lys Thr Arg Pro Gln Asn	
56 61 66 71	
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Gly Ser Ile Ile Leu Tyr Asn Arg Lys Lys Val Lys Tyr Arg Lys Asp	
72 77 82 87	
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Gly Tyr Leu Trp Lys Lys Arg Lys Asp Gly Lys Thr Thr Arg Glu Asp	
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His Met Lys Leu Lys Val Gln Gly Met Glu Cys Leu Tyr Gly Cys Tyr	
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Val His Ser Ser Ile Val Pro Thr Phe His Arg Arg Cys Tyr Trp Leu	
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Leu Gln Asn Pro Asp Ile Val Leu Val His Tyr Leu Asn Val Pro Ala	
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Leu Glu Asp Cys Gly Lys Gly Cys Ser Pro Ile Phe Cys Ser Ile Ser	
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Ser Asp Arg Arg Glu Trp Leu Lys Trp Ser Arg Glu Glu Leu Leu Gly	
168 173 178 183	
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Gln Leu Lys Pro Met Phe His Gly Ile Lys Trp Ser Cys Gly Asn Gly	
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His Pro Thr Lys Pro Ala Pro Arg Thr His Ala Cys Leu Cys Ser Gly	
216 221 226 231	
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Gly Leu Gly Ser Gly Ser Leu Thr His Lys Cys Ser Ser Thr Lys His	
232 237 242 247	
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Arg Ile Ile Ser Pro Lys Val Glu Pro Arg Ala Leu Thr Leu Thr Ser	
248 253 258 263	
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Ile Pro His Pro His Pro Pro Glu Pro Pro Pro Leu Ile Ala Pro Leu	
264 269 274 279	
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ccc	act	tct	cga	ggg	ggc	tct	tca	aga	gga	ggc	act	gct	atc	ctc	ctc		1131
Pro	Thr	Ser	Arg	Gly	Gly	Ser	Ser	Arg	Gly	Gly	Thr	Ala	Ile	Leu	Leu		
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ctg	aca	gga	ctg	gag	cag	cgg	gct	gga	ggc	ttg	acg	ccc	acc	agg	cac		1179
Leu	Thr	Gly	Leu	Glu	Gln	Arg	Ala	Gly	Gly	Leu	Thr	Pro	Thr	Arg	His		
328					333					338						343	
ttg	gct	cca	cag	gct	gat	cct	agg	cct	tcc	atg	agt	ttg	gca	gtg	gtt		1227
Leu	Ala	Pro	Gln	Ala	Asp	Pro	Arg	Pro	Ser	Met	Ser	Leu	Ala	Val	Val		
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Val	Gly	Thr	Glu	Pro	Ser	Ala	Pro	Pro	Ala	Pro	Pro	Ser	Pro	Ala	Phe		
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Asp	Pro	Asp	Arg	Phe	Leu	Asn	Ser	Pro	Gln	Arg	Gly	Gln	Thr	Tyr	Gly		
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ggg	ggg	cag	gga	gta	agc	cca	gac	ttc	ccc	gag	gca	gag	gcc	gct	cat		1371
Gly	Gly	Gln	Gly	Val	Ser	Pro	Asp	Phe	Pro	Glu	Ala	Glu	Ala	Ala	His		
392					397					402						407	
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Thr	Pro	Cys	Ser	Ala	Leu	Glu	Pro	Ala	Ala	Ala	Leu	Glu	Pro	Gln	Ala		
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Asn	Cys	Phe	Phe	Ile	Gln	Asp	Asp	Asp	Ser	Gly	Glu	Glu	Leu	Lys	Gly		
440					445					450						455	
cac	ggg	gct	gcc	cca	ccc	ata	cct	tca	ccc	cct	ccc	tca	ccc	cca	ccc		1563
His	Gly	Ala	Ala	Pro	Pro	Ile	Pro	Ser	Pro	Pro	Pro	Ser	Pro	Pro	Pro		
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Ser	Pro	Ala	Pro	Leu	Glu	Pro	Ser	Ser	Arg	Val	Gly	Arg	Gly	Glu	Ala		
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Leu	Phe	Gly	Gly	Pro	Val	Gly	Ala	Ser	Glu	Leu	Glu	Pro	Phe	Ser	Leu		
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Ser	Ser	Phe	Pro	Asp	Leu	Met	Gly	Glu	Leu	Ile	Ser	Asp	Glu	Ala	Pro		

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Ser Ile Pro Ala Pro Thr Pro Gln Leu Ser Pro Ala Leu Ser Thr Ile				
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Thr Asp Phe Ser Pro Glu Trp Ser Tyr Pro Glu Gly Gly Val Lys Val				
536	541	546	551	
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Leu Ile Thr Gly Pro Trp Thr Glu Ala Ala Glu His Tyr Ser Cys Val				
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Phe Asp His Ile Ala Val Pro Ala Ser Leu Val Gln Pro Gly Val Leu				
568	573	578	583	
cgc tgc tac tgt ccc gcc cat gag gta ggg ctg gtg tct ttg cag gtg				1947
Arg Cys Tyr Cys Pro Ala His Glu Val Gly Leu Val Ser Leu Gln Val				
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Ala Gly Arg Glu Gly Pro Leu Ser Ala Ser Val Leu Phe Glu Tyr Arg				
600	605	610	615	
gcc cgc cga ttc ctg tct ctg cct agt act caa ctt gac tgg ctg tca				2043
Ala Arg Arg Phe Leu Ser Leu Pro Ser Thr Gln Leu Asp Trp Leu Ser				
616	621	626	631	
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Leu Asp Asp Asn Gln Phe Arg Met Ser Ile Leu Glu Arg Leu Glu Gln				
632	637	642	647	
atg gag aag cgg atg gca gag atc gca gca gct ggg cag gtg cct tgc				2139
Met Glu Lys Arg Met Ala Glu Ile Ala Ala Ala Gly Gln Val Pro Cys				
648	653	658	663	
cag ggt cct gat gct cct cca gtt cag gat gaa ggc cag ggg cct ggg				2187
Gln Gly Pro Asp Ala Pro Pro Val Gln Asp Glu Gly Gln Gly Pro Gly				
664	669	674	679	
ttc gaa gca cgg gta gtg gtc ttg gta gaa agc atg atc cca cgc tcc				2235
Phe Glu Ala Arg Val Val Val Leu Val Glu Ser Met Ile Pro Arg Ser				
680	685	690	695	
acc tgg aag ggt cct gaa cgt ctg gcc cat gga agc ccc ttc cgg ggc				2283
Thr Trp Lys Gly Pro Glu Arg Leu Ala His Gly Ser Pro Phe Arg Gly				
696	701	706	711	
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Met Ser Leu Leu His Leu Ala Ala Ala Gln Gly Tyr Ala Arg Leu Ile				
712	717	722	727	
gag acc ctg agc cag tgg cgg agt gtg gag act gga agc ttg gac tta				2379
Glu Thr Leu Ser Gln Trp Arg Ser Val Glu Thr Gly Ser Leu Asp Leu				
728	733	738	743	

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Glu Gln Glu Val Asp Pro Leu Asn Val Asp His Phe Ser Cys Thr Pro	
744 749 754 759	
ctg atg tgg gct tgt gcc ctg gga cac ctg gaa gct gct gtg ctc ctt	2475
Leu Met Trp Ala Cys Ala Leu Gly His Leu Glu Ala Ala Val Leu Leu	
760 765 770 775	
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Phe Arg Trp Asn Arg Gln Ala Leu Ser Ile Pro Asp Ser Leu Gly Arg	
776 781 786 791	
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Leu Pro Leu Ser Val Ala His Ser Arg Gly His Val Arg Leu Ala Arg	
792 797 802 807	
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Cys Leu Glu Glu Leu Gln Arg Gln Glu Pro Ser Val Glu Pro Pro Phe	
808 813 818 823	
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1192

1197

1202

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424 429 434 439	
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Val	Ile	Lys	Trp	His	Gly	Pro	Lys	Cys	Asn	Lys	Leu	Asn	Ser	Lys	Phe	
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Thr	Tyr	Cys	Asn	Ile	Pro	Met	Thr	Leu	Ile	Asn	Gly	Gln	Arg	Pro	Gln	
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Thr	Lys	Ser	Ser	Arg	Glu	Gln	Asn	Pro	Asp	Glu	Ala	His	Thr	Asn	Ser	

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Trp *				
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Phe Asp Ala Val Met Val Cys Thr Gly His Phe Leu Asn Pro His Leu				
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Pro Leu Glu Ala Phe Pro Gly Ile His Lys Phe Lys Gly Gln Ile Leu				
156	161	166	171	
cat agt caa gag tac aag atc cca gaa ggc ttt cag ggc aaa cgc gtc				939
His Ser Gln Glu Tyr Lys Ile Pro Glu Gly Phe Gln Gly Lys Arg Val				
172	177	182	187	
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Leu Val Ile Gly Leu Gly Asn Thr Gly Gly Asp Ile Ala Val Glu Leu				
188	193	198	203	
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Ser Arg Thr Ala Ala Gln Val Leu Leu Ser Thr Arg Thr Gly Thr Trp				
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Val Leu Gly Arg Ser Ser Asp Trp Gly Tyr Pro Tyr Asn Met Met Val				
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268 273 278 283	
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Cys Lys Ile Pro Pro Ser Gln Lys Leu Met Met Glu Ala Thr Glu Lys	
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Glu Gln Leu Ile Lys Arg Gly Val Phe Lys Asp Thr Ser Lys Asp Lys	
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Phe Asp Tyr Ile Ala Tyr Met Asp Asp Ile Ala Ala Cys Ile Gly Thr	
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Lys Pro Ser Ile Pro Leu Leu Phe Leu Lys Asp Pro Arg Leu Ala Trp	
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Glu Val Phe Phe Gly Pro Cys Thr Pro Tyr Gln Tyr Arg Leu Met Gly	
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Pro Gly Lys Trp Asp Gly Ala Arg Asn Ala Ile Leu Thr Gln Trp Asp	
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Arg Thr Leu Lys Pro Leu Lys Thr Arg Ile Val Pro Asp Ser Ser Lys	
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cct gcc tcc atg tca cat tat tta aaa gcc tgg ggg gca cct gtc cta	1947
Pro Ala Ser Met Ser His Tyr Leu Lys Ala Trp Gly Ala Pro Val Leu	
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Leu Ala Ser Leu Leu Leu Ile Cys Lys Ser Ser Leu Phe Leu Lys Leu	
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Trp Arg Gly *	
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Glu Cys Val Gly Ile Ala Ser Lys Ala Leu Cys Gly Leu Thr Glu Ala	

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Ala Ala Gln Ala Ala Tyr Leu Val Gly Ile Phe Asp Pro Asn Ser Gln				
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Ala Gly His Gln Gly Leu Val Asp Pro Ile Gln Phe Ala Arg Ala Asn				
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Gln Ala Ile Gln Met Ala Cys Gln Asn Leu Val Asp Pro Gly Ser Ser				
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cca tca cag gtc ctg tca gcc gcc aca att gtt gcc aag cac acg tca				403
Pro Ser Gln Val Leu Ser Ala Ala Thr Ile Val Ala Lys His Thr Ser				
82	87	92	97	
gcc ttg tgt aat gcc tgc cgc atc gcc tca tcc aag acg gcc aac cca				451
Ala Leu Cys Asn Ala Cys Arg Ile Ala Ser Ser Lys Thr Ala Asn Pro				
98	103	108	113	
gta gcc aag agg cac ttc gtc cag tcg gcc aag gaa gtc gcc aac agc				499
Val Ala Lys Arg His Phe Val Gln Ser Ala Lys Glu Val Ala Asn Ser				
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Thr Ala Asn Leu Val Lys Thr Ile Lys Ala Leu Asp Gly Asp Phe Ser				
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Ile Pro Ala Gln Ile Ser Ser Glu Gly Ser Gln Ala Gln Glu Pro Ile				
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Leu Val Ser Ala Lys Thr Met Leu Glu Ser Ser Ser Tyr Leu Ile Arg				
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act gca cgc tct ctg gcc atc aac ccc aaa gac cca ccc acc tgg tct				787
Thr Ala Arg Ser Leu Ala Ile Asn Pro Lys Asp Pro Pro Thr Trp Ser				
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Val Leu Ala Gly His Ser His Thr Val Ser Asp Ser Ile Lys Ser Leu				
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Ile Thr Ser Ile Arg Asp Lys Ala Pro Gly Gln Arg Glu Cys Asp Tyr				
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Ser Ile Asp Gly Ile Asn Arg Cys Ile Arg Asp Ile Glu Gln Ala Ser	
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Leu Ala Ala Val Ser Gln Ser Leu Ala Thr Arg Asp Asp Ile Ser Val	
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Thr Val Leu Asp Gln Thr Lys Thr Leu Ala Glu Ser Ala Leu Gln Met	
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Leu Tyr Ala Ala Lys Glu Gly Gly Gly Asn Pro Lys Ala Gln His Thr	
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His Asp Ala Ile Thr Glu Ala Ala Gln Leu Met Lys Glu Ala Val Asp	
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Asp Ile Met Val Thr Leu Asn Glu Ala Ala Ser Glu Val Gly Leu Val	
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Gly Gly Met Val Asp Ala Ile Ala Glu Ala Met Ser Lys Leu Asp Glu	
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Thr Lys Ser Val Thr Asn Pro Glu Glu Leu Gly Gly Leu Ala Ser Gln	
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Met Thr Ser Asp Tyr Gly His Leu Ala Phe Gln Gly Gln Met Ala Ala	
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Ala Thr Ala Glu Pro Glu Glu Ile Gly Phe Gln Ile Arg Thr Arg Val	
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Ala Gly Thr Leu Asn Ala Glu Asn Ser Glu Thr Phe Ala Asp His Arg	
594 599 604 609	
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738					743					748					753	
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Gln	Ser	Lys	Asp	Val	Pro	Glu	Lys	Thr	Ser	Ser	Pro	Glu	Glu	Ser	Ile	
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cgg	aaa	gcc	gtg	tca	gat	atg	ttg	acg	gct	tgc	aag	caa	gca	tcc	ttc	2563
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His	Pro	Asp	Val	Ser	Asp	Glu	Val	Arg	Thr	Arg	Ala	Leu	Arg	Phe	Gly	
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Ile	Leu	Gln	Lys	Pro	Thr	Pro	Glu	Phe	Lys	Gln	Gln	Leu	Ala	Ala	Phe	
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Ser	Lys	Arg	Val	Ala	Gly	Ala	Val	Thr	Glu	Leu	Ile	Gln	Ala	Ala	Glu	
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Ala	Glu	Thr	Glu	Leu	Leu	Gly	Ala	Ala	Ala	Ser	Ile	Glu	Ala	Ala	Ala	
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Lys Ala Asp Asp Asp Asp Val Val Val Lys Thr Lys Phe Val Gly Gly				
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Lys Ala Ala Ala Leu Asn Leu Ser Ala Leu His Ser Pro Ala His Arg
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Pro Pro Gly Phe Ser Val Ala Gln Lys Pro Phe Gly Ala Thr Tyr Val
23 28 33 38
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Trp Ser Ser Ile Ile Asn Thr Leu Gln Thr Gln Val Glu Val Lys Lys
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Asp	Lys	Lys	Pro	Thr	Phe	Glu	Asp	Ser	Ser	Cys	Ser	Leu	Tyr	Arg	Phe	
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Thr	Thr	Ile	Pro	Asn	Gln	Asp	Ser	Gln	Leu	Gly	Lys	Glu	Asn	Lys	Leu	
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Ala	Asn	Ser	Pro	His	Val	Asn	Ile	Ser	Thr	Thr	Leu	Ser	Pro	Gln	Val	
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Ile	Asn	Glu	Val	Trp	Gln	Glu	Glu	Thr	Ile	Gly	Arg	Leu	Leu	Gln	Leu	
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Thr Gln Leu Leu Leu Lys Leu Leu Asp Phe Gln Asn Arg Glu Glu Phe				
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aga aga cta ctg tat ttc atg gct gtt gca gca aat cct tct gag ttt				1157
Arg Arg Leu Leu Tyr Phe Met Ala Val Ala Ala Asn Pro Ser Glu Phe				
359	364	369	374	
aaa tta cag aaa gaa agt gac aac cga atg gtt gtg aaa agg ata ttc				1205
Lys Leu Gln Lys Glu Ser Asp Asn Arg Met Val Val Lys Arg Ile Phe				
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Ser Lys Ala Ile Val Asp Asn Lys Asn Leu Ser Lys Gly Lys Thr Asp				
391	396	401	406	
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Leu Leu Val Leu Phe Leu Met Asp His Gln Lys Asp Val Phe Lys Ile				
407	412	417	422	
cct gga act cta cat aaa att gta agt gtt aag ctt atg gcc ata cag				1349
Pro Gly Thr Leu His Lys Ile Val Ser Val Lys Leu Met Ala Ile Gln				
423	428	433	438	
aac gga aga gat cca aat aga gat gca gga tat att tat tgc cag aga				1397
Asn Gly Arg Asp Pro Asn Arg Asp Ala Gly Tyr Ile Tyr Cys Gln Arg				
439	444	449	454	
att gat caa cgt gac tat tcc aac aat aca gag aag aca acc aaa gat				1445
Ile Asp Gln Arg Asp Tyr Ser Asn Asn Thr Glu Lys Thr Thr Lys Asp				
455	460	465	470	
gag ctg ttg aat tta cta aaa act ctt gat gag gat tca aaa ctt tct				1493
Glu Leu Leu Asn Leu Leu Lys Thr Leu Asp Glu Asp Ser Lys Leu Ser				
471	476	481	486	
gcc aaa gag aag aaa aaa ttg cta ggt caa ttc tat aag tgt cac cca				1541
Ala Lys Glu Lys Lys Lys Leu Leu Gly Gln Phe Tyr Lys Cys His Pro				
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Asp Ile Phe Ile Glu His Phe Gly Asp *				
503	508			
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Pro Asp Tyr Glu Ser Ile Asn His Val Val Val Phe Met Leu Gly Thr						
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92 97	102	107				
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Val Ala Gln Ile Gly Ile Ser Val Glu Leu Leu Asp Ser Met Ala Gln						
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Gln Thr Pro Val Gly Asn Ala Ala Val Ser Ser Val Asp Ser Phe Thr						
124 129	134	139				
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Gln Phe Thr Gln Lys Met Leu Asp Asn Phe Tyr Asn Phe Ala Ser Ser						
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Val Glu Ile Ile Glu Lys Asp Thr Lys Tyr Ser Val Ile Val Ile Arg	
142 147 152 157	
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Arg Phe Asp Pro Lys Leu Phe Leu Val Phe Leu Leu Gly Leu Met Leu	
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1,1,1,2-Tetrachloroethane	0.1 M	25 °C	24 h	72%	92%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	25 °C	24 h	75%	96%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	25 °C	24 h	70%	90%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	25 °C	24 h	73%	94%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	25 °C	24 h	68%	88%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	25 °C	24 h	71%	91%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	25 °C	24 h	65%	85%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	25 °C	24 h	69%	89%	¹ H NMR, IR, MS
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1,1,2,2-Tetrachloroethane	0.1 M	25 °C	24 h	59%	79%	¹ H NMR, IR, MS
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1,1,1,2-Tetrachloroethane	0.1 M	25 °C	24 h	48%	68%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	25 °C	24 h	51%	71%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	25 °C	24 h	45%	65%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	25 °C	24 h	49%	69%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	25 °C	24 h	42%	62%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	25 °C	24 h	46%	66%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	25 °C	24 h	40%	60%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	25 °C	24 h	43%	63%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	25 °C	24 h	38%	58%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	25 °C	24 h	41%	61%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	25 °C	24 h	35%	55%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	25 °C	24 h	39%	59%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	25 °C	24 h	32%	52%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	25 °C	24 h	36%	56%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	25 °C	24 h	30%	50%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	25 °C	24 h	33%	53%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	25 °C	24 h	28%	48%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	25 °C	24 h	31%	51%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	25 °C	24 h	25%	45%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	25 °C	24 h	29%	49%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	25 °C	24 h	22%	42%	¹ H NMR, IR, MS
1,1,2,2-Tetrachloroethane	0.1 M	25 °C	24 h	26%	46%	¹ H NMR, IR, MS
1,1,1,2-Tetrachloroethane	0.1 M	25 °C	24 h	20%	40%</	

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120

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240

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 Thr Val Val Leu Gln Asp Ala Ser Met Glu Ala Gln Pro Ala Glu Thr
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 Leu Pro Glu Gly Pro Gln Gln Asp Leu Pro Pro Glu Ala Ser Ala Ala
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Tyr	Cys	Asp	Phe	Arg	Ser	His	Asp	Met	Thr	Gln	Phe	Val	Gly	His	Met	
81					86					91					96	
aac	tca	gag	cac	aca	gac	ttt	aat	aaa	gac	cca	acc	ttt	gta	tgc	agt	396
Asn	Ser	Glu	His	Thr	Asp	Phe	Asn	Lys	Asp	Pro	Thr	Phe	Val	Cys	Ser	
97					102					107					112	
ggg	tgc	agt	ttt	ctg	gca	aaa	acc	cct	gag	ggg	ctt	tcc	ttg	cac	aat	444
Gly	Cys	Ser	Phe	Leu	Ala	Lys	Thr	Pro	Glu	Gly	Leu	Ser	Leu	His	Asn	
113					118					123					128	
gcc	aca	tgt	cac	tcc	ggg	gaa	gcc	agc	ttt	gtg	tgg	aac	gtg	gcc	aag	492
Ala	Thr	Cys	His	Ser	Gly	Glu	Ala	Ser	Phe	Val	Trp	Asn	Val	Ala	Lys	
129					134					139					144	
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Pro	Asp	Asn	His	Val	Val	Val	Glu	Gln	Ser	Ile	Pro	Glu	Ser	Thr	Ser	
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Lys	Ala	Glu	Ala	Lys	Lys	Ile	His	Thr	Leu	Lys	Glu	Asn	Val	Pro	Ser	
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Gln	Ala	Ser	Ala	Ser	Ser	Ala	Lys	Asn	Pro	His	Ala	Ala	Asn	Gly	Pro	
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Ser	Leu	Gln	Gln	Gln	Pro	Pro	Val	His	Ala	Gln	His	His	Val	His	Gln	
273					278					283					288	
cca	ctg	ccc	acg	gcc	aag	gcc	ctt	ccc	aaa	gtg	atg	atc	ccc	ctg	agc	972
Pro	Leu	Pro	Thr	Ala	Lys	Ala	Leu	Pro	Lys	Val	Met	Ile	Pro	Leu	Ser	

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Asn Ser Phe His Lys	Phe Pro Tyr Pro Thr	Lys Ala Glu Leu Cys Tyr		
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Glu Asp Ala Arg Lys	Lys Met Phe Asn Thr	Val Ile Gln Ser Val Pro		
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Gln Pro Thr Ile Thr	Val Leu Asn Thr Pro	Leu Val Ala Ser Ala Gly		
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Asn Val Gln His Leu	Ile Gln Ala Ala Leu	Pro Gly His Val Val Gly		
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Gln Pro Glu Gly Thr	Gly Gly Gly Leu Leu	Val Thr Gln Pro Leu Met		
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Ser Val Pro Lys Gln	Pro Gly Val Ala Pro	Ile Asn Thr Val Cys Ser		
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Thr Ala Cys Pro Ser	Ile Thr Ser Gln Ala	Phe Leu Asp Ala Ser Ile		
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Lys Val Thr Gly Leu Ser Thr Arg Glu Val Arg Lys Trp Phe Ser Asp	
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Arg Arg Tyr His Cys Arg Asn Leu Lys Gly Ser Arg Ala Met Ile Pro	
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Gly Asp His Ser Ser Ile Ile Ile Asp Ser Val Pro Glu Val Ser Phe	
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Ser Pro Ser Ser Lys Val Pro Glu Val Thr Cys Ile Pro Thr Thr Ala	
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Glu Lys Ile Pro Gln Ser His Ile Gln Gln Ile Cys Glu Thr Ile Leu	
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Ala Cys Lys Phe Ala Glu Trp Cys Leu Glu Tyr Gly Glu His Gly Cys	
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Met Pro Gln Thr Pro Val Pro Pro Glu
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Gly Gln Gly Gln Leu Pro Arg Arg Ala Gly Ser Arg Glu Ala Val Pro
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Gly Lys Leu Tyr Ala Met Lys Val Leu Arg Lys Ala Ala Leu Val Gln
122 127 132 137
cgc gcc aag acg cag gag cac acg cgc acc gag cgc tcg gtg ctg gag 604
Arg Ala Lys Thr Gln Glu His Thr Arg Thr Glu Arg Ser Val Leu Glu

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Thr Asp Ala Lys Leu His Leu Ile Leu Asp Tyr Val Ser Gly Gly Glu				
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Met Phe Thr His Leu Tyr Gln Arg Gln Tyr Phe Lys Glu Ala Glu Val				
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Arg Val Tyr Gly Gly Glu Ile Val Leu Ala Leu Glu His Leu His Lys				
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Leu Gly Ile Ile Tyr Arg Asp Leu Lys Leu Glu Asn Val Leu Leu Asp				
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Ser Glu Gly His Ile Val Leu Thr Asp Phe Gly Leu Ser Lys Glu Phe				
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Ala Ser Pro Phe Thr Leu Glu Gly Glu Arg Asn Thr Gln Ala Glu Val				
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Arg	Met	Gly	Phe	Asn	Ala	Ser	Ser	Met	Leu	Arg	Lys	Ser	Gln	Leu	Gly	
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Ser	Cys	Met	Glu	Arg	Lys	Lys	Val	Gln	Ile	Arg	Ser	Met	Asp	Pro	Ser	
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Phe Val Asn Ser His Pro Gly Ile Asp Arg Pro Gly Met Leu Cys Ser				
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Asn Val Val Thr Gly His Arg Gln Ser Phe Gly Thr Asn Ser Asp Val				
312	317	322	327	
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Leu Ala Gln Gln Phe Ala Phe Met Ala Pro Leu Leu Phe Asn Gly Cys				
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Arg Ser Gly Glu Ile Phe Ala Ile Asp Leu Arg Cys Gly Asn Gln Gly				
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Lys Gly Trp Lys Ala Thr Arg Leu Phe His Asp Ser Ala Val Thr Ser				
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Val Arg Ile Leu Gln Asp Glu Gln Tyr Leu Met Ala Ser Asp Met Ala				
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392	397	402	407	
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Tyr Glu Gly His Val Asn Glu Tyr Ala Tyr Leu Pro Leu His Val His				
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Leu Ala Leu Trp Ile Thr Leu Ser Leu Leu Gln Thr Gly Leu Ala Glu	
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Pro Glu Arg Cys Asn Phe Thr Leu Ala Glu Ser Lys Ala Ser Ser His	
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Leu Ile Tyr Ser Ser Asp Thr Leu Gly Ala Ala Leu Cys Pro Thr Phe	
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Arg Ile Asp Asn Thr Thr Tyr Gly Cys Asn Leu Gln Asp Leu Gln Ala	
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Val Val Leu Gln Thr Asp Pro Leu Pro Pro Ala Arg Phe Gly Val Ser	
104 109 114 119	
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Lys Glu Lys Thr Thr Ser Thr Gly Leu His Val Trp Trp Thr Pro Ser	
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Ser Gly Lys Val Thr Ser Tyr Glu Val Gln Leu Phe Asp Glu Asn Asn	
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Gln Lys Ile Gln Gly Val Gln Ile Gln Glu Ser Thr Ser Trp Asn Glu	
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Thr Ala Val Ser Gly Gly Lys Arg Ser Phe Ser Val Tyr Thr Asn Gly	
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Tyr Arg Leu Met Leu Met Asp Lys Gly Ile Leu Val His Gly Gly Val				
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Val Asp Lys His Ala Thr Ser Tyr Ala Phe His Gly Leu Ser Pro Gly				
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Tyr Arg Trp Lys Leu Val Arg Thr Ala Pro Met Glu Val Ser Asn Leu				
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Lys Val Thr Asn Asp Gly Ser Leu Thr Ser Leu Lys Val Lys Trp Gln				
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Arg Pro Pro Gly Asn Val Asp Ser Tyr Asn Ile Thr Leu Ser His Lys				
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Arg Ser Leu Val Val Ser Trp Ser Pro Pro Ala Gly Asp Trp Glu Gln				
392	397	402	407	
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Tyr Arg Ile Leu Leu Phe Asn Asp Ser Val Val Leu Leu Asn Ile Thr				
408	413	418	423	
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Pro Gly Arg Gln Tyr Glu Val Glu Val Ile Val Glu Ser Gly Asn Leu				
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Lys Asn Ser Glu Arg Cys Gln Gly Arg Thr Val Pro Leu Ala Val Leu	
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Glu Ser Arg Thr Ala Pro Ser Pro Pro Ser Leu Met Ser Phe Ala Asp				
1256	1261	1266	1271	
att gca aac aca tcc ttg gcc atc acg tgg aaa ggg ccc cca gac tgg				3891
Ile Ala Asn Thr Ser Leu Ala Ile Thr Trp Lys Gly Pro Pro Asp Trp				
1272	1277	1282	1287	
aca gac tac aac gac ttt gag ctg cag tgg ttg ccc aga gat gca ctt				3939
Thr Asp Tyr Asn Asp Phe Glu Leu Gln Trp Leu Pro Arg Asp Ala Leu				
1288	1293	1298	1303	
act gtc ttc aac ccc tac aac aac aga aaa tca gaa gga cgc att gtg				3987
Thr Val Phe Asn Pro Tyr Asn Asn Arg Lys Ser Glu Gly Arg Ile Val				
1304	1309	1314	1319	
tat ggt ctt cgt cca ggg aga tcc tat caa ttc aac gtc aag act gtc				4035
Tyr Gly Leu Arg Pro Gly Arg Ser Tyr Gln Phe Asn Val Lys Thr Val				
1320	1325	1330	1335	
agt ggt gat tcc tgg aaa act tac agc aaa cca att ttt gga tct gtg				4083
Ser Gly Asp Ser Trp Lys Thr Tyr Ser Lys Pro Ile Phe Gly Ser Val				
1336	1341	1346	1351	
agg aca aag cct gac aag ata caa aac ctg cat tgc cgg cct cag aac				4131
Arg Thr Lys Pro Asp Lys Ile Gln Asn Leu His Cys Arg Pro Gln Asn				
1352	1357	1362	1367	

tcc acg gcc att gcc tgt tct tgg atc cct cct gat tct gac ttt gat	4179
Ser Thr Ala Ile Ala Cys Ser Trp Ile Pro Pro Asp Ser Asp Phe Asp	
1368 1373 1378 1383	
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Gly Tyr Ser Ile Glu Cys Arg Lys Met Asp Thr Gln Glu Val Glu Phe	
1384 1389 1394 1399	
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Ser Arg Lys Leu Glu Lys Glu Lys Ser Leu Leu Asn Ile Met Met Leu	
1400 1405 1410 1415	
gtg ccc cat aag agg tac ctg gtg tcc atc aaa gtg cag tcg gcc ggc	4323
Val Pro His Lys Arg Tyr Leu Val Ser Ile Lys Val Gln Ser Ala Gly	
1416 1421 1426 1431	
atg acc agc gag gtg gtt gaa gac agc act atc aca atg ata gac cgc	4371
Met Thr Ser Glu Val Val Glu Asp Ser Thr Ile Thr Met Ile Asp Arg	
1432 1437 1442 1447	
ccc cct cct cca ccc cca cac att cgt gtg aat gaa aag gat gtg cta	4419
Pro Pro Pro Pro Pro Pro His Ile Arg Val Asn Glu Lys Asp Val Leu	
1448 1453 1458 1463	
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Ile Ser Lys Ser Ser Ile Asn Phe Thr Val Asn Cys Ser Trp Phe Ser	
1464 1469 1474 1479	
gac acc aat gga gct gtg aaa tac ttc aca gtg gtg gtg aga gag gct	4515
Asp Thr Asn Gly Ala Val Lys Tyr Phe Thr Val Val Val Arg Glu Ala	
1480 1485 1490 1495	
gat ggc agt gat gag ctg aag cca gaa cag cag cac cct ctc cct tcc	4563
Asp Gly Ser Asp Glu Leu Lys Pro Glu Gln Gln His Pro Leu Pro Ser	
1496 1501 1506 1511	
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Tyr Leu Glu Tyr Arg His Asn Ala Ser Ile Arg Val Tyr Gln Thr Asn	
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tat ttt gcc agc aaa tgt gcc gaa aat cct aac agc aac tcc aag agt	4659
Tyr Phe Ala Ser Lys Cys Ala Glu Asn Pro Asn Ser Asn Ser Lys Ser	
1528 1533 1538 1543	
ttt aac att aag ctt gga gca gag atg gag agc cta ggt gga aaa tgc	4707
Phe Asn Ile Lys Leu Gly Ala Glu Met Glu Ser Leu Gly Gly Lys Cys	
1544 1549 1554 1559	
gat ccc act cag caa aaa ttc tgt gat gga cca ctg aag cca cac act	4755
Asp Pro Thr Gln Gln Lys Phe Cys Asp Gly Pro Leu Lys Pro His Thr	
1560 1565 1570 1575	
gcc tac aga atc agc att cga gct ttt aca cag ctc ttt gat gag gac	4803
Ala Tyr Arg Ile Ser Ile Arg Ala Phe Thr Gln Leu Phe Asp Glu Asp	
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Leu Lys Glu Phe Thr Lys Pro Leu Tyr Ser Asp Thr Phe Phe Ser Leu	
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Pro Ile Thr Thr Glu Ser Glu Pro Leu Phe Gly Ala Ile Glu Gly Val	
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Ser Ala Gly Leu Phe Leu Ile Gly Met Leu Val Ala Val Val Ala Leu	
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Leu Ile Cys Arg Gln Lys Val Ser His Gly Arg Glu Arg Pro Ser Ala	
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Arg Leu Ser Ile Arg Arg Asp Arg Pro Leu Ser Val His Leu Asn Leu	
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Gly Gln Lys Gly Asn Arg Lys Thr Ser Cys Pro Ile Lys Ile Asn Gln	
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Phe Glu Gly His Phe Met Lys Leu Gln Ala Asp Ser Asn Tyr Leu Leu	
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Ser Lys Glu Tyr Glu Glu Leu Lys Asp Val Gly Arg Asn Gln Ser Cys	
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Asp Ile Ala Leu Leu Pro Glu Asn Arg Gly Lys Asn Arg Tyr Asn Asn	
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ata ttg ccc tat gat gcc acg cga gtg aag ctc tcc aat gta gat gat	5283
Ile Leu Pro Tyr Asp Ala Thr Arg Val Lys Leu Ser Asn Val Asp Asp	
1736 1741 1746 1751	
gat cct tgc tct gac tac atc aat gcc agc tac atc cct ggc aac aac	5331
Asp Pro Cys Ser Asp Tyr Ile Asn Ala Ser Tyr Ile Pro Gly Asn Asn	
1752 1757 1762 1767	
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Phe Arg Arg Glu Tyr Ile Val Thr Gln Gly Pro Leu Pro Gly Thr Lys	
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Asp Asp Phe Trp Lys Met Val Trp Glu Gln Asn Val His Asn Ile Val	
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Met Val Thr Gln Cys Val Glu Lys Gly Arg Val Lys Cys Asp His Tyr	
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Met	Leu	Ser	Glu	Ser	Val	Leu	Pro	Glu	Trp	Thr	Ile	Arg	Glu	Phe	Lys		
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Ile	Cys	Gly	Glu	Glu	Gln	Leu	Asp	Ala	His	Arg	Leu	Ile	Arg	His	Phe		
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cac	tat	acg	gtg	tgg	cca	gac	cat	gga	gtc	cca	gaa	acc	acc	cag	tct	5667	
His	Tyr	Thr	Val	Trp	Pro	Asp	His	Gly	Val	Pro	Glu	Thr	Thr	Gln	Ser		
1864					1869					1874					1879		
ctg	atc	cag	ttt	gtg	aga	act	gtc	agg	gac	tac	atc	aac	aga	agc	ccg	5715	
Leu	Ile	Gln	Phe	Val	Arg	Thr	Val	Arg	Asp	Tyr	Ile	Asn	Arg	Ser	Pro		
1880					1885					1890					1895		
ggg	gct	ggg	ccc	act	gtg	gtg	cac	tgc	agt	gct	ggg	gtg	ggg	agg	act	5763	
Gly	Ala	Gly	Pro	Thr	Val	Val	His	Cys	Ser	Ala	Gly	Val	Gly	Arg	Thr		
1896					1901					1906					1911		
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Gly	Thr	Phe	Ile	Ala	Leu	Asp	Arg	Ile	Leu	Gln	Gln	Leu	Asp	Ser	Lys		
1912					1917					1922					1927		
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Asp	Ser	Val	Asp	Ile	Tyr	Gly	Ala	Val	His	Asp	Leu	Arg	Leu	His	Arg		
1928					1933					1938					1943		
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Val	His	Met	Val	Gln	Thr	Glu	Cys	Gln	Tyr	Val	Tyr	Leu	His	Gln	Cys		
1944					1949					1954					1959		
gta	aga	gat	gtc	ctc	aga	gca	aga	aag	cta	cgg	agt	gaa	caa	gaa	aac	5955	
Val	Arg	Asp	Val	Leu	Arg	Ala	Arg	Lys	Leu	Arg	Ser	Glu	Gln	Glu	Asn		
1960					1965					1970					1975		
ccc	ttg	ttt	cca	atc	tat	gaa	aat	gtg	aat	cca	gag	tat	cac	aga	gat	6003	
Pro	Leu	Phe	Pro	Ile	Tyr	Glu	Asn	Val	Asn	Pro	Glu	Tyr	His	Arg	Asp		
1976					1981					1986					1991		
cca	gtc	tat	tca	agg	cat	tga	ga	atgtacctga	agagctcctg	gataaaaatt						6056	
Pro	Val	Tyr	Ser	Arg	His	*											
1992					1997												
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Val Pro Leu Gly Arg Tyr Thr Glu Glu Glu His Lys Ala Thr Glu Lys				
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atc ctg aaa atg ttt gga gag agg gct aga agt ttc atg att ctc ata				904
Ile Leu Lys Met Phe Gly Glu Arg Ala Arg Ser Phe Met Ile Leu Ile				
137	142	147	152	
ttc acc cgg aaa gat gac tta ggt gac acc aat ttg cat gac tac tta				952
Phe Thr Arg Lys Asp Asp Leu Gly Asp Thr Asn Leu His Asp Tyr Leu				
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Arg Glu Ala Pro Glu Asp Ile Gln Asp Leu Met Asp Ile Phe Gly Asp				
169	174	179	184	
cgc tac tgt gcg tta aac aac aag gca aca ggc gct gag cag gag gcc				1048
Arg Tyr Cys Ala Leu Asn Asn Lys Ala Thr Gly Ala Glu Gln Glu Ala				
185	190	195	200	
cag agg gca cag ttg ctg ggc ctg atc cag cgc gtg gtg agg gag aac				1096
Gln Arg Ala Gln Leu Leu Gly Leu Ile Gln Arg Val Val Arg Glu Asn				
201	206	211	216	
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Lys Glu Gly Cys Tyr Thr Asn Arg Met Tyr Gln Arg Ala Glu Glu Glu				
217	222	227	232	
atc cag aag caa aca caa gca atg caa gaa ctc cac aga gtg gag ctg				1192
Ile Gln Lys Gln Thr Gln Ala Met Gln Glu Leu His Arg Val Glu Leu				
233	238	243	248	
gag aga gag aaa gcg cgg ata aga gag gag tat gaa gag aaa atc aga				1240
Glu Arg Glu Lys Ala Arg Ile Arg Glu Glu Tyr Glu Glu Lys Ile Arg				
249	254	259	264	
aag ctg gaa gat aaa gtg gag cag gaa aag aga aag aag caa atg gag				1288
Lys Leu Glu Asp Lys Val Glu Gln Glu Lys Arg Lys Lys Gln Met Glu				
265	270	275	280	
aag aaa cta gca gaa cag gag gct cac tat gct gta agg cag caa agg				1336
Lys Lys Leu Ala Glu Gln Glu Ala His Tyr Ala Val Arg Gln Gln Arg				
281	286	291	296	
gca aga acg gaa gtg gag agt aag gat ggg ata ctt gaa tta atc atg				1384
Ala Arg Thr Glu Val Glu Ser Lys Asp Gly Ile Leu Glu Leu Ile Met				
297	302	307	312	
aca gcg tta cag att gct tcc ttt att ttg tta cgt ctg ttc gcg gaa				1432
Thr Ala Leu Gln Ile Ala Ser Phe Ile Leu Leu Arg Leu Phe Ala Glu				
313	318	323	328	
gat taa acttaatgaa aatctgtttg tattttctgc atattctctg gcaaccttgc				1488
Asp *				
329				

cccataactta cttatttagc atagtcgagt gctctagttt ctgtctctca ggcactcgta 1548
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 tgactgtgga atccttaagg gccattaca tttctgaaga agaaagctaa gatgaaggac 240
 atg cca ctc cga att cat gtg cta ctt ggc cta gct atc act aca cta 288
 Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile Thr Thr Leu
 1 5 10 15
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 Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu Cys Thr Cys
 17 22 27 32
 gaa atc agg cct tgg ttt aca ccc aga tcc att tat atg gaa gca tct 384
 Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met Glu Ala Ser
 33 38 43 48
 aca gtg gat tgt aat gat tta ggt ctt tta act ttc cca gcc aga ttg 432
 Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro Ala Arg Leu
 49 54 59 64
 cca gct aac aca cag att ctt ctc cta cag act aac aat att gca aaa 480
 Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn Ile Ala Lys
 65 70 75 80
 att gaa tac tcc aca gac ttt cca gta aac ctt act ggc ctg gat tta 528

Ile	Glu	Tyr	Ser	Thr	Asp	Phe	Pro	Val	Asn	Leu	Thr	Gly	Leu	Asp	Leu		
81					86					91					96		
tct	caa	aac	aat	tta	tct	tca	gtc	acc	aat	att	aat	gta	aaa	aag	atg	576	
Ser	Gln	Asn	Asn	Leu	Ser	Ser	Val	Thr	Asn	Ile	Asn	Val	Lys	Lys	Met		
97					102					107					112		
cct	cag	ctc	ctt	tct	gtg	tac	cta	gag	gaa	aac	aaa	ctt	act	gaa	ctg	624	
Pro	Gln	Leu	Leu	Ser	Val	Tyr	Leu	Glu	Glu	Asn	Lys	Leu	Thr	Glu	Leu		
113					118					123					128		
cct	gaa	aaa	tgt	ctg	tcc	gaa	ctg	agc	aac	tta	caa	gaa	ctc	tat	att	672	
Pro	Glu	Lys	Cys	Leu	Ser	Glu	Leu	Ser	Asn	Leu	Gln	Glu	Leu	Tyr	Ile		
129					134					139					144		
aat	cac	aac	ttg	ctt	tct	aca	att	tca	cct	gga	gcc	ttt	att	ggc	cta	720	
Asn	His	Asn	Leu	Leu	Ser	Thr	Ile	Ser	Pro	Gly	Ala	Phe	Ile	Gly	Leu		
145					150					155					160		
cat	aat	ctt	ctt	cga	ctt	cat	ctc	aat	tca	aat	aga	ttg	cag	atg	atc	768	
His	Asn	Leu	Leu	Arg	Leu	His	Leu	Asn	Ser	Asn	Arg	Leu	Gln	Met	Ile		
161					166					171					176		
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Asn	Ser	Lys	Trp	Phe	Asp	Ala	Leu	Pro	Asn	Leu	Glu	Ile	Leu	Met	Ile		
177					182					187					192		
ggg	gaa	aat	cca	att	atc	aga	atc	aaa	gac	atg	aac	ttt	aag	cct	ctt	864	
Gly	Glu	Asn	Pro	Ile	Ile	Arg	Ile	Lys	Asp	Met	Asn	Phe	Lys	Pro	Leu		
193					198					203					208		
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Ile	Asn	Leu	Arg	Ser	Leu	Val	Ile	Ala	Gly	Ile	Asn	Leu	Thr	Glu	Ile		
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Pro	Asp	Asn	Ala	Leu	Val	Gly	Leu	Glu	Asn	Leu	Glu	Ser	Ile	Ser	Phe		
225					230					235					240		
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Tyr	Asp	Asn	Arg	Leu	Ile	Lys	Val	Pro	His	Val	Ala	Leu	Gln	Lys	Val		
241					246					251					256		
gta	aat	ctc	aaa	ttt	ttg	gat	cta	aat	aaa	aat	cct	att	aat	aga	ata	1056	
Val	Asn	Leu	Lys	Phe	Leu	Asp	Leu	Asn	Lys	Asn	Pro	Ile	Asn	Arg	Ile		
257					262					267					272		
cga	agg	ggt	gat	ttt	agc	aat	atg	cta	cac	tta	aaa	gag	ttg	ggg	ata	1104	
Arg	Arg	Gly	Asp	Phe	Ser	Asn	Met	Leu	His	Leu	Lys	Glu	Leu	Gly	Ile		
273					278					283					288		
aat	aat	atg	cct	gag	ctg	att	tcc	atc	gat	agt	ctt	gct	gtg	gat	aac	1152	
Asn	Asn	Met	Pro	Glu	Leu	Ile	Ser	Ile	Asp	Ser	Leu	Ala	Val	Asp	Asn		
289					294					299					304		
ctg	cca	gat	tta	aga	aaa	ata	gaa	gct	act	aac	aac	cct	aga	ttg	tct	1200	
Leu	Pro	Asp	Leu	Arg	Lys	Ile	Glu	Ala	Thr	Asn	Asn	Pro	Arg	Leu	Ser		

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tac att cac ccc aat gca ttt ttc aga ctc ccc aag ctg gaa tca ctc				1248
Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu Glu Ser Leu				
321	326	331	336	
atg ctg aac agc aat gct ctc agt gcc ctg tac cat ggt acc att gag				1296
Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly Thr Ile Glu				
337	342	347	352	
tct ctg cca aac ctc aag gaa atc agc ata cac agt aac ccc atc agg				1344
Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn Pro Ile Arg				
353	358	363	368	
tgt gac tgt gtc atc cgt tgg atg aac atg aac aaa acc aac att cga				1392
Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr Asn Ile Arg				
369	374	379	384	
ttc atg gag cca gat tca ctg ttt tgc gtg gac cca cct gaa ttc caa				1440
Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro Glu Phe Gln				
385	390	395	400	
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Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met Glu Ile Cys				
401	406	411	416	
ctc cct ctt ata gct cct gag agc ttt cct tct aat cta aat gta gaa				1536
Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu Asn Val Glu				
417	422	427	432	
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Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala Glu Pro Gln				
433	438	443	448	
cct gaa atc tac tgg ata aca cct tct ggt caa aaa ctc ttg cct aat				1632
Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu Leu Pro Asn				
449	454	459	464	
acc ctg aca gac aag ttc tat gtc cat tct gag gga aca cta gat ata				1680
Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr Leu Asp Ile				
465	470	475	480	
aat ggc gta act ccc aaa gaa ggg ggt tta tat act tgt ata gca act				1728
Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys Ile Ala Thr				
481	486	491	496	
aac cta gtt ggc gct gac ttg aag tct gtt atg atc aaa gtg gat gga				1776
Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys Val Asp Gly				
497	502	507	512	
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Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys Ile Arg Asp				
513	518	523	528	
att cag gcc aat tca gtt ttg gtg tcc tgg aaa gca agt tct aaa att				1872
Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser Ser Lys Ile				
529	534	539	544	

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Glu	Gly	Lys	Glu	Glu	Glu	Gly	Gly	Glu	Glu	Glu	Glu	Ala	Glu	Gly	Gly	
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gaa	gaa	gaa	aca	aag	tct	ccc	cca	gta	gaa	gag	gct	gca	tcc	cca	gag	5491
Glu	Glu	Glu	Thr	Lys	Ser	Pro	Pro	Val	Glu	Glu	Ala	Ala	Ser	Pro	Glu	
498					503					508					513	
aag	gaa	gcc	aag	tca	cca	gta	aag	gaa	gag	gca	aag	tca	ccg	gct	gag	5539
Lys	Glu	Ala	Lys	Ser	Pro	Val	Lys	Glu	Glu	Ala	Lys	Ser	Pro	Ala	Glu	
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gcc	aag	tcc	cca	gag	aag	gag	gaa	gca	aaa	tcc	cca	gcc	gaa	gtc	aag	5587
Ala	Lys	Ser	Pro	Glu	Lys	Glu	Glu	Ala	Lys	Ser	Pro	Ala	Glu	Val	Lys	
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Ser	Pro	Glu	Lys	Ala	Lys	Ser	Pro	Ala	Lys	Glu	Glu	Ala	Lys	Ser	Pro	
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Pro	Glu	Ala	Lys	Ser	Pro	Glu	Lys	Glu	Glu	Ala	Lys	Ser	Pro	Ala	Glu	
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Val	Lys	Ser	Pro	Glu	Lys	Ala	Lys	Ser	Pro	Ala	Lys	Glu	Glu	Ala	Lys	
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Ser	Pro	Ala	Glu	Ala	Lys	Ser	Pro	Glu	Lys	Ala	Lys	Ser	Pro	Val	Lys	
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Ala	Lys	Ser	Pro	Ala	Glu	Val	Lys	Ser	Pro	Glu	Lys	Ala	Lys	Ser	Pro	
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Thr	Lys	Glu	Glu	Ala	Lys	Ser	Pro	Glu	Lys	Ala	Lys	Ser	Pro	Glu	Lys	

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tcc cca gtg aag gca gaa gca aag tcc cct gag aag gcc aag tcc cca				6019
Ser Pro Val Lys Ala Glu Ala Lys Ser Pro Glu Lys Ala Lys Ser Pro				
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gtg aag gca gaa gca aag tcc cct gag aag gcc aag tcc cca gtg aag				6067
Val Lys Ala Glu Ala Lys Ser Pro Glu Lys Ala Lys Ser Pro Val Lys				
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gaa gaa gca aag tcc cct gag aag gcc aag tcc cca gtg aag gaa gaa				6115
Glu Glu Ala Lys Ser Pro Glu Lys Ala Lys Ser Pro Val Lys Glu Glu				
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Ala Lys Ser Pro Glu Lys Ala Lys Ser Pro Val Lys Glu Glu Ala Lys				
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acc ccc gag aag gcc aag tcc cca gtg aag gaa gaa gcc aag tcc cca				6211
Thr Pro Glu Lys Ala Lys Ser Pro Val Lys Glu Glu Ala Lys Ser Pro				
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Glu Lys Ala Lys Ser Pro Glu Lys Ala Lys Thr Leu Asp Val Lys Ser				
754	759	764	769	
cca gaa gcc aag act cca gcg aag gag gaa gca agg tcc cct gca gac				6307
Pro Glu Ala Lys Thr Pro Ala Lys Glu Glu Ala Arg Ser Pro Ala Asp				
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Lys Phe Pro Glu Lys Ala Lys Ser Pro Val Lys Glu Glu Val Lys Ser				
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Pro Glu Lys Ala Lys Ser Pro Leu Lys Glu Asp Ala Lys Ala Pro Glu				
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Lys Glu Ile Pro Lys Lys Glu Glu Val Lys Ser Pro Val Lys Glu Glu				
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Glu Lys Pro Gln Glu Val Lys Val Lys Glu Pro Pro Lys Lys Ala Glu				
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Glu Glu Lys Ala Pro Ala Thr Pro Lys Thr Glu Glu Lys Lys Asp Ser				
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Lys Lys Glu Glu Ala Pro Lys Lys Glu Ala Pro Lys Pro Lys Val Glu				
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Ala Lys Lys Glu Glu Ala Glu Asp Lys Lys Lys Val Pro Thr Pro Glu	
898 903 908 913	
aag gag gct cct gcc aag gtg gag gtg aag gaa gac gct aaa ccc aaa	6739
Lys Glu Ala Pro Ala Lys Val Glu Val Lys Glu Asp Ala Lys Pro Lys	
914 919 924 929	
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Glu Lys Thr Glu Val Ala Lys Lys Glu Pro Asp Asp Ala Lys Ala Lys	
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Glu Pro Ser Lys Pro Ala Glu Lys Lys Glu Ala Ala Pro Glu Lys Lys	
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Asp Thr Lys Glu Glu Lys Ala Lys Lys Pro Glu Glu Lys Pro Lys Thr	
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Glu Ala Lys Ala Lys Glu Asp Asp Lys Thr Leu Ser Lys Glu Pro Ser	
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Lys Pro Lys Ala Glu Lys Ala Glu Lys Ser Ser Ser Thr Asp Gln Lys	
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 Pro Leu Lys Thr Gly Phe Leu His Asn Gly Arg Ala Met Gly Asn Met
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 Arg Lys Thr Tyr Trp Ser Ser Arg Ser Glu Phe Lys Asn Asn Phe Leu
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 aat att gac ccg ata acc atg gcc tac agt ctg aac tct tct gct cag 373
 Asn Ile Asp Pro Ile Thr Met Ala Tyr Ser Leu Asn Ser Ser Ala Gln
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 Glu Arg Leu Ile Pro Leu Gly His Ala Ser Lys Ser Ala Pro Met Asn
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 Gly His Cys Phe Ala Glu Asn Gly Pro Ser Gln Lys Ser Ser Leu Pro
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 Pro Leu Leu Ile Pro Pro Ser Glu Asn Leu Gly Pro His Glu Glu Asp
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Ser Thr Pro Pro Leu Thr Pro Ile Lys Asn Ser Pro Ser Leu Phe Pro	
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Cys Ala Pro Leu Cys Glu Arg Gly Ser Arg Pro Leu Pro Pro Leu Pro	
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Ile Ser Glu Ala Leu Ser Leu Asp Asp Thr Asp Cys Glu Val Glu Phe	
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Gln Ile Asn Tyr Ala Tyr Phe Asp Thr Pro Ala Val Ser Ala Ala Asp	
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Leu Ser Tyr Val Ser Asp Gln Asn Gly Gly Val Pro Asp Pro Asn Pro	
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Ala Gly Ser Phe Asn Lys Pro Ala Ile Arg Ile Ser Asn Cys Cys Ile	
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Ser Pro Lys Ser Leu Pro Ser Tyr Leu Asn Gly Val Met Pro Pro Thr	
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Ile Ile Glu Asn Gly Lys Lys Val Ser Ser Thr His Tyr Tyr Leu Leu	
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Cys Gly Ile Ser Ser Ala Thr Glu Lys Pro Asp Ser Lys Thr Lys Met	
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Asp Leu Gly Gly His Val Lys Arg Lys His Leu Ser Tyr Val Val Ser	
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Glu Val Gly Thr Asp Ser Trp Ser Gln Cys Asn Asp Thr Pro Val Lys	
414 419 424 429	
ttt gct cgt ttt cct gtc act gga ttg atc gaa ggt cgt tcc tat atc	2004
Phe Ala Arg Phe Pro Val Thr Gly Leu Ile Glu Gly Arg Ser Tyr Ile	
430 435 440 445	

ttc cga gtt cga gct gtg aat aaa atg gga ata ggt ttc cca tct cga	2052
Phe Arg Val Arg Ala Val Asn Lys Met Gly Ile Gly Phe Pro Ser Arg	
446 451 456 461	
gtt tcc gag gcc gtg gct gct ctg gat ccg gct gag aaa gct aga cta	2100
Val Ser Glu Ala Val Ala Ala Leu Asp Pro Ala Glu Lys Ala Arg Leu	
462 467 472 477	
aag tcc ccc ctc agc acc ctg gac tgg aca gtc att gtt act gaa gag	2148
Lys Ser Pro Leu Ser Thr Leu Asp Trp Thr Val Ile Val Thr Glu Glu	
478 483 488 493	
gaa cct tca gag ggt att gtg cct ggc ccc ccg aca gac ctc tct gtc	2196
Glu Pro Ser Glu Gly Ile Val Pro Gly Pro Pro Thr Asp Leu Ser Val	
494 499 504 509	
act gag gcc acc cgg agc tat gtg gtg ctc agc tgg aag ccc cct ggc	2244
Thr Glu Ala Thr Arg Ser Tyr Val Val Leu Ser Trp Lys Pro Pro Gly	
510 515 520 525	
cag cgt ggt cat gag ggc att atg tac ttt gtg gaa aag tgt gag gca	2292
Gln Arg Gly His Glu Gly Ile Met Tyr Phe Val Glu Lys Cys Glu Ala	
526 531 536 541	
gga aca gaa aac tgg cag cga gtg aac acg gag ctc cct gtg aag tct	2340
Gly Thr Glu Asn Trp Gln Arg Val Asn Thr Glu Leu Pro Val Lys Ser	
542 547 552 557	
ccc cgc ttt gct ctg ttt gac ttg gcc gag ggg aaa tcc tac tgt ttc	2388
Pro Arg Phe Ala Leu Phe Asp Leu Ala Glu Gly Lys Ser Tyr Cys Phe	
558 563 568 573	
cgt gtc cgc tgt tct aat tct gca gga gtt ggt gag ccc tca gag gca	2436
Arg Val Arg Cys Ser Asn Ser Ala Gly Val Gly Glu Pro Ser Glu Ala	
574 579 584 589	
acg gag gtg act gtg gta ggg gac aaa ctt gat atc ccc aag gct cct	2484
Thr Glu Val Thr Val Val Gly Asp Lys Leu Asp Ile Pro Lys Ala Pro	
590 595 600 605	
ggc aaa atc atc cca agc aga aac aca gac acc tca gtg gta gtt tcc	2532
Gly Lys Ile Ile Pro Ser Arg Asn Thr Asp Thr Ser Val Val Val Ser	
606 611 616 621	
tgg gag gag tcc aaa gat gcc aaa gag ctg gtc ggg tac tac ata gag	2580
Trp Glu Glu Ser Lys Asp Ala Lys Glu Leu Val Gly Tyr Tyr Ile Glu	
622 627 632 637	
gcg agc gtt gct ggc tct ggc aag tgg gag ccc tgt aac aac aac ccc	2628
Ala Ser Val Ala Gly Ser Gly Lys Trp Glu Pro Cys Asn Asn Asn Pro	
638 643 648 653	
gtg aag ggc tca cga ttc act tgt cat gga tta gtg act ggt cag agt	2676
Val Lys Gly Ser Arg Phe Thr Cys His Gly Leu Val Thr Gly Gln Ser	
654 659 664 669	
tat att ttc cgg gtc aga gca gtc aat gca gct gga ctt agt gaa tat	2724

Tyr Ile Phe Arg Val Arg Ala Val Asn Ala Ala Gly Leu Ser Glu Tyr	
670 675 680 685	
tcc cag gat tca gaa gct att gaa gtc aaa gct gct att gca cca cca	2772
Ser Gln Asp Ser Glu Ala Ile Glu Val Lys Ala Ala Ile Ala Pro Pro	
686 691 696 701	
tct cca ccc tgt gat atc acc tgt ctt gaa agt ttt cgt gac tca atg	2820
Ser Pro Pro Cys Asp Ile Thr Cys Leu Glu Ser Phe Arg Asp Ser Met	
702 707 712 717	
gtt ctt gga tgg aag caa cca gat aag att gga ggg gca gaa att act	2868
Val Leu Gly Trp Lys Gln Pro Asp Lys Ile Gly Gly Ala Glu Ile Thr	
718 723 728 733	
ggc tat tat gtg aac tat cgc gag gtc att gat ggg gta cca gga aaa	2916
Gly Tyr Tyr Val Asn Tyr Arg Glu Val Ile Asp Gly Val Pro Gly Lys	
734 739 744 749	
tgg aga gaa gcc aat gtc aag gct gtc agt gag gag gca tac aag att	2964
Trp Arg Glu Ala Asn Val Lys Ala Val Ser Glu Glu Ala Tyr Lys Ile	
750 755 760 765	
agc aac ttg aag gaa aac atg gtg tat cag ttc caa gtg gca gcc atg	3012
Ser Asn Leu Lys Glu Asn Met Val Tyr Gln Phe Gln Val Ala Ala Met	
766 771 776 781	
aac atg gct ggg ctg ggc gcg ccc tcc gca gta agc gaa tgc ttc aaa	3060
Asn Met Ala Gly Leu Gly Ala Pro Ser Ala Val Ser Glu Cys Phe Lys	
782 787 792 797	
tgt gaa gag tgg acc atc gcc gtc cca gga cca ccg cac agt ctc aag	3108
Cys Glu Glu Trp Thr Ile Ala Val Pro Gly Pro Pro His Ser Leu Lys	
798 803 808 813	
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Cys Ser Glu Val Arg Lys Asp Ser Leu Val Leu Gln Trp Lys Pro Pro	
814 819 824 829	
gtc cac tcc ggg cgg act ccg gtc act ggt tac ttc gtg gac ttg aag	3204
Val His Ser Gly Arg Thr Pro Val Thr Gly Tyr Phe Val Asp Leu Lys	
830 835 840 845	
gag gcc aag gcc aaa gaa gac cag tgg cga ggg ctc aat gag gcg gct	3252
Glu Ala Lys Ala Lys Glu Asp Gln Trp Arg Gly Leu Asn Glu Ala Ala	
846 851 856 861	
att aaa aac gta tac ctg aag gtt cga ggc ctc aag gag ggc gtc agc	3300
Ile Lys Asn Val Tyr Leu Lys Val Arg Gly Leu Lys Glu Gly Val Ser	
862 867 872 877	
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Tyr Val Phe Arg Val Arg Ala Ile Asn Gln Ala Gly Val Gly Lys Pro	
878 883 888 893	
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Ser Asp Leu Ala Gly Pro Val Val Ala Glu Thr Arg Pro Gly Thr Lys	

Tyr Ile Phe Arg Val Arg Ala Val Asn Ala Ala Gly Leu Ser Glu Tyr	
670 675 680 685	
tcc cag gat tca gaa gct att gaa gtc aaa gct gct att gca cca cca	2772
Ser Gln Asp Ser Glu Ala Ile Glu Val Lys Ala Ala Ile Ala Pro Pro	
686 691 696 701	
tct cca ccc tgt gat atc acc tgt ctt gaa agt ttt cgt gac tca atg	2820
Ser Pro Pro Cys Asp Ile Thr Cys Leu Glu Ser Phe Arg Asp Ser Met	
702 707 712 717	
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Val Leu Gly Trp Lys Gln Pro Asp Lys Ile Gly Gly Ala Glu Ile Thr	
718 723 728 733	
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Gly Tyr Tyr Val Asn Tyr Arg Glu Val Ile Asp Gly Val Pro Gly Lys	
734 739 744 749	
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Trp Arg Glu Ala Asn Val Lys Ala Val Ser Glu Glu Ala Tyr Lys Ile	
750 755 760 765	
agc aac ttg aag gaa aac atg gtg tat cag ttc caa gtg gca gcc atg	3012
Ser Asn Leu Lys Glu Asn Met Val Tyr Gln Phe Gln Val Ala Ala Met	
766 771 776 781	
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Asn Met Ala Gly Leu Gly Ala Pro Ser Ala Val Ser Glu Cys Phe Lys	
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tgt gaa gag tgg acc atc gcc gtc cca gga cca ccg cac agt ctc aag	3108
Cys Glu Glu Trp Thr Ile Ala Val Pro Gly Pro Pro His Ser Leu Lys	
798 803 808 813	
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Cys Ser Glu Val Arg Lys Asp Ser Leu Val Leu Gln Trp Lys Pro Pro	
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gtc cac tcc ggg cgg act ccg gtc act ggt tac ttc gtg gac ttg aag	3204
Val His Ser Gly Arg Thr Pro Val Thr Gly Tyr Phe Val Asp Leu Lys	
830 835 840 845	
gag gcc aag gcc aaa gaa gac cag tgg cga ggg ctc aat gag gcg gct	3252
Glu Ala Lys Ala Lys Glu Asp Gln Trp Arg Gly Leu Asn Glu Ala Ala	
846 851 856 861	
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Ile Lys Asn Val Tyr Leu Lys Val Arg Gly Leu Lys Glu Gly Val Ser	
862 867 872 877	
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Tyr Val Phe Arg Val Arg Ala Ile Asn Gln Ala Gly Val Gly Lys Pro	
878 883 888 893	
tct gac ctt gct ggc cct gtt gtg gca gag acc cgt cca gga acc aaa	3396
Ser Asp Leu Ala Gly Pro Val Val Ala Glu Thr Arg Pro Gly Thr Lys	

894	899	904	909	
gag gtt gtt gta aat	gtg gat gat gat gga	gtc att tca ttg aac ttc		3444
Glu Val Val Val Asn	Val Asp Asp Asp Gly	Val Ile Ser Leu Asn Phe		
910	915	920	925	
gag tgt gat aag atg	act cca aag tcc gag	ttc tcc tgg tcc aaa gat		3492
Glu Cys Asp Lys Met	Thr Pro Lys Ser Glu	Phe Ser Trp Ser Lys Asp		
926	931	936	941	
tat gta tcc act gag	gac tct cca cga ttg	gaa gtc gaa agc aag ggc		3540
Tyr Val Ser Thr Glu	Asp Ser Pro Arg Leu	Glu Val Glu Ser Lys Gly		
942	947	952	957	
aac aag acg aaa atg	acc ttc aaa gac ctt	ggg atg gat gac ttg ggt		3588
Asn Lys Thr Lys Met	Thr Phe Lys Asp Leu	Gly Met Asp Asp Leu Gly		
958	963	968	973	
att tac tct tgc gat	gta aca gac act gat	gga ata gca tca agc tac		3636
Ile Tyr Ser Cys Asp	Val Thr Asp Thr Asp	Gly Ile Ala Ser Ser Tyr		
974	979	984	989	
tta ata gat gag gaa	gaa ttg aaa cgt tta	ctt gct ctc agc cat gaa		3684
Leu Ile Asp Glu Glu	Glu Leu Lys Arg Leu	Leu Ala Leu Ser His Glu		
990	995	1000	1005	
cac aag ttc cca act	gtc cca gtt aaa tca	gag ttg gca gtt gaa att		3732
His Lys Phe Pro Thr	Val Pro Val Lys Ser	Glu Leu Ala Val Glu Ile		
1006	1011	1016	1021	
ttg gag aaa ggc cag	gtc cgg ttt tgg atg	cag gct gag aaa ctg tct		3780
Leu Glu Lys Gly Gln	Val Arg Phe Trp Met	Gln Ala Glu Lys Leu Ser		
1022	1027	1032	1037	
ggc aat gcc aaa gtc	aac tac ata ttt aac	gag aag gaa att ttt gaa		3828
Gly Asn Ala Lys Val	Asn Tyr Ile Phe Asn	Glu Lys Glu Ile Phe Glu		
1038	1043	1048	1053	
ggc ccg aaa tat aaa	atg cat att gac cga	aac act ggc atc atc gaa		3876
Gly Pro Lys Tyr Lys	Met His Ile Asp Arg	Asn Thr Gly Ile Ile Glu		
1054	1059	1064	1069	
atg ttc atg gaa aag	cta cag gat gag gat	gag gga acg tac act ttc		3924
Met Phe Met Glu Lys	Leu Gln Asp Glu Asp	Glu Gly Thr Tyr Thr Phe		
1070	1075	1080	1085	
cag ctt caa gat gga	aaa gca act aac cat	tct act gtt gtt ctc gtt		3972
Gln Leu Gln Asp Gly	Lys Ala Thr Asn His	Ser Thr Val Val Leu Val		
1086	1091	1096	1101	
gga gat gtt ttc aaa	aag ctc cag aaa gaa	gct gaa ttc cag cgg caa		4020
Gly Asp Val Phe Lys	Lys Leu Gln Lys Glu	Ala Glu Phe Gln Arg Gln		
1102	1107	1112	1117	
gaa tgg atc agg aaa	caa ggt cct cac ttt	ggt gag tat ttg agc tgg		4068
Glu Trp Ile Arg Lys	Gln Gly Pro His Phe	Val Glu Tyr Leu Ser Trp		
1118	1123	1128	1133	

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Glu Val Thr Gly Glu Cys Asn Val Leu Leu Lys Cys Lys Val Ala Asn	
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Ile Lys Lys Glu Thr His Ile Val Trp Tyr Lys Asp Glu Arg Glu Ile	
1150 1155 1160 1165	
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Ser Val Asp Glu Lys His Asp Phe Lys Asp Gly Ile Cys Thr Leu Leu	
1166 1171 1176 1181	
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Ile Thr Glu Phe Ser Lys Lys Asp Ala Gly Ile Tyr Glu Val Ile Leu	
1182 1187 1192 1197	
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Lys Asp Asp Arg Gly Lys Asp Lys Ser Arg Leu Lys Leu Val Asp Glu	
1198 1203 1208 1213	
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Ala Phe Lys Glu Leu Met Met Glu Val Cys Lys Lys Ile Ala Leu Ser	
1214 1219 1224 1229	
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Ala Thr Asp Leu Lys Ile Gln Ser Thr Ala Glu Gly Ile Gln Leu Tyr	
1230 1235 1240 1245	
tct ttt gta act tac tat gtg gag gat ttg aaa gtt aac tgg tcc cac	4452
Ser Phe Val Thr Tyr Tyr Val Glu Asp Leu Lys Val Asn Trp Ser His	
1246 1251 1256 1261	
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Asn Gly Ser Ala Ile Arg Tyr Ser Asp Arg Val Lys Thr Gly Val Thr	
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Gly Glu Gln Ile Trp Leu Gln Ile Asn Glu Pro Thr Pro Asn Asp Lys	
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Gly Lys Tyr Val Met Glu Leu Phe Asp Gly Lys Thr Gly His Gln Lys	
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Thr Val Asp Leu Ser Gly Gln Ala Tyr Asp Glu Ala Tyr Ala Glu Phe	
1310 1315 1320 1325	
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Gln Arg Leu Lys Gln Ala Ala Ile Ala Glu Lys Asn Arg Ala Arg Val	
1326 1331 1336 1341	
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Leu Gly Gly Leu Pro Asp Val Val Thr Ile Gln Glu Gly Lys Ala Leu	
1342 1347 1352 1357	

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Ser Asp Lys Glu Lys Glu Asn Gly Lys Met Gly Cys Trp Ser Ile Glu	
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His Val Glu Gln Tyr Leu Gly Thr Asp Glu Leu Pro Lys Asn Asp Leu	
316 321 326 331	
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Ile Thr Tyr Leu Gln Lys Asn Ala Asp Ala Ala Phe Leu Arg His Trp	
332 337 342 347	
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Lys Leu Thr Gly Thr Asn Lys Ser Ile Arg Lys Asn Arg Asn Cys Ser	
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Gln Leu Ile Ala Ala Tyr Lys Asp Phe Cys Glu His Gly Thr Lys Ser	
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Gly Leu Asn Gln Gly Ala Ile Ser Thr Leu Gln Ser Ser Asp Ile Leu	
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Asn Leu Thr Lys Glu Gln Pro Gln Ala Lys Ala Gly Asn Gly Gln Asn	
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Ser Cys Gly Val Glu Asp Val Leu Gln Leu Leu Arg Ile Leu Tyr Ile	
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Val Ala Ser Asp Pro Tyr Ser Arg Ile Ser Gln Glu Asp Gly Asp Glu	
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Gln Pro Gln Phe Thr Phe Pro Pro Asp Glu Phe Thr Ser Lys Lys Ile	
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Leu Ile Pro Phe Glu Thr Arg Gln Leu Tyr Phe Thr Cys Thr Ala Phe	
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Gly Ala Ser Arg Ala Ile Val Trp Leu Gln Asn Arg Arg Glu Ala Thr	
508 513 518 523	
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Val	Glu	Arg	Thr	Arg	Thr	Thr	Ser	Ser	Val	Arg	Arg	Asp	Asp	Pro	Gly	
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Glu	Phe	Arg	Val	Gly	Arg	Leu	Lys	His	Glu	Arg	Val	Lys	Val	Pro	Arg	
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Gly	Glu	Ser	Leu	Met	Glu	Trp	Ala	Glu	Asn	Val	Met	Gln	Ile	His	Ala	
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Asp	Arg	Lys	Ser	Val	Leu	Glu	Val	Glu	Phe	Leu	Gly	Glu	Glu	Gly	Thr	
572					577					582					587	
ggc	ttg	gga	ccc	aca	tta	gag	ttt	tat	gct	ctg	gtg	gca	gca	gaa	ttc	6507
Gly	Leu	Gly	Pro	Thr	Leu	Glu	Phe	Tyr	Ala	Leu	Val	Ala	Ala	Glu	Phe	
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Gln	Arg	Thr	Asp	Leu	Gly	Ala	Trp	Leu	Cys	Asp	Asp	Asn	Phe	Pro	Asp	
604					609					614					619	
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Asp	Glu	Ser	Arg	His	Val	Asp	Leu	Gly	Gly	Gly	Leu	Lys	Pro	Pro	Gly	
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Asp	Ser	Asp	Glu	Leu	Glu	Arg	Ile	Thr	Lys	Leu	Phe	His	Phe	Leu	Gly	
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Ile	Ser	Lys	Pro	Phe	Phe	Lys	Leu	Met	Cys	Met	Gly	Asp	Ile	Lys	Ser	
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Cys	Thr	Glu	Ser	Gln	Ser	Glu	Ala	Ser	Thr	Glu	Glu	Gly	His	Asp	Ser	
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Leu	Ser	Val	Gly	Ser	Phe	Glu	Glu	Asp	Ser	Lys	Ser	Glu	Phe	Ile	Leu	
732					737					742					747	
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Asp	Pro	Pro	Lys	Pro	Lys	Pro	Pro	Ala	Trp	Phe	Asn	Gly	Ile	Leu	Thr	

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Trp Glu Asp Phe Glu Leu Val Asn Pro His Arg Ala Arg Phe Leu Lys				
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Glu Ile Lys Asp Leu Ala Ile Lys Arg Arg Gln Ile Leu Ser Asn Lys				
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ggg ctt tct gaa gat gag aag aac aca aaa tta cag gaa cta gtg ctg				7131
Gly Leu Ser Glu Asp Glu Lys Asn Thr Lys Leu Gln Glu Leu Val Leu				
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aag aat cca tca ggt tct ggg cct cca ctt agc ata gag gat tta ggt				7179
Lys Asn Pro Ser Gly Ser Gly Pro Pro Leu Ser Ile Glu Asp Leu Gly				
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Leu Asn Phe Gln Phe Cys Pro Ser Ser Arg Ile Tyr Gly Phe Thr Ala				
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gtg gat ctc aag cca agt ggt gaa gat gag atg ata aca atg gat aat				7275
Val Asp Leu Lys Pro Ser Gly Glu Asp Glu Met Ile Thr Met Asp Asn				
844	849	854	859	
gca gaa gaa tat gtg gat ttg atg ttt gac ttt tgt atg cat acg ggt				7323
Ala Glu Glu Tyr Val Asp Leu Met Phe Asp Phe Cys Met His Thr Gly				
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att cag aaa caa atg gaa gcc ttt aga gat ggg ttt aat aaa gtt ttt				7371
Ile Gln Lys Gln Met Glu Ala Phe Arg Asp Gly Phe Asn Lys Val Phe				
876	881	886	891	
cca atg gag aaa tta agt tcc ttc agc cat gaa gaa gtc caa atg att				7419
Pro Met Glu Lys Leu Ser Ser Phe Ser His Glu Glu Val Gln Met Ile				
892	897	902	907	
ctt tgt gga aac cag tca cca tcc tgg gca gca gag gat att atc aat				7467
Leu Cys Gly Asn Gln Ser Pro Ser Trp Ala Ala Glu Asp Ile Ile Asn				
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tac act gaa cct aag ctg ggt tat aca cgt gac agc cct ggt ttc ctg				7515
Tyr Thr Glu Pro Lys Leu Gly Tyr Thr Arg Asp Ser Pro Gly Phe Leu				
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Arg Phe Val Arg Val Leu Cys Gly Met Ser Ser Asp Glu Arg Lys Ala				
940	945	950	955	
ttc ttg cag ttt acc act ggt tgt tca act cta ccc cca ggt gga ctg				7611
Phe Leu Gln Phe Thr Thr Gly Cys Ser Thr Leu Pro Pro Gly Gly Leu				
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gct aac ctg cat ccc agg ctc acg gtt gta cgc aag gtt gat gct act				7659
Ala Asn Leu His Pro Arg Leu Thr Val Val Arg Lys Val Asp Ala Thr				
972	977	982	987	

Met Thr Lys Ile Lys

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Ala Asp Pro Asp Gly Pro Glu Ala Gln Ala Glu Ala Cys Ser Gly Glu	
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Arg Thr Tyr Gln Glu Leu Leu Val Asn Gln Asn Pro Ile Ala Gln Pro	
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ctg gct tct cgc cgc ctc acg cgg aag ctc tac aaa tgc atc aag aaa	259
Leu Ala Ser Arg Arg Leu Thr Arg Lys Leu Tyr Lys Cys Ile Lys Lys	
38 43 48 53	
gcg gtg aag cag aag cag att cgg cgc ggg gtg aaa gag gtt cag aaa	307
Ala Val Lys Gln Lys Gln Ile Arg Arg Gly Val Lys Glu Val Gln Lys	
54 59 64 69	
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Phe Val Asn Lys Gly Glu Lys Gly Ile Met Val Leu Ala Gly Asp Thr	
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ctg ccc att gag gta tac tgc cat ctc cca gtc atg tgt gag gac cga	403
Leu Pro Ile Glu Val Tyr Cys His Leu Pro Val Met Cys Glu Asp Arg	
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aat ttg ccc tat gtc tat atc ccc tct aag acg gac ctg ggt gca gcc	451
Asn Leu Pro Tyr Val Tyr Ile Pro Ser Lys Thr Asp Leu Gly Ala Ala	
102 107 112 117	
gca ggc tcc aag cgc ccc acc tgt gtg ata atg gtc aag ccc cat gag	499
Ala Gly Ser Lys Arg Pro Thr Cys Val Ile Met Val Lys Pro His Glu	
118 123 128 133	
gag tac cag gag gct tac gat gag tgc ctg gag gag gtg cag tcc ctg	547
Glu Tyr Gln Glu Ala Tyr Asp Glu Cys Leu Glu Glu Val Gln Ser Leu	
134 139 144 149	
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Pro Leu Pro Leu *	
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cagttcccca aggcacgcct tcttccagg cagctctaac agccctttca tgaaggtaat	722
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Glu Glu Lys Thr Leu Lys Lys Asp Glu Glu Asn Asp Ser Lys Ala Pro	
183 188 193 198	
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Pro His Glu Leu Thr Glu Glu Glu Lys Gln Gln Ile Leu His Ser Glu	
199 204 209 214	
gaa ttt tta agt ttc ttt gac cat tct aca aga att gta gaa aga gct	904
Glu Phe Leu Ser Phe Phe Asp His Ser Thr Arg Ile Val Glu Arg Ala	
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Leu Ser Glu Gln Ile Asn Ile Phe Phe Asp Tyr Ser Gly Arg Asp Leu	
231 236 241 246	
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Glu Asp Lys Glu Gly Glu Ile Gln Ala Gly Ala Lys Leu Ser Leu Asn	
247 252 257 262	
cga caa ttt ttt gac gaa cgt tgg tca aag cat cgg gtg gtt agt tgt	1048
Arg Gln Phe Phe Asp Glu Arg Trp Ser Lys His Arg Val Val Ser Cys	
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Leu Asp Trp Ser Ser Gln Tyr Pro Glu Leu Leu Val Ala Ser Tyr Asn	
279 284 289 294	
aac aat gaa gat gcc cct cat gag cct gat ggt gtg gcc ctt gta tgg	1144
Asn Asn Glu Asp Ala Pro His Glu Pro Asp Gly Val Ala Leu Val Trp	
295 300 305 310	
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Asn Met Lys Tyr Lys Lys Thr Thr Pro Glu Tyr Val Phe His Cys Gln	
311 316 321 326	
tca gct gtg atg tct gcc aca ttt gca aaa ttt cat cca aat ctt gtt	1240
Ser Ala Val Met Ser Ala Thr Phe Ala Lys Phe His Pro Asn Leu Val	
327 332 337 342	
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Val Gly Gly Thr Tyr Ser Gly Gln Ile Val Leu Trp Asp Asn Arg Ser	
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Thr His Pro Val Tyr Cys Val Asn Val Val Gly Thr Gln Asn Ala His	
375 380 385 390	
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Asp	Ser	Glu	Gly	Gln	Ile	Val	Ile	Tyr	Asp	Val	Gly	Glu	Gln	Ile	Ala	
583					588					593					598	
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Ile	Asn	Ala	Asn	Arg	Ala	Asp	Ala	Glu	Glu	Glu	Ala	Ala	Thr	Arg	Ile	

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Pro Ala *				
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Glu Glu Lys Lys Arg Lys Glu Glu Glu Arg Lys Lys Lys Glu Thr Asp	
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Gln Lys Lys Glu Ala Val Ala Pro Val Gln Glu Glu Ser Asp Leu Glu	

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Sample	Age	Grade	Sex	Height	Weight	Arm span	Fore arm length	Hand length	Hand breadth	Mid finger length	Mid finger breadth	2 nd finger length	2 nd finger breadth	3 rd finger length	3 rd finger breadth	4 th finger length	4 th finger breadth	5 th finger length	5 th finger breadth
1	10	4	M	135	25	155	35	18	8	10	2.5	12	2.5	10	2.5	9	2.5	8	2.5
2	11	5	F	140	28	160	38	19	9	11	2.8	13	2.8	11	2.8	10	2.8	9	2.8
3	12	6	M	145	30	165	40	20	10	12	3.0	14	3.0	12	3.0	11	3.0	10	3.0
4	13	7	F	150	32	170	42	21	11	13	3.2	15	3.2	13	3.2	12	3.2	11	3.2
5	14	8	M	155	35	175	45	22	12	14	3.5	16	3.5	14	3.5	13	3.5	12	3.5
6	15	9	F	160	38	180	48	23	13	15	3.8	17	3.8	15	3.8	14	3.8	13	3.8
7	16	10	M	165	40	185	50	24	14	16	4.0	18	4.0	16	4.0	15	4.0	14	4.0
8	17	11	F	170	42	190	52	25	15	17	4.2	19	4.2	17	4.2	16	4.2	15	4.2
9	18	12	M	175	45	195	55	26	16	18	4.5	20	4.5	18	4.5	17	4.5	16	4.5
10	19	13	F	180	48	200	58	27	17	19	4.8	21	4.8	19	4.8	18	4.8	17	4.8
11	20	14	M	185	50	205	60	28	18	20	5.0	22	5.0	20	5.0	19	5.0	18	5.0
12	21	15	F	190	52	210	62	29	19	21	5.2	23	5.2	21	5.2	20	5.2	19	5.2
13	22	16	M	195	55	215	65	30	20	22	5.5	24	5.5	22	5.5	21	5.5	20	5.5
14	23	17	F	200	58	220	68	31	21	23	5.8	25	5.8	23	5.8	22	5.8	21	5.8
15	24	18	M	205	60	225	70	32	22	24	6.0	26	6.0	24	6.0	23	6.0	22	6.0
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17	26	20	M	215	65	235	75	34	24	26	6.5	28	6.5	26	6.5	25	6.5	24	6.5
18	27	21	F	220	68	240	78	35	25	27	6.8	29	6.8	27	6.8	26	6.8	25	6.8
19	28	22	M	225	70	245	80	36	26	28	7.0	30	7.0	28	7.0	27	7.0	26	7.0
20	29	23	F	230	72	250	82	37	27	29	7.2	31	7.2	29	7.2	28	7.2	27	7.2
21	30	24	M	235	75	255	85	38	28	30	7.5	32	7.5	30	7.5	29	7.5	28	7.5
22	31	25	F	240	78	260	88	39	29	31	7.8	33	7.8	31	7.8	30	7.8	29	7.8
23	32	26	M	245	80	265	90	40	30	32</									

[illegible][illegible]

Sample	Age	Grade	Sex	Height	Weight	Arm span	Fore arm length	Hand length	Hand breadth	Mid finger length	Mid finger breadth	2 nd finger length	2 nd finger breadth	3 rd finger length	3 rd finger breadth	4 th finger length	4 th finger breadth	5 th finger length	5 th finger breadth
1	10	4	M	135	25	155	35	18	8	10	2.5	12	2.5	10	2.5	9	2.5	8	2.5
2	11	5	F	140	28	160	38	19	9	11	2.8	13	2.8	11	2.8	10	2.8	9	2.8
3	12	6	M	145	30	165	40	20	10	12	3.0	14	3.0	12	3.0	11	3.0	10	3.0
4	13	7	F	150	32	170	42	21	11	13	3.2	15	3.2	13	3.2	12	3.2	11	3.2
5	14	8	M	155	35	175	45	22	12	14	3.5	16	3.5	14	3.5	13	3.5	12	3.5
6	15	9	F	160	38	180	48	23	13	15	3.8	17	3.8	15	3.8	14	3.8	13	3.8
7	16	10	M	165	40	185	50	24	14	16	4.0	18	4.0	16	4.0	15	4.0	14	4.0
8	17	11	F	170	42	190	52	25	15	17	4.2	19	4.2	17	4.2	16	4.2	15	4.2
9	18	12	M	175	45	195	55	26	16	18	4.5	20	4.5	18	4.5	17	4.5	16	4.5
10	19	13	F	180	48	200	58	27	17	19	4.8	21	4.8	19	4.8	18	4.8	17	4.8
11	20	14	M	185	50	205	60	28	18	20	5.0	22	5.0	20	5.0	19	5.0	18	5.0
12	21	15	F	190	52	210	62	29	19	21	5.2	23	5.2	21	5.2	20	5.2	19	5.2
13	22	16	M	195	55	215	65	30	20	22	5.5	24	5.5	22	5.5	21	5.5	20	5.5
14	23	17	F	200	58	220	68	31	21	23	5.8	25	5.8	23	5.8	22	5.8	21	5.8
15	24	18	M	205	60	225	70	32	22	24	6.0	26	6.0	24	6.0	23	6.0	22	6.0
16	25	19	F	210	62	230	72	33	23	25	6.2	27	6.2	25	6.2	24	6.2	23	6.2
17	26	20	M	215	65	235	75	34	24	26	6.5	28	6.5	26	6.5	25	6.5	24	6.5
18	27	21	F	220	68	240	78	35	25	27	6.8	29	6.8	27	6.8	26	6.8	25	6.8
19	28	22	M	225	70	245	80	36	26	28	7.0	30	7.0	28	7.0	27	7.0	26	7.0
20	29	23	F	230	72	250	82	37	27	29	7.2	31	7.2	29	7.2	28	7.2	27	7.2
21	30	24	M	235	75	255	85	38	28	30	7.5	32	7.5	30	7.5	29	7.5	28	7.5
22	31	25	F	240	78	260	88	39	29	31	7.8	33	7.8	31	7.8	30	7.8	29	7.8
23	32	26	M	245	80	265	90	40	30	32</									

gtg aga aag ctg gac cgg gag agg gta gga gct tgg tgg aga ggc gcc	768
Val Arg Lys Leu Asp Arg Glu Arg Val Gly Ala Trp Trp Arg Gly Ala	
241 246 251 256	
tgg gcc aga cat ccg cgg cag gag gcg ggg gaa cat gcc aag agg cgg	816
Trp Ala Arg His Pro Arg Gln Glu Ala Gly Glu His Ala Lys Arg Arg	
257 262 267 272	
aag ggg cac gcg gag acc ccc agg ggg cgc cgg aag ggg cgc gcc ggg	864
Lys Gly His Ala Glu Thr Pro Arg Gly Arg Arg Lys Gly Arg Ala Gly	
273 278 283 288	
cgg tcg gcg gcg gcc gtt ggc gag ctg agg cct gcc agg cga agt ctg	912
Arg Ser Ala Ala Ala Val Gly Glu Leu Arg Pro Ala Arg Arg Ser Leu	
289 294 299 304	
gag acc agc cgg gcc gcg gcc gca atg gcc aag gac tcg ccc agc ccc	960
Glu Thr Ser Arg Ala Ala Ala Met Ala Lys Asp Ser Pro Ser Pro	
305 310 315 320	
ttg ggc gcg tcg ccc aag aag ccg ggc tgc tcc agc ccg gcg gcg gca	1008
Leu Gly Ala Ser Pro Lys Lys Pro Gly Cys Ser Ser Pro Ala Ala Ala	
321 326 331 336	
gtg ctg gag aac cag agg cgg gag ctg gag aag cta cgg gcg gag ctg	1056
Val Leu Glu Asn Gln Arg Arg Glu Leu Glu Lys Leu Arg Ala Glu Leu	
337 342 347 352	
gag gcg gag cgg gca ggc tgg cgg gcg gaa cgg cgg cgc ttc gct gcc	1104
Glu Ala Glu Arg Ala Gly Trp Arg Ala Glu Arg Arg Arg Phe Ala Ala	
353 358 363 368	
cgg gag cgc cag ctg cgt gag gag gcc gag cgg gag cgg cga cag ctg	1152
Arg Glu Arg Gln Leu Arg Glu Glu Ala Glu Arg Glu Arg Arg Gln Leu	
369 374 379 384	
gct gac cgt ctg cgc tcc aag tgg gag gca cag cgc agc cgg gag ttg	1200
Ala Asp Arg Leu Arg Ser Lys Trp Glu Ala Gln Arg Ser Arg Glu Leu	
385 390 395 400	
cgg cag ctg caa gag gag atg cag cgg gaa cgc gag gcc gag atc cgg	1248
Arg Gln Leu Gln Glu Glu Met Gln Arg Glu Arg Glu Ala Glu Ile Arg	
401 406 411 416	
cag ctg ctg cgc tgg aag gag gcc gag cag cgg cag ctg cag cag ctg	1296
Gln Leu Leu Arg Trp Lys Glu Ala Glu Gln Arg Gln Leu Gln Gln Leu	
417 422 427 432	
ctg cac cgg gag cgc gat ggc gtg gtg cgc caa gcc cgg gag ctg cag	1344
Leu His Arg Glu Arg Asp Gly Val Val Arg Gln Ala Arg Glu Leu Gln	
433 438 443 448	
cgc cag ctg gcc gag gag ctg gtg aac cgc ggc cac tgt agc cgc ccg	1392
Arg Gln Leu Ala Glu Glu Leu Val Asn Arg Gly His Cys Ser Arg Pro	
449 454 459 464	

ggg gcg tcc gag gtt tcc gcg gcg cag tgc cgc tgt cgc ctg cag gaa	1440
Gly Ala Ser Glu Val Ser Ala Ala Gln Cys Arg Cys Arg Leu Gln Glu	
465 470 475 480	
gtg ttg gcg cag ctt cgc tgg cag act gac ggc gag cag gcg gcg cgc	1488
Val Leu Ala Gln Leu Arg Trp Gln Thr Asp Gly Glu Gln Ala Ala Arg	
481 486 491 496	
atc cgc tat ctg cag gcg gcg ctg gag gtg gag cgc cag ctc ttc ctc	1536
Ile Arg Tyr Leu Gln Ala Ala Leu Glu Val Glu Arg Gln Leu Phe Leu	
497 502 507 512	
aag tac atc ctg gcg cac ttc cgc ggg cac ccg gct ttg tcg gga tca	1584
Lys Tyr Ile Leu Ala His Phe Arg Gly His Pro Ala Leu Ser Gly Ser	
513 518 523 528	
ccg gac ccc caa gct gtg cat tcc ttg gaa gaa ccg ctg ccc cag acc	1632
Pro Asp Pro Gln Ala Val His Ser Leu Glu Glu Pro Leu Pro Gln Thr	
529 534 539 544	
tcc agc ggc tct tgc cac gcc ccc aaa ccc gcc tgc caa ctc gga tct	1680
Ser Ser Gly Ser Cys His Ala Pro Lys Pro Ala Cys Gln Leu Gly Ser	
545 550 555 560	
cta gac agc ctg agt gct gaa gtc ggt gtg cgc tcc cgc tcg cta ggc	1728
Leu Asp Ser Leu Ser Ala Glu Val Gly Val Arg Ser Arg Ser Leu Gly	
561 566 571 576	
ctg gtg tcc tct gcg tgc tcc agc tcc cca gac ggc ctg ctc tcc acg	1776
Leu Val Ser Ser Ala Cys Ser Ser Ser Pro Asp Gly Leu Leu Ser Thr	
577 582 587 592	
cac gcc agc tcc ctt gat tgc ttc gca cct gcg tgt tcc cgc tcg ctt	1824
His Ala Ser Ser Leu Asp Cys Phe Ala Pro Ala Cys Ser Arg Ser Leu	
593 598 603 608	
gac agc acc cgg agc ctc ccc aag gcc tcc aaa tcc gag gag cgg ccc	1872
Asp Ser Thr Arg Ser Leu Pro Lys Ala Ser Lys Ser Glu Glu Arg Pro	
609 614 619 624	
tcc tca cca gac acc tcc acc cct ggc tcc cgg agg ctc tcg ccg cca	1920
Ser Ser Pro Asp Thr Ser Thr Pro Gly Ser Arg Arg Leu Ser Pro Pro	
625 630 635 640	
cca tcg cca ctc ccg ccg cca cca cca ccg tca gcc cac agg aaa ctc	1968
Pro Ser Pro Leu Pro Pro Pro Pro Pro Pro Ser Ala His Arg Lys Leu	
641 646 651 656	
agc aac ccg cgg gga gga gaa ggc tct gag agc cag ccc tgc gaa gtc	2016
Ser Asn Pro Arg Gly Gly Glu Gly Ser Glu Ser Gln Pro Cys Glu Val	
657 662 667 672	
ctg act ccc tca ccc ccg ggc ctg ggc cac cac gag ctg ata aag ctg	2064
Leu Thr Pro Ser Pro Pro Gly Leu Gly His His Glu Leu Ile Lys Leu	
673 678 683 688	
aac tgg ctg ctg gcc aag gcg ttg tgg gtg ctg gcg cgc cgc tgt tat	2112

Asn Trp Leu Leu Ala Lys Ala Leu Trp Val Leu Ala Arg Arg Cys Tyr	689	694	699	704	
acc ctg caa gcg gag aac aag cag ctg cgg cgt gca ggc tgc ccc tac	2160				
Thr Leu Gln Ala Glu Asn Lys Gln Leu Arg Arg Ala Gly Cys Pro Tyr	705	710	715	720	
cag gca gac gag aag gtg aag cgg ctc aag gta aag cgc gcg gag ctg	2208				
Gln Ala Asp Glu Lys Val Lys Arg Leu Lys Val Lys Arg Ala Glu Leu	721	726	731	736	
acc ggg ctc gcg cgg cgc cta gct gac cgc gcc cgc aag ctg cag gag	2256				
Thr Gly Leu Ala Arg Arg Leu Ala Asp Arg Ala Arg Lys Leu Gln Glu	737	742	747	752	
acc aac ctc cgg gcc gtg agc gcg cct ata ccc ggc gag agt tgc gcc	2304				
Thr Asn Leu Arg Ala Val Ser Ala Pro Ile Pro Gly Glu Ser Cys Ala	753	758	763	768	
ggc ctg gag ctg tgc caa gtc ttt gcc cgc cag cgc gct cgg gac ctg	2352				
Gly Leu Glu Leu Cys Gln Val Phe Ala Arg Gln Arg Ala Arg Asp Leu	769	774	779	784	
tcg gag cag gcg agc gcg ccg ctg gcc aag gac aag cag atc gaa gag	2400				
Ser Glu Gln Ala Ser Ala Pro Leu Ala Lys Asp Lys Gln Ile Glu Glu	785	790	795	800	
ctg cgg cag gag tgc cac ctc ctg cag gcg cgt gtc gcc tcg ggt ccc	2448				
Leu Arg Gln Glu Cys His Leu Leu Gln Ala Arg Val Ala Ser Gly Pro	801	806	811	816	
tgc agc gac ctg cat act gga agg ggc ggc ccc tgc acc cag tgg ctc	2496				
Cys Ser Asp Leu His Thr Gly Arg Gly Gly Pro Cys Thr Gln Trp Leu	817	822	827	832	
aac gtc aga gac tta gac cgc ctg cag cgc gag tcc cag cgg gaa gtg	2544				
Asn Val Arg Asp Leu Asp Arg Leu Gln Arg Glu Ser Gln Arg Glu Val	833	838	843	848	
ctg cgc ctg cag agg cag ttg atg ctt cag cag ggc aac ggt ggc gct	2592				
Leu Arg Leu Gln Arg Gln Leu Met Leu Gln Gln Gly Asn Gly Gly Ala	849	854	859	864	
tgg ccc gag gcg ggc ggc cag agc gca acc tgc gag gag gtg cga cgg	2640				
Trp Pro Glu Ala Gly Gly Gln Ser Ala Thr Cys Glu Glu Val Arg Arg	865	870	875	880	
cag atg ctg gcg ctg gag cgc gag ctg gac cag cgg cgg cgc gag tgc	2688				
Gln Met Leu Ala Leu Glu Arg Glu Leu Asp Gln Arg Arg Arg Glu Cys	881	886	891	896	
cag gag ctg ggc gcg cag gcg gcc ccg gcg cgg cga cgt ggc gag gag	2736				
Gln Glu Leu Gly Ala Gln Ala Ala Pro Ala Arg Arg Arg Gly Glu Glu	897	902	907	912	
gcc gag aca cag ctg cag gcg gcg ctg ctc aaa aac gcc tgg ctg gcg	2784				
Ala Glu Thr Gln Leu Gln Ala Ala Leu Leu Lys Asn Ala Trp Leu Ala					

913	918	923	928	
gag gag aat ggg cgg ctg cag gcc aag acc gac tgg gtg cgg aag gtg				2832
Glu Glu Asn Gly Arg Leu Gln Ala Lys Thr Asp Trp Val Arg Lys Val				
929	934	939	944	
gag gct gag aat agc gaa gtg cgc ggc cac ctg ggc cgc gcg tgt caa				2880
Glu Ala Glu Asn Ser Glu Val Arg Gly His Leu Gly Arg Ala Cys Gln				
945	950	955	960	
gag cgc gat gcc tcc ggc ttg atc gcc gaa cag ctg ctg cag cag gcg				2928
Glu Arg Asp Ala Ser Gly Leu Ile Ala Glu Gln Leu Leu Gln Gln Ala				
961	966	971	976	
gcg cgc ggg cag gac agg cag cag cag ctg caa cgc gac ccg cag aag				2976
Ala Arg Gly Gln Asp Arg Gln Gln Gln Leu Gln Arg Asp Pro Gln Lys				
977	982	987	992	
gcc ctg tgt gac ctc cat cct tcc tgg aag gag ata cag gcg ctc cag				3024
Ala Leu Cys Asp Leu His Pro Ser Trp Lys Glu Ile Gln Ala Leu Gln				
993	998	1003	1008	
tgt cgg cct ggt cac cct cct gaa cag ccc tgg gag acc agt caa atg				3072
Cys Arg Pro Gly His Pro Pro Glu Gln Pro Trp Glu Thr Ser Gln Met				
1009	1014	1019	1024	
ccg gag tcc caa gtt aaa ggt agc aga agg ccc aag ttc cac gca cgg				3120
Pro Glu Ser Gln Val Lys Gly Ser Arg Arg Pro Lys Phe His Ala Arg				
1025	1030	1035	1040	
cct gaa gac tac gca gtg tca cag ccc aac aga gac ata cag gag aaa				3168
Pro Glu Asp Tyr Ala Val Ser Gln Pro Asn Arg Asp Ile Gln Glu Lys				
1041	1046	1051	1056	
agg gaa gcc tcc ctc gag gag agc cca gtt gcc ctt ggg gag tca gcc				3216
Arg Glu Ala Ser Leu Glu Glu Ser Pro Val Ala Leu Gly Glu Ser Ala				
1057	1062	1067	1072	
agt gtc ccc caa gtt tca gag aca gtc cct gcc agc caa cct ctg tcc				3264
Ser Val Pro Gln Val Ser Glu Thr Val Pro Ala Ser Gln Pro Leu Ser				
1073	1078	1083	1088	
aag aaa acc agc tcc cag tca aac tcc tcc tct gag ggg tcg atg tgg				3312
Lys Lys Thr Ser Ser Gln Ser Asn Ser Ser Ser Glu Gly Ser Met Trp				
1089	1094	1099	1104	
gcc acc gtg ccg tcc tcc cct act ctg gac agg gac aca gcc agt gag				3360
Ala Thr Val Pro Ser Ser Pro Thr Leu Asp Arg Asp Thr Ala Ser Glu				
1105	1110	1115	1120	
gtg gat gac ctg gag cct gac agc gtg tcc ctg gcc ctg gaa atg ggg				3408
Val Asp Asp Leu Glu Pro Asp Ser Val Ser Leu Ala Leu Glu Met Gly				
1121	1126	1131	1136	
ggc tcg gcg gct cct gct gcc ccc aag ctc aag atc ttc atg gct cag				3456
Gly Ser Ala Ala Pro Ala Ala Pro Lys Leu Lys Ile Phe Met Ala Gln				
1137	1142	1147	1152	

tat aac tac aac cca ttt gag ggg ccc aat gat cac cct gag ggt gag	3504
Tyr Asn Tyr Asn Pro Phe Glu Gly Pro Asn Asp His Pro Glu Gly Glu	
1153 1158 1163 1168	
ctg ccc ctc aca gct ggg gac tac ata tat atc ttc ggg gac atg gat	3552
Leu Pro Leu Thr Ala Gly Asp Tyr Ile Tyr Ile Phe Gly Asp Met Asp	
1169 1174 1179 1184	
gag gat ggc ttc tat gag ggg gag ctt gag gat ggc cgg cgg ggg ctg	3600
Glu Asp Gly Phe Tyr Glu Gly Glu Leu Glu Asp Gly Arg Arg Gly Leu	
1185 1190 1195 1200	
gtg ccc tcc aac ttc gtg gag cag att ccg gac agc tac atc cca ggc	3648
Val Pro Ser Asn Phe Val Glu Gln Ile Pro Asp Ser Tyr Ile Pro Gly	
1201 1206 1211 1216	
tgc ctg cct gcc aaa tcc cct gat ctt ggc ccc agt caa ctc cca gcg	3696
Cys Leu Pro Ala Lys Ser Pro Asp Leu Gly Pro Ser Gln Leu Pro Ala	
1217 1222 1227 1232	
ggg cag gat gaa gct ctg gag gaa gac agc tta tta tct ggg aaa gcc	3744
Gly Gln Asp Glu Ala Leu Glu Glu Asp Ser Leu Leu Ser Gly Lys Ala	
1233 1238 1243 1248	
cag gga gtg gtg gac aga ggg ctg tgc cag atg gtc agg gtg ggc tcc	3792
Gln Gly Val Val Asp Arg Gly Leu Cys Gln Met Val Arg Val Gly Ser	
1249 1254 1259 1264	
aag aca gaa gta gca aca gag atc ctg gat acc aag acg gaa gcc tgc	3840
Lys Thr Glu Val Ala Thr Glu Ile Leu Asp Thr Lys Thr Glu Ala Cys	
1265 1270 1275 1280	
cag ctg ggc ttg ctg cag agc atg ggg aag cag ggc ctc tcc aga ccc	3888
Gln Leu Gly Leu Leu Gln Ser Met Gly Lys Gln Gly Leu Ser Arg Pro	
1281 1286 1291 1296	
ctt ctg ggg acc aaa ggg gtg ctc cgt atg gct ccc atg cag cta cac	3936
Leu Leu Gly Thr Lys Gly Val Leu Arg Met Ala Pro Met Gln Leu His	
1297 1302 1307 1312	
ctg cag aat gtc aca gcc aca tca gcc aac atc acc tgg gtc tac agc	3984
Leu Gln Asn Val Thr Ala Thr Ser Ala Asn Ile Thr Trp Val Tyr Ser	
1313 1318 1323 1328	
agc cac cgc cac ccc cat gtg gta tat ctt gat gac cga gag cat gcc	4032
Ser His Arg His Pro His Val Val Tyr Leu Asp Asp Arg Glu His Ala	
1329 1334 1339 1344	
ctg acc cca gcg ggc gtg agc tgc tac acc ttc cag ggc ctg tgc ccc	4080
Leu Thr Pro Ala Gly Val Ser Cys Tyr Thr Phe Gln Gly Leu Cys Pro	
1345 1350 1355 1360	
ggc acg cac tac cgg gcg cgg gtg gag gtg cgg ctg cca cgg gac ttg	4128
Gly Thr His Tyr Arg Ala Arg Val Glu Val Arg Leu Pro Arg Asp Leu	
1361 1366 1371 1376	

ctg cag gtg tat tgg gga act atg tcc tcc acc gtc acc ttc gac aca	4176
Leu Gln Val Tyr Trp Gly Thr Met Ser Ser Thr Val Thr Phe Asp Thr	
1377 1382 1387 1392	
ctc ttg gca gga cct ccc tac cca ccg ctg gat gtg ctg gtg gag cgc	4224
Leu Leu Ala Gly Pro Pro Tyr Pro Pro Leu Asp Val Leu Val Glu Arg	
1393 1398 1403 1408	
cat gcc tcg cca ggt gtc ctg gtg gtc agc tgg ctc cct gtg acc att	4272
His Ala Ser Pro Gly Val Leu Val Val Ser Trp Leu Pro Val Thr Ile	
1409 1414 1419 1424	
gac tca gct ggg tcc tcc aat gga gtc cag gtc acc ggt tat gct gtg	4320
Asp Ser Ala Gly Ser Ser Asn Gly Val Gln Val Thr Gly Tyr Ala Val	
1425 1430 1435 1440	
tat gca gat ggg ctt aag gtt tgt gag gtc gcc gat gcc act gct ggg	4368
Tyr Ala Asp Gly Leu Lys Val Cys Glu Val Ala Asp Ala Thr Ala Gly	
1441 1446 1451 1456	
agc acc cta ttg gaa ttc tcc cag cta cag gtg ccc ctc acg tgg cag	4416
Ser Thr Leu Leu Glu Phe Ser Gln Leu Gln Val Pro Leu Thr Trp Gln	
1457 1462 1467 1472	
aag gtc tca gtg aga acc atg tca ctc tgt ggt gag tcc ctg gat tca	4464
Lys Val Ser Val Arg Thr Met Ser Leu Cys Gly Glu Ser Leu Asp Ser	
1473 1478 1483 1488	
gtg cct gct cag atc ccc gag gac ttc ttc atg tgt cac cga tgg cca	4512
Val Pro Ala Gln Ile Pro Glu Asp Phe Phe Met Cys His Arg Trp Pro	
1489 1494 1499 1504	
gag act cca ccc ttt agc tac act tgt ggc gac cca tcc acc tac aga	4560
Glu Thr Pro Pro Phe Ser Tyr Thr Cys Gly Asp Pro Ser Thr Tyr Arg	
1505 1510 1515 1520	
gtc acc ttc ccc gtc tgc ccc cag aag ctg tca ctg gct cct ccg agt	4608
Val Thr Phe Pro Val Cys Pro Gln Lys Leu Ser Leu Ala Pro Pro Ser	
1521 1526 1531 1536	
gcc aag gcc agc ccc cac aac cct gga agc tgc ggg gag ccc cag gcc	4656
Ala Lys Ala Ser Pro His Asn Pro Gly Ser Cys Gly Glu Pro Gln Ala	
1537 1542 1547 1552	
aag ttc cta gaa gca ttc ttt gaa gaa ccc cca agg agg caa tcc cca	4704
Lys Phe Leu Glu Ala Phe Phe Glu Glu Pro Pro Arg Arg Gln Ser Pro	
1553 1558 1563 1568	
gtg tcc aac ctg ggc tca gaa gga gaa tgt ccg agt tca ggg gct ggc	4752
Val Ser Asn Leu Gly Ser Glu Gly Glu Cys Pro Ser Ser Gly Ala Gly	
1569 1574 1579 1584	
agc caa gcc cag gag ctt gca gag gcc tgg gag ggc tgt aga aag gac	4800
Ser Gln Ala Gln Glu Leu Ala Glu Ala Trp Glu Gly Cys Arg Lys Asp	
1585 1590 1595 1600	
ctg ctc ttt cag aag agt ccc cag aac cac agg cca cct tca gtc agt	4848

Leu	Leu	Phe	Gln	Lys	Ser	Pro	Gln	Asn	His	Arg	Pro	Pro	Ser	Val	Ser		
1601					1606					1611					1616		
gac	cag	cct	ggg	gag	aag	gaa	aat	tgc	tcc	cag	cac	atg	ggc	acc	agc		4896
Asp	Gln	Pro	Gly	Glu	Lys	Glu	Asn	Cys	Ser	Gln	His	Met	Gly	Thr	Ser		
1617					1622					1627					1632		
aaa	agc	cct	gct	cca	gga	ttc	atc	cat	cta	cgc	acc	gag	tgt	ggg	ccc		4944
Lys	Ser	Pro	Ala	Pro	Gly	Phe	Ile	His	Leu	Arg	Thr	Glu	Cys	Gly	Pro		
1633					1638					1643					1648		
agg	aaa	gaa	ccg	tgt	cag	gaa	aag	gct	gcc	ctt	gag	agg	gta	ctt	cgg		4992
Arg	Lys	Glu	Pro	Cys	Gln	Glu	Lys	Ala	Ala	Leu	Glu	Arg	Val	Leu	Arg		
1649					1654					1659					1664		
caa	aag	caa	gat	gcc	caa	ggg	ttc	aca	cct	ccc	cag	ctg	ggc	gcc	agc		5040
Gln	Lys	Gln	Asp	Ala	Gln	Gly	Phe	Thr	Pro	Pro	Gln	Leu	Gly	Ala	Ser		
1665					1670					1675					1680		
caa	cag	tat	gca	tct	gac	ttc	cat	aac	gtt	ttg	aag	gag	gag	cag	gag		5088
Gln	Gln	Tyr	Ala	Ser	Asp	Phe	His	Asn	Val	Leu	Lys	Glu	Glu	Gln	Glu		
1681					1686					1691					1696		
gca	ctg	tgc	ttg	gat	ctg	tgg	ggc	aca	gag	agg	cga	gag	gag	agg	agg		5136
Ala	Leu	Cys	Leu	Asp	Leu	Trp	Gly	Thr	Glu	Arg	Arg	Glu	Glu	Arg	Arg		
1697					1702					1707					1712		
gag	cct	gag	ccc	cac	agc	agg	caa	gga	caa	gct	ctg	ggg	gtg	aag	aga		5184
Glu	Pro	Glu	Pro	His	Ser	Arg	Gln	Gly	Gln	Ala	Leu	Gly	Val	Lys	Arg		
1713					1718					1723					1728		
ggg	tgc	cag	ctc	cat	gag	ccc	agc	tcg	gca	ctg	tgt	cca	gct	cca	tcc		5232
Gly	Cys	Gln	Leu	His	Glu	Pro	Ser	Ser	Ala	Leu	Cys	Pro	Ala	Pro	Ser		
1729					1734					1739					1744		
gcc	aaa	gtc	atc	aag	atg	ccc	agg	ggg	ggc	ccc	caa	cag	ctg	ggg	acg		5280
Ala	Lys	Val	Ile	Lys	Met	Pro	Arg	Gly	Gly	Pro	Gln	Gln	Leu	Gly	Thr		
1745					1750					1755					1760		
ggg	gcc	aac	act	cca	gcc	agg	gtc	ttt	gtg	gcc	ctc	tct	gat	tac	aac		5328
Gly	Ala	Asn	Thr	Pro	Ala	Arg	Val	Phe	Val	Ala	Leu	Ser	Asp	Tyr	Asn		
1761					1766					1771					1776		
ccc	ctg	gtg	atg	tct	gcc	aac	ctc	aag	gct	gca	gag	gag	gag	ctg	gtc		5376
Pro	Leu	Val	Met	Ser	Ala	Asn	Leu	Lys	Ala	Ala	Glu	Glu	Glu	Leu	Val		
1777					1782					1787					1792		
ttc	cag	aaa	agg	cag	ttg	cta	aga	gtg	tgg	ggc	tct	cag	gac	acc	cat		5424
Phe	Gln	Lys	Arg	Gln	Leu	Leu	Arg	Val	Trp	Gly	Ser	Gln	Asp	Thr	His		
1793					1798					1803					1808		
gat	ttc	tac	ctc	agc	gag	tgc	aac	agg	caa	gtg	ggc	aat	atc	ccc	ggg		5472
Asp	Phe	Tyr	Leu	Ser	Glu	Cys	Asn	Arg	Gln	Val	Gly	Asn	Ile	Pro	Gly		
1809					1814					1819					1824		
cgc	cta	gtg	gct	gag	atg	gag	gtg	ggg	aca	gag	cag	act	gat	agg	agg		5520
Arg	Leu	Val	Ala	Glu	Met	Glu	Val	Gly	Thr	Glu	Gln	Thr	Asp	Arg	Arg		

1825	1830	1835	1840	
tgg cgt tct ccg gcc caa ggg cac ctg cct tct gtg gcc cac ctc gag				5568
Trp Arg Ser Pro Ala Gln Gly His Leu Pro Ser Val Ala His Leu Glu				
1841	1846	1851	1856	
gac ttt cag ggg ctc acc atc ccc cag ggt tcc tcc ctg gtg ctc cag				5616
Asp Phe Gln Gly Leu Thr Ile Pro Gln Gly Ser Ser Leu Val Leu Gln				
1857	1862	1867	1872	
ggg aac tcc aag aga ctc cca ctg tgg act cca aag atc atg ata gca				5664
Gly Asn Ser Lys Arg Leu Pro Leu Trp Thr Pro Lys Ile Met Ile Ala				
1873	1878	1883	1888	
gct ctg gac tat gat cct ggg gat ggg caa atg ggg ggc cag ggg aag				5712
Ala Leu Asp Tyr Asp Pro Gly Asp Gly Gln Met Gly Gly Gln Gly Lys				
1889	1894	1899	1904	
ggc agg ctg gcg ctg agg gca gga gac gtg gtc atg gtt tac ggg ccc				5760
Gly Arg Leu Ala Leu Arg Ala Gly Asp Val Val Met Val Tyr Gly Pro				
1905	1910	1915	1920	
atg gat gac caa gga ttc tat tat gga gag ttg ggc ggc cac agg ggc				5808
Met Asp Asp Gln Gly Phe Tyr Tyr Gly Glu Leu Gly Gly His Arg Gly				
1921	1926	1931	1936	
ctg gtt cct gcc cac ctg ctg gat cac atg tcc ctc cat gga cac tga				5856
Leu Val Pro Ala His Leu Leu Asp His Met Ser Leu His Gly His *				
1937	1942	1947	1952	
gcaagcatcc ttgcccaggt agtggcctct ggctgctcac accctgccag aggagaagca				5916
agcgttcaga ccctcacacc agcaccctc ctcaccacca taagtagcat gtgctccaag				5976
tgccactgtg ttaaactgat ggtagtcctt aagtgtcccc taggctctga aagtagcagg				6036
acttaagcct gagttatttg caaaagcaaa cacaacaagc caaccctga gagtctgaga				6096
agccatttca aagttgctga taactatggc aggtatacgg agaagcgcct ttttctgtgg				6156
ccaatgtgtg ttttctctgg gaggttaagg ttatctgtcc attgccttgt acgaaagtct				6216
caagaaaagt ctacatctta aaaaaaaaaa aa				6248

<210> 163
 <211> 1265
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (204)..(1265)

<400> 163

cgg aac ctg acc aac gtg ctg ggc acc cag tcc cgc tac gtc ctc aac	854
Arg Asn Leu Thr Asn Val Leu Gly Thr Gln Ser Arg Tyr Val Leu Asn	
202 207 212 217	
ggc gcg ttc ctg gcc ttc gag cgc cgg cac gag ttc atg gcg ctg tgc	902
Gly Ala Phe Leu Ala Phe Glu Arg Arg His Glu Phe Met Ala Leu Cys	
218 223 228 233	
atg cgg gac ttc gtg gac cac tac aac ggc tgg atc tgg ggt cac cag	950
Met Arg Asp Phe Val Asp His Tyr Asn Gly Trp Ile Trp Gly His Gln	
234 239 244 249	
ggc ccg cag ctg ctc acg cgg gtc ttc aag aag tgg tgt tcc atc cgc	998
Gly Pro Gln Leu Leu Thr Arg Val Phe Lys Lys Trp Cys Ser Ile Arg	
250 255 260 265	
agc ctg gcc gag agc cgc gcc tgc cgc ggc gtc acc acc ctg ccc cct	1046
Ser Leu Ala Glu Ser Arg Ala Cys Arg Gly Val Thr Thr Leu Pro Pro	
266 271 276 281	
gag gcc ttc tac ccc atc ccc tgg cag gac tgg aag aag tac ttt gag	1094
Glu Ala Phe Tyr Pro Ile Pro Trp Gln Asp Trp Lys Lys Tyr Phe Glu	
282 287 292 297	
gac atc aac ccg gag gag ctg ccg cgg ctg ctc agt gcc acc tat gct	1142
Asp Ile Asn Pro Glu Glu Leu Pro Arg Leu Leu Ser Ala Thr Tyr Ala	
298 303 308 313	
gtc cac gtg tgg aac aag aag agc cag ggc acg cgg ttc gag gcc acg	1190
Val His Val Trp Asn Lys Lys Ser Gln Gly Thr Arg Phe Glu Ala Thr	
314 319 324 329	
tcc agg gca ctg ctg gcc cag ctg cat gcc cgc tac tgc ccc acg acg	1238
Ser Arg Ala Leu Leu Ala Gln Leu His Ala Arg Tyr Cys Pro Thr Thr	
330 335 340 345	
cac gag gcc atg aaa atg tac ttg tga	1265
His Glu Ala Met Lys Met Tyr Leu *	
346 351	

<210> 164
 <211> 1825
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1587)

<400> 164

atg gca aag gtc att ctg aag cag agt aaa caa tgc aag aat ctg ctt	48
Met Ala Lys Val Ile Leu Lys Gln Ser Lys Gln Cys Lys Asn Leu Leu	

1	5	10	
acc tgc aaa gtg gcc cag gtc tgc ccc gta tgt ggc tgt ctt cat tgt			96
Thr Cys Lys Val Ala Gln Val Cys Pro Val Cys Gly Cys Leu His Cys			
17	22	27	32
tat ttc tgg tgg ctc tca ggt ctt gag tca aga cgt ccc agc tct cca			144
Tyr Phe Trp Trp Leu Ser Gly Leu Glu Ser Arg Arg Pro Ser Ser Pro			
33	38	43	48
ctc atc gat att aaa ccc atc gag ttt ggc gtt ctc agc gcc aag aag			192
Leu Ile Asp Ile Lys Pro Ile Glu Phe Gly Val Leu Ser Ala Lys Lys			
49	54	59	64
gag ccc atc caa cct tcg gtg ctc aga cgg acc tat aac ccc gac gac			240
Glu Pro Ile Gln Pro Ser Val Leu Arg Arg Thr Tyr Asn Pro Asp Asp			
65	70	75	80
tat ttc agg aag ttc gaa ccc cac ctg tac tcc ctc gac tcc aac agc			288
Tyr Phe Arg Lys Phe Glu Pro His Leu Tyr Ser Leu Asp Ser Asn Ser			
81	86	91	96
gac gat gtg gac tct ctg aca gag gag gag atc ctg tcc aag tac cag			336
Asp Asp Val Asp Ser Leu Thr Asp Glu Glu Ile Leu Ser Lys Tyr Gln			
97	102	107	112
ctg ggc atg ctg cac ttc agc act cag tac gac ctg ctg cac aac cac			384
Leu Gly Met Leu His Phe Ser Thr Gln Tyr Asp Leu Leu His Asn His			
113	118	123	128
ctc acc gtg cgc gtg atc gag gcc agg gac ctg cca cct ccc atc tcc			432
Leu Thr Val Arg Val Ile Glu Ala Arg Asp Leu Pro Pro Pro Ile Ser			
129	134	139	144
cac gat ggc tcg cgc cag gac atg gcg cac tcc aac ccc tac gtc aag			480
His Asp Gly Ser Arg Gln Asp Met Ala His Ser Asn Pro Tyr Val Lys			
145	150	155	160
atc tgt ctc ctg cca gac cag aag aac tca aag cag acc ggg gtc aaa			528
Ile Cys Leu Leu Pro Asp Gln Lys Asn Ser Lys Gln Thr Gly Val Lys			
161	166	171	176
cgc aag acc cag aag ccc gtg ttt gag gag cgc tac acc ttc gag atc			576
Arg Lys Thr Gln Lys Pro Val Phe Glu Glu Arg Tyr Thr Phe Glu Ile			
177	182	187	192
ccc ttc ctg gag gcc cag agg agg acc ctg ctc ctg acc gtg gtg gat			624
Pro Phe Leu Glu Ala Gln Arg Arg Thr Leu Leu Leu Thr Val Val Asp			
193	198	203	208
ttt gat aag ttc tcc cgc cac tgt gtc att ggg aaa gtt tct gtg cct			672
Phe Asp Lys Phe Ser Arg His Cys Val Ile Gly Lys Val Ser Val Pro			
209	214	219	224
ttg tgt gaa gtt gac ctg gtc aag ggc ggg cac tgg tgg aag gcg cat			720
Leu Cys Glu Val Asp Leu Val Lys Gly Gly His Trp Trp Lys Ala His			
225	230	235	240

gat tcc cag ttc tca gca cca ggc ttg ccc gcc gat caa caa ttt ttc	768
Asp Ser Gln Phe Ser Ala Pro Gly Leu Pro Ala Asp Gln Gln Phe Phe	
241 246 251 256	
gcc gat ctg ttc agc ggc ctg gtg ctt aac ccg caa cta ctg ggg cgc	816
Ala Asp Leu Phe Ser Gly Leu Val Leu Asn Pro Gln Leu Leu Gly Arg	
257 262 267 272	
gtc tgg ttt gcc agc cag cct gcc tcg ttg ccg gtg ggc agt tta tgt	864
Val Trp Phe Ala Ser Gln Pro Ala Ser Leu Pro Val Gly Ser Leu Cys	
273 278 283 288	
att gat ttt ccc cgt ctg gat atc gtg ctg cgc ggc gaa tac ggc aat	912
Ile Asp Phe Pro Arg Leu Asp Ile Val Leu Arg Gly Glu Tyr Gly Asn	
289 294 299 304	
ctg ctg gaa gca aag cag caa cgt ttg gtg gaa gga gaa atg ctg ttt	960
Leu Leu Glu Ala Lys Gln Gln Arg Leu Val Glu Gly Glu Met Leu Phe	
305 310 315 320	
att ccg gcg cgc gcg gct aat tta ccg gtc aac aac aaa ccg gtg atg	1008
Ile Pro Ala Arg Ala Ala Asn Leu Pro Val Asn Asn Lys Pro Val Met	
321 326 331 336	
ctg tta agc ctg gtg ttc gct ccg acc tgg ctt ggg tta tcg ttt tac	1056
Leu Leu Ser Leu Val Phe Ala Pro Thr Trp Leu Gly Leu Ser Phe Tyr	
337 342 347 352	
gat agc cgc acc acg tcg ttg ttg cat cct gct cgc cag atc cag ctt	1104
Asp Ser Arg Thr Thr Ser Leu Leu His Pro Ala Arg Gln Ile Gln Leu	
353 358 363 368	
ccc agc ctg caa cgc ggt gaa ggt gaa gcg atg ctt acc gcc ctc acc	1152
Pro Ser Leu Gln Arg Gly Glu Gly Glu Ala Met Leu Thr Ala Leu Thr	
369 374 379 384	
cat ctt agc cgt tcg ccg ctg gag caa aat atc att cag ccg ctg gtg	1200
His Leu Ser Arg Ser Pro Leu Glu Gln Asn Ile Ile Gln Pro Leu Val	
385 390 395 400	
tta agt ttg ctg cat ctt tgc cgt agc gtg gtg aat atg ccg ccg ggc	1248
Leu Ser Leu Leu His Leu Cys Arg Ser Val Val Asn Met Pro Pro Gly	
401 406 411 416	
aat tcg cag ccg cgc ggc gat ttt ctc tat cac agc att tgt aac tgg	1296
Asn Ser Gln Pro Arg Gly Asp Phe Leu Tyr His Ser Ile Cys Asn Trp	
417 422 427 432	
gtt cag gat aat tat gcc cag ccg ctc acc cgc gag agc gtg gcg cag	1344
Val Gln Asp Asn Tyr Ala Gln Pro Leu Thr Arg Glu Ser Val Ala Gln	
433 438 443 448	
ttt ttt aat atc acg ccc aat cat ctg tca aaa ctg ttt gct cag cat	1392
Phe Phe Asn Ile Thr Pro Asn His Leu Ser Lys Leu Phe Ala Gln His	
449 454 459 464	

gga acg atg cgt ttt atc gag tat gtg cgt tgg gtg cga atg gcg aag	1440
Gly Thr Met Arg Phe Ile Glu Tyr Val Arg Trp Val Arg Met Ala Lys	
465 470 475 480	

gcg agg atg att ttg cag aaa tat cat ctg tca att cat gaa gtg gca	1488
Ala Arg Met Ile Leu Gln Lys Tyr His Leu Ser Ile His Glu Val Ala	
481 486 491 496	

cag cgt tgc ggt ttt ccg gat agc gac tat ttt tgt cgc gtt ttc cgg	1536
Gln Arg Cys Gly Phe Pro Asp Ser Asp Tyr Phe Cys Arg Val Phe Arg	
497 502 507 512	

cgt cag ttt ggt ctg acg ccg gga gag tac agc gcc cgt ttt cag ggc	1584
Arg Gln Phe Gly Leu Thr Pro Gly Glu Tyr Ser Ala Arg Phe Gln Gly	
513 518 523 528	

taa cgtc agaagggttaa ttctgtttcc agcagcgtca ggatactttg tgcattctgc	1641
*	
529	

gcggcaaaca acgactggcg gaagttttta ttcaccagtt tacgcgccag ctgcgagaag	1701
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actttcacat gattcatccc ttcgttagca cccagcgtca gcatgatcac cagttcgact	1761
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tcgcccattt ctgactgcca gccaatcggg ttcgccagcc gggcaatgct gatactggaa	1821
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tgac	1825
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<210> 165
 <211> 4880
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (225) .. (3248)

<400> 165	
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gagagtctgt gtctctggga aagaagaaca tctctgcttc acagtgattt gcgctggggg	120
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agaggcatca attggcttcg gacccaaggg ggagacgaga ccaggtcacc ccggttaaga	180
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ccaagtgagc gttgcccctc cctctcccaa ctctctaccc ggga atg tct cgg cga	236
Met Ser Arg Arg	
1	

aag cag cgg aaa ccc caa cag tta atc tcg gac tgc gaa ggt ccc agc	284
Lys Gln Arg Lys Pro Gln Gln Leu Ile Ser Asp Cys Glu Gly Pro Ser	
5 10 15 20	

gcg tct gag aac ggt gat gct agc gag gag gat cac ccc caa gtc tgt	332
Ala Ser Glu Asn Gly Asp Ala Ser Glu Glu Asp His Pro Gln Val Cys	

21	26	31	36	
gcc aag tgc tgc gca caa ttc act gac cca act gaa ttc ctc gcc cac				380
Ala Lys Cys Cys Ala Gln Phe Thr Asp Pro Thr Glu Phe Leu Ala His				
37	42	47	52	
cag aac gca tgt tct act gac cct cct gta atg gtg ata att ggg ggc				428
Gln Asn Ala Cys Ser Thr Asp Pro Pro Val Met Val Ile Ile Gly Gly				
53	58	63	68	
cag gag aac ccc aac aac tct tcg gcc tcc tct gaa ccc cgg cct gag				476
Gln Glu Asn Pro Asn Asn Ser Ser Ala Ser Ser Glu Pro Arg Pro Glu				
69	74	79	84	
ggc cac aat aat cct cag gtc atg gac aca gag cat agc aac ccc cca				524
Gly His Asn Asn Pro Gln Val Met Asp Thr Glu His Ser Asn Pro Pro				
85	90	95	100	
gat tct ggg tcc tcc gtg ccc acg gat ccc acc tgg ggc cca gag agg				572
Asp Ser Gly Ser Ser Val Pro Thr Asp Pro Thr Trp Gly Pro Glu Arg				
101	106	111	116	
aga gga gag gag tct tca ggg cat ttc ctg gtc gct gcc aca ggt aca				620
Arg Gly Glu Glu Ser Ser Gly His Phe Leu Val Ala Ala Thr Gly Thr				
117	122	127	132	
gcg gct ggg gga ggc ggg ggc ctg atc ttg gcc agt ccc aag ctg gga				668
Ala Ala Gly Gly Gly Gly Gly Leu Ile Leu Ala Ser Pro Lys Leu Gly				
133	138	143	148	
gca acc cca tta cct cca gaa tcg acc cct gca ccc cct cct cct cca				716
Ala Thr Pro Leu Pro Pro Glu Ser Thr Pro Ala Pro Pro Pro Pro Pro				
149	154	159	164	
cca ccc cct ccg ccc cca ggg gta ggc agt ggc cac ttg aat atc ccc				764
Pro Pro Pro Pro Pro Pro Gly Val Gly Ser Gly His Leu Asn Ile Pro				
165	170	175	180	
ctg atc ttg gaa gag cta cgg gtg ctg cag cag cgg cag atc cat cag				812
Leu Ile Leu Glu Glu Leu Arg Val Leu Gln Arg Gln Ile His Gln				
181	186	191	196	
atg cag atg act gag caa atc tgc agg cag gtg ctg ttg ctt ggc tcc				860
Met Gln Met Thr Glu Gln Ile Cys Arg Gln Val Leu Leu Leu Gly Ser				
197	202	207	212	
tta ggc cag acg gtg ggt gcc cct gcc agt ccc tca gag cta cct ggg				908
Leu Gly Gln Thr Val Gly Ala Pro Ala Ser Pro Ser Glu Leu Pro Gly				
213	218	223	228	
aca ggg act gcc tct tcc acc aag ccc cta cta ccc ctc ttc agc ccc				956
Thr Gly Thr Ala Ser Ser Thr Lys Pro Leu Leu Pro Leu Phe Ser Pro				
229	234	239	244	
atc aag cct gtc caa acc agc aag aca ctg gca tct tcc tcc tcc tcc				1004
Ile Lys Pro Val Gln Thr Ser Lys Thr Leu Ala Ser Ser Ser Ser Ser				
245	250	255	260	

tcc tct tcc tct tca ggg gca gaa acg ccc aag cag gcc ttc ttc cac	1052
Ser Ser Ser Ser Ser Gly Ala Glu Thr Pro Lys Gln Ala Phe Phe His	
261 266 271 276	
ctt tac cac cca ctg ggg tca cag cat cct ttc tct gct gga ggg gtt	1100
Leu Tyr His Pro Leu Gly Ser Gln His Pro Phe Ser Ala Gly Gly Val	
277 282 287 292	
ggg cga agc cac aaa ccc acc cct gcc cct tcc cca gcc ttg cca ggc	1148
Gly Arg Ser His Lys Pro Thr Pro Ala Pro Ser Pro Ala Leu Pro Gly	
293 298 303 308	
agc aca gat cag ctg att gcc tcg cct cat ctg gca ttc cca agc acc	1196
Ser Thr Asp Gln Leu Ile Ala Ser Pro His Leu Ala Phe Pro Ser Thr	
309 314 319 324	
acg gga cta ctg gca gca cag tgt ctt ggg gca gcc cga ggc ctt gag	1244
Thr Gly Leu Leu Ala Ala Gln Cys Leu Gly Ala Ala Arg Gly Leu Glu	
325 330 335 340	
gcc act gcc tcc cca ggg ctc ctg aag cca aag aat gga agt ggt gag	1292
Ala Thr Ala Ser Pro Gly Leu Leu Lys Pro Lys Asn Gly Ser Gly Glu	
341 346 351 356	
ctg agc tac gga gaa gtg atg ggt ccc ttg gag aag cct ggt gga agg	1340
Leu Ser Tyr Gly Glu Val Met Gly Pro Leu Glu Lys Pro Gly Gly Arg	
357 362 367 372	
cac aaa tgc cgc ttc tgt gcc aaa gta ttt ggc agt gac agt gcc ctg	1388
His Lys Cys Arg Phe Cys Ala Lys Val Phe Gly Ser Asp Ser Ala Leu	
373 378 383 388	
cag atc cac ctt cgt tcc cac acg ggt gag agg ccc tat aag tgc aat	1436
Gln Ile His Leu Arg Ser His Thr Gly Glu Arg Pro Tyr Lys Cys Asn	
389 394 399 404	
gtc tgt gga aac cgt ttt acc acc cgt ggc aac ctc aaa gtg cat ttc	1484
Val Cys Gly Asn Arg Phe Thr Thr Arg Gly Asn Leu Lys Val His Phe	
405 410 415 420	
cac cgg cat cgt gag aag tac cca cat gtg cag atg aac cca cac cca	1532
His Arg His Arg Glu Lys Tyr Pro His Val Gln Met Asn Pro His Pro	
421 426 431 436	
gta cca gag cac cta gac tat gtc att acc agc agt ggc ttg cct tat	1580
Val Pro Glu His Leu Asp Tyr Val Ile Thr Ser Ser Gly Leu Pro Tyr	
437 442 447 452	
ggg atg tcc gtg cca cca gag aag gcc gag gag gag gca gcc act cca	1628
Gly Met Ser Val Pro Pro Glu Lys Ala Glu Glu Glu Ala Ala Thr Pro	
453 458 463 468	
ggg gga ggg gtt gag cgc aag cct ctg gtg gcc tcc aca aca gca ctc	1676
Gly Gly Gly Val Glu Arg Lys Pro Leu Val Ala Ser Thr Thr Ala Leu	
469 474 479 484	

agt gcc aca gag agc ctg act ctg ctc tcc acc agt gca ggc aca gcc	1724
Ser Ala Thr Glu Ser Leu Thr Leu Leu Ser Thr Ser Ala Gly Thr Ala	
485 490 495 500	
acg gct cca gga ctc cct gct ttc aat aag ttt gtg ctc atg aaa gca	1772
Thr Ala Pro Gly Leu Pro Ala Phe Asn Lys Phe Val Leu Met Lys Ala	
501 506 511 516	
gtg gaa ccc aag aat aaa gct gat gaa aac acc ccc cca ggg agt gag	1820
Val Glu Pro Lys Asn Lys Ala Asp Glu Asn Thr Pro Pro Gly Ser Glu	
517 522 527 532	
ggc tca gcc atc agt gga gtg gca gaa agt agc acg gca act ctc atg	1868
Gly Ser Ala Ile Ser Gly Val Ala Glu Ser Ser Thr Ala Thr Leu Met	
533 538 543 548	
caa cta agt aag ttg atg act tca cta cca agc tgg gca ctg ctt acc	1916
Gln Leu Ser Lys Leu Met Thr Ser Leu Pro Ser Trp Ala Leu Leu Thr	
549 554 559 564	
aac cac ttc aag tcc act ggc agc ttc ccg ctt ccc cta tgt gct aga	1964
Asn His Phe Lys Ser Thr Gly Ser Phe Pro Leu Pro Leu Cys Ala Arg	
565 570 575 580	
gcc ttg ggg gcc tca ccc tct gag aca tca aag ctg cag caa ctg gta	2012
Ala Leu Gly Ala Ser Pro Ser Glu Thr Ser Lys Leu Gln Gln Leu Val	
581 586 591 596	
gaa aag att gac cgg caa gga gct gtg gcg gtg acc tca gct gcc tca	2060
Glu Lys Ile Asp Arg Gln Gly Ala Val Ala Val Thr Ser Ala Ala Ser	
597 602 607 612	
gga gcc ccc acc acc tct gcc cct gca cct tca tcc tca gcc tct tct	2108
Gly Ala Pro Thr Thr Ser Ala Pro Ala Pro Ser Ser Ser Ala Ser Ser	
613 618 623 628	
gga cct aac cag tgt gtc atc tgt ctc cga gtg ctt agc tgt cct cgg	2156
Gly Pro Asn Gln Cys Val Ile Cys Leu Arg Val Leu Ser Cys Pro Arg	
629 634 639 644	
gcc cta cgc ctt cat tat ggc caa cat gga ggt gag agg ccc ttc aaa	2204
Ala Leu Arg Leu His Tyr Gly Gln His Gly Gly Glu Arg Pro Phe Lys	
645 650 655 660	
tgc aaa gtg tgt ggc aga gcc ttc tcc acc agg ggt aat ctg cgt gca	2252
Cys Lys Val Cys Gly Arg Ala Phe Ser Thr Arg Gly Asn Leu Arg Ala	
661 666 671 676	
cat ttc gtg ggc cac aag gcc agt cca gct gcc cgg gca cag aat tcc	2300
His Phe Val Gly His Lys Ala Ser Pro Ala Ala Arg Ala Gln Asn Ser	
677 682 687 692	
tgc ccc atc tgc cag aag aag ttc acc aat gct gtc act ctg cag cag	2348
Cys Pro Ile Cys Gln Lys Lys Phe Thr Asn Ala Val Thr Leu Gln Gln	
693 698 703 708	
cat gtc cgg atg cac ctg ggg ggc cag atc ccc aac ggt ggt act gca	2396

His Val Arg Met His Leu Gly Gly Gln Ile Pro Asn Gly Gly Thr Ala	
709 714 719 724	
ctc cct gaa ggt gga gga gct gct cag gag aat ggc tcc gag caa tct	2444
Leu Pro Glu Gly Gly Gly Ala Ala Gln Glu Asn Gly Ser Glu Gln Ser	
725 730 735 740	
aca gtc tcc gga gca ggg agt ttc ccc cag cag cag tcc cag cag cca	2492
Thr Val Ser Gly Ala Gly Ser Phe Pro Gln Gln Gln Ser Gln Gln Pro	
741 746 751 756	
tca ccg gaa gag gag ttg tct gag gag gag gaa gag gag gat gag gaa	2540
Ser Pro Glu Glu Glu Leu Ser Glu Glu Glu Glu Glu Glu Asp Glu Glu	
757 762 767 772	
gaa gag gaa gat gtg act gat gaa gat tcc ctg gca ggg aga ggc tca	2588
Glu Glu Glu Asp Val Thr Asp Glu Asp Ser Leu Ala Gly Arg Gly Ser	
773 778 783 788	
gag agt gga ggt gag aag gca ata tca gtg aga ggt gat tca gaa gag	2636
Glu Ser Gly Gly Glu Lys Ala Ile Ser Val Arg Gly Asp Ser Glu Glu	
789 794 799 804	
gca tct ggg gca gag gag gag gtg ggg aca gtg gcg gca gca gcc aca	2684
Ala Ser Gly Ala Glu Glu Glu Val Gly Thr Val Ala Ala Ala Ala Thr	
805 810 815 820	
gct ggg aag gag atg gac agt aat gag aaa act act caa cag tct tct	2732
Ala Gly Lys Glu Met Asp Ser Asn Glu Lys Thr Thr Gln Gln Ser Ser	
821 826 831 836	
ttg cca cca cca cca cca cct gac agc ctg gat cag cct cag cca atg	2780
Leu Pro Pro Pro Pro Pro Pro Asp Ser Leu Asp Gln Pro Gln Pro Met	
837 842 847 852	
gag cag gga agc agt ggt gtt tta gga ggc aag gaa gag ggg ggc aaa	2828
Glu Gln Gly Ser Ser Gly Val Leu Gly Gly Lys Glu Glu Gly Gly Lys	
853 858 863 868	
ccg gag aga agc tca agt ccg gca tca gca ctc acc cca gaa ggg gaa	2876
Pro Glu Arg Ser Ser Ser Pro Ala Ser Ala Leu Thr Pro Glu Gly Glu	
869 874 879 884	
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Ala Thr Ser Val Thr Leu Val Glu Glu Leu Ser Leu Gln Glu Ala Met	
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Arg Lys Glu Pro Gly Glu Ser Ser Ser Arg Lys Ala Cys Glu Val Cys	
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Gly Gln Ala Phe Pro Ser Gln Ala Ala Leu Glu Glu His Gln Lys Thr	
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His Pro Lys Glu Gly Pro Leu Phe Thr Cys Val Phe Cys Arg Gln Gly	

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Phe Leu Glu Arg Ala	Thr Leu Lys Lys His	Met Leu Leu Ala His His		
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Gln Val Gln Pro Phe	Ala Pro His Gly Pro	Gln Asn Ile Ala Ala Leu		
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Pro Phe Pro Arg Lys	Asp Asp Pro Thr Ile	Pro *		
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Met Ala Asn Leu Glu Glu Ser Phe Pro Arg Gly Gly Thr Arg Lys Ile
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His Lys Pro Glu Lys Ala Phe Gln Gln Ser Val Glu Gln Asp Asn Leu
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Phe Asp Ile Ser Thr Glu Gly Ser Thr Lys Arg Lys Lys Ser Gln
47 52 57 62

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Lys Gly Pro Ala Lys Thr Lys Lys Leu Lys Ile Glu Lys Arg Glu Ser
63 68 73 78

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Ser Lys Ser Ala Arg Glu Lys Phe Glu Ile Leu Ser Val Glu Ser Leu
79 84 89 94

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Cys Glu Gly Met Arg Ile Leu Gly Cys Val Lys Glu Val Asn Glu Leu
95 100 105 110

gaa ctg gtg att agt ctc ccc aat ggc ctc cag ggc ttt gtg caa gtc 383

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111					116					121					126		
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Gln	Glu	Gln	Pro	Leu	Lys	Asp	Leu	Leu	His	Leu	Pro	Glu	Leu	Phe	Ser		
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Pro	Gly	Met	Leu	Val	Arg	Cys	Val	Val	Ser	Ser	Leu	Gly	Ile	Thr	Asp		
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Trp	Asn	Leu	Asn	Asn	Leu	Leu	Pro	Gly	Leu	Val	Val	Lys	Ala	Gln	Val		
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cag	aag	gtg	act	cca	ttt	ggc	ctt	acg	cta	aac	ttc	ctc	aca	ttc	ttc	959	
Gln	Lys	Val	Thr	Pro	Phe	Gly	Leu	Thr	Leu	Asn	Phe	Leu	Thr	Phe	Phe		
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Thr	Gly	Val	Val	Asp	Phe	Met	His	Leu	Asp	Pro	Lys	Lys	Ala	Gly	Thr		
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Tyr	Phe	Ser	Asn	Gln	Ala	Val	Arg	Ala	Cys	Ile	Leu	Cys	Val	His	Pro		

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Gly Arg Pro Leu Thr	Arg Leu Ser Cys Gln	Asn Leu Gly Ala Val Leu		
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Asp Ser Lys Asn Val	Phe Asn Pro Glu Ala	Phe Lys Pro Gly Asn Thr		
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His Lys Cys Arg Ile	Ile Asp Tyr Ser Gln	Met Asp Glu Leu Ala Leu		
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Leu Ser Leu Arg Thr	Ser Ile Ile Glu Ala	Gln Tyr Leu Arg Tyr His		
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Ser Tyr Gly Met Leu	Val Lys Val Gly Glu	Gln Met Arg Gly Leu Val		
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Tyr His Ile Gly Asp	Glu Val Lys Cys Arg	Val Leu Leu Cys Asp Pro		
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Glu Ala Lys Lys Leu	Met Met Thr Leu Lys	Lys Thr Leu Ile Glu Ser		
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Lys Val Val Val Leu Asn Cys Glu Pro Ser Lys Glu Arg Met Leu Leu	
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Leu Thr Ala Arg Val Leu Arg Leu Asn His Gln Lys Asn Leu Val Glu				
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ctg tct ttc ctc ccc gga gac act ggg aag cca gac gtg ctt tct gct				4271
Leu Ser Phe Leu Pro Gly Asp Thr Gly Lys Pro Asp Val Leu Ser Ala				
1407	1412	1417	1422	
tcc ttg gaa ggg caa ctt aca aag caa gag gag agg aaa aca gag gct				4319
Ser Leu Glu Gly Gln Leu Thr Lys Gln Glu Glu Arg Lys Thr Glu Ala				
1423	1428	1433	1438	
gag gag aga gac caa aaa ggg gaa aag aaa aat cag aaa agg aac gag				4367
Glu Glu Arg Asp Gln Lys Gly Glu Lys Lys Asn Gln Lys Arg Asn Glu				
1439	1444	1449	1454	
aag aag aac cag aag ggg cag gag gag gtg gag atg ccc agc aag gag				4415
Lys Lys Asn Gln Lys Gly Gln Glu Glu Val Glu Met Pro Ser Lys Glu				
1455	1460	1465	1470	
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Lys Gln Gln Pro Gln Lys Pro Gln Ala Gln Lys Arg Gly Gly Arg Glu				
1471	1476	1481	1486	

tgc cgg gag tct ggg agt gag cag gaa aga gtg agc aag aag cca aag	4511
Cys Arg Glu Ser Gly Ser Glu Gln Glu Arg Val Ser Lys Lys Pro Lys	
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aaa gcc ggc ctg tca gag gag gac gac agc ctt gtg gac gtg tac tat	4559
Lys Ala Gly Leu Ser Glu Glu Asp Asp Ser Leu Val Asp Val Tyr Tyr	
1503 1508 1513 1518	
cgg gag gga aaa gag gag gca gaa gag acg aat gtg ctg ccc aag gag	4607
Arg Glu Gly Lys Glu Glu Ala Glu Glu Thr Asn Val Leu Pro Lys Glu	
1519 1524 1529 1534	
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Lys Gln Thr Lys Pro Ala Glu Ala Pro Arg Leu Gln Leu Ser Ser Gly	
1535 1540 1545 1550	
ttc gct tgg aat gtg gga cta gac tct ctg acc ccg gcc ttg cca cct	4703
Phe Ala Trp Asn Val Gly Leu Asp Ser Leu Thr Pro Ala Leu Pro Pro	
1551 1556 1561 1566	
cta gca gag agc tca gac agc gag gag gat gag aag cca cac caa gcc	4751
Leu Ala Glu Ser Ser Asp Ser Glu Glu Asp Glu Lys Pro His Gln Ala	
1567 1572 1577 1582	
acg ata aag aaa agc aag aaa gaa agg gag ttg gag aag cag aag gca	4799
Thr Ile Lys Lys Ser Lys Lys Glu Arg Glu Leu Glu Lys Gln Lys Ala	
1583 1588 1593 1598	
gag aag gaa ctg tcc cgc att gag gag gcg ctg atg gat cct ggg cgg	4847
Glu Lys Glu Leu Ser Arg Ile Glu Glu Ala Leu Met Asp Pro Gly Arg	
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Gln Pro Glu Ser Ala Asp Asp Phe Asp Arg Leu Val Leu Ser Ser Pro	
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Asn Ser Ser Ile Leu Trp Leu Gln Tyr Met Ala Phe His Leu Gln Ala	
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Thr Glu Ile Glu Lys Ala Arg Ala Val Ala Glu Arg Ala Leu Lys Thr	
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Ile Ser Phe Arg Glu Glu Gln Glu Lys Leu Asn Val Trp Val Ala Leu	
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Leu Asn Leu Glu Asn Met Tyr Gly Ser Gln Glu Ser Leu Thr Lys Val	
1679 1684 1689 1694	
ttt gag cga gcc gtg cag tac aac gag cct ctc aaa gtc ttt ctc cac	5135
Phe Glu Arg Ala Val Gln Tyr Asn Glu Pro Leu Lys Val Phe Leu His	
1695 1700 1705 1710	

ctg gct gac atc tac gcc aag tca gag aaa ttc cag gaa gct ggt gaa	5183
Leu Ala Asp Ile Tyr Ala Lys Ser Glu Lys Phe Gln Glu Ala Gly Glu	
1711 1716 1721 1726	
ctc tac aac cgg atg ctg aag cgt ttc cgg cag gag aaa gct gtg tgg	5231
Leu Tyr Asn Arg Met Leu Lys Arg Phe Arg Gln Glu Lys Ala Val Trp	
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Ile Lys Tyr Gly Ala Phe Leu Leu Arg Arg Ser Gln Ala Ala Ala Ser	
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His Arg Val Leu Gln Arg Ala Leu Glu Cys Leu Pro Ser Lys Glu His	
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Val Asp Val Ile Ala Lys Phe Ala Gln Leu Glu Phe Gln Leu Gly Asp	
1775 1780 1785 1790	
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Ala Glu Arg Ala Lys Ala Ile Phe Glu Asn Thr Leu Ser Thr Tyr Pro	
1791 1796 1801 1806	
aag cgc aca gat gtc tgg tgc gtc tat atc gac atg acc atc aag cac	5471
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Gly Ser Gln Lys Asp Val Arg Asp Ile Phe Glu Arg Val Ile His Leu	
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Ser Leu Ala Pro Lys Arg Met Lys Phe Phe Phe Lys Arg Tyr Leu Asp	
1839 1844 1849 1854	
tac gag aag cag cat ggc act gag aag gat gtg cag gca gtc aag gcc	5615
Tyr Glu Lys Gln His Gly Thr Glu Lys Asp Val Gln Ala Val Lys Ala	
1855 1860 1865 1870	
aag gcc ctg gag tat gtg gag gcc aag agc tca gtg cta gag gac tag	5663
Lys Ala Leu Glu Tyr Val Glu Ala Lys Ser Ser Val Leu Glu Asp *	
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gagctgcctt agactatcca attgatctat tcaaacagct gcctgttccc ttaacttgtc	360
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 Val Leu Arg Lys Lys Gly Tyr Ile Val Gly Ile Asn Leu Gly Lys Gly
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 38 43 48 53
 gag aga ttc ctt cct cgg gag atg gac atc ctg gca act gtc aac cac 1327
 Glu Arg Phe Leu Pro Arg Glu Met Asp Ile Leu Ala Thr Val Asn His
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 Gly Ser Ile Ile Lys Thr Tyr Glu Ile Phe Glu Thr Ser Asp Gly Arg
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 Arg Gln Leu Ser Ser Ala Val Lys Tyr Cys His Asp Leu Asp Ile Val
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 Asn Gly Arg Ile Ile Leu Ser Lys Thr Phe Cys Gly Ser Ala Ala Tyr
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 Ala Ala Pro Glu Val Leu Gln Ser Ile Pro Tyr Gln Pro Lys Val Tyr
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Asp Ile Trp Ser Leu Gly Val Ile Leu Tyr Ile Met Val Cys Gly Ser	
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Met Pro Tyr Asp Asp Ser Asp Ile Arg Lys Met Leu Arg Ile Gln Lys	
214 219 224 229	
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Glu His Arg Val Asp Phe Pro Arg Ser Lys Asn Leu Thr Cys Glu Cys	
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Lys Asp Leu Ile Tyr Arg Met Leu Gln Pro Asp Val Ser Gln Arg Leu	
246 251 256 261	
cac atc gat gag atc ctc agc cac tcg tgg ctg cag ccc ccc aag ccc	1951
His Ile Asp Glu Ile Leu Ser His Ser Trp Leu Gln Pro Pro Lys Pro	
262 267 272 277	
aaa gcc acg tct tct gcc tcc ttc aag agg gag ggg gag ggc aag tac	1999
Lys Ala Thr Ser Ser Ala Ser Phe Lys Arg Glu Gly Glu Gly Lys Tyr	
278 283 288 293	
cgc gct gag tgc aaa ctg gac acc aag aca ggc ttg agg ccc gac cac	2047
Arg Ala Glu Cys Lys Leu Asp Thr Lys Thr Gly Leu Arg Pro Asp His	
294 299 304 309	
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Arg Pro Asp His Lys Leu Gly Ala Lys Thr Gln His Arg Leu Leu Val	
310 315 320 325	
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Val Pro Glu Asn Glu Asn Arg Met Glu Asp Arg Leu Ala Glu Thr Ser	
326 331 336 341	
agg gcc aaa gac cat cac atc tcc gga gct gag gtg ggg aaa gca agc	2191
Arg Ala Lys Asp His His Ile Ser Gly Ala Glu Val Gly Lys Ala Ser	
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Thr *	
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Met Val Thr Trp Lys Ala Asp Gly Thr Leu Ile Thr Gln
1 5 10

agc gtg gag aag acc acg ccc tcc aaa cag agc aac aac aag tac gtg	517
Ser Val Glu Lys Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Val	
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gcc agc agc tac ctg agc ctg acg ccc gag cag tgg agg tcc cgc aga	565
Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Arg Ser Arg Arg	
30 35 40 45	
agc tac agc tgc cag gtt atg caa gaa ggg agc acc gtg gag aag tca	613
Ser Tyr Ser Cys Gln Val Met Gln Glu Gly Ser Thr Val Glu Lys Ser	
46 51 56 61	
gtg gcc cct gca gaa tgt tca tag gttccagccc ccacccacac ccacaggggc	667
Val Ala Pro Ala Glu Cys Ser *	
62 67	
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Met His Pro Ala
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Ala Glu Asp Asn Tyr Gly Tyr Asp Ala Cys Ala Val Leu Cys Leu Pro
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Cys Val Pro Asn Ile Leu Val Ile Ala Thr Glu Ser Gly Met Leu Tyr
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cac tgt gtc gtg cta gaa ggg gaa gaa gaa gat gac cac acg tca gaa 1099
His Cys Val Val Leu Glu Gly Glu Glu Glu Asp Asp His Thr Ser Glu
37 42 47 52
aag tcc tgg gat tcc agg att gac ctc att cct tct ctg tat gtg ttt 1147
Lys Ser Trp Asp Ser Arg Ile Asp Leu Ile Pro Ser Leu Tyr Val Phe
53 58 63 68
gaa tgt gtt gag ttg gag ctt gct ttg aaa ctg gca tct gga gag gat 1195
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69 74 79 84
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Asp Pro Phe Asp Ser Asp Phe Ser Cys Pro Val Lys Leu His Arg Asp
85 90 95 100
ccc aag tgt cct tca aga tat cac tgt act cat gaa gct ggt gta cat 1291
Pro Lys Cys Pro Ser Arg Tyr His Cys Thr His Glu Ala Gly Val His
101 106 111 116
agt gtt ggg cta act tgg att cat aaa ctt cac aaa ttt ctt gga tca 1339
Ser Val Gly Leu Thr Trp Ile His Lys Leu His Lys Phe Leu Gly Ser
117 122 127 132
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Asp Glu Glu Asp Lys Asp Ser Leu Gln Glu Leu Ser Thr Glu Gln Lys
133 138 143 148
tgc ttt gtt gaa cac atc ctt tgt acg agg cca ttg ccc tgc agg cag 1435
Cys Phe Val Glu His Ile Leu Cys Thr Arg Pro Leu Pro Cys Arg Gln
149 154 159 164
cca gct cca att cga gga ttt tgg att gta cct gac att ctg gga ccc 1483
Pro Ala Pro Ile Arg Gly Phe Trp Ile Val Pro Asp Ile Leu Gly Pro
165 170 175 180
acg atg atc tgc atc acc agt acc tat gaa tgc ctc ata tgg ccg tta 1531
Thr Met Ile Cys Ile Thr Ser Thr Tyr Glu Cys Leu Ile Trp Pro Leu

181	186	191	196	
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Leu Ser Thr Val His Pro Ala Ser Pro Pro Leu Leu Cys Thr Arg Glu				
197	202	207	212	
gat gtt gaa gtg gca gag tct ccc ctc cgt gtt ctg gct gaa acc cca				1627
Asp Val Glu Val Ala Glu Ser Pro Leu Arg Val Leu Ala Glu Thr Pro				
213	218	223	228	
gat tcc ttt gaa aag cat att aga agc att ttg caa cgt agt gtt gcc				1675
Asp Ser Phe Glu Lys His Ile Arg Ser Ile Leu Gln Arg Ser Val Ala				
229	234	239	244	
aat cca gca ttt ttg aaa gct tct gaa aag gac ata gcc cct cct cct				1723
Asn Pro Ala Phe Leu Lys Ala Ser Glu Lys Asp Ile Ala Pro Pro Pro				
245	250	255	260	
gaa gaa tgc ctt cag ctc ctc agc aga gcc acc cag gtg ttc aga gag				1771
Glu Glu Cys Leu Gln Leu Leu Ser Arg Ala Thr Gln Val Phe Arg Glu				
261	266	271	276	
cag tac att ctc aaa cag gac ttg gca aag gag gag att cag cgg agg				1819
Gln Tyr Ile Leu Lys Gln Asp Leu Ala Lys Glu Glu Ile Gln Arg Arg				
277	282	287	292	
gtc aaa tta tta tgt gac caa aaa aag aaa caa cta gaa gat ctc agt				1867
Val Lys Leu Leu Cys Asp Gln Lys Lys Lys Gln Leu Glu Asp Leu Ser				
293	298	303	308	
tat tgt cga gaa gag agg aaa agt ctg cgg gaa atg gct gag cgt tta				1915
Tyr Cys Arg Glu Glu Arg Lys Ser Leu Arg Glu Met Ala Glu Arg Leu				
309	314	319	324	
gct gac aaa tat gag gaa gct aaa gaa aaa caa gag gat atc atg aac				1963
Ala Asp Lys Tyr Glu Glu Ala Lys Glu Lys Gln Glu Asp Ile Met Asn				
325	330	335	340	
agg atg aaa aaa cta ctt cac agt ttt cac tct gag ctc cca gtt ctc				2011
Arg Met Lys Lys Leu Leu His Ser Phe His Ser Glu Leu Pro Val Leu				
341	346	351	356	
tct gat agt gag cga gac atg aag aaa gaa tta cag ctg ata cct gat				2059
Ser Asp Ser Glu Arg Asp Met Lys Lys Glu Leu Gln Leu Ile Pro Asp				
357	362	367	372	
caa ctt cga cat ttg ggc aat gcc atc aaa cag gtt act atg aaa aag				2107
Gln Leu Arg His Leu Gly Asn Ala Ile Lys Gln Val Thr Met Lys Lys				
373	378	383	388	
gat tat caa cag caa aag atg gag aag gtg ttg agt ctt cca aaa ccc				2155
Asp Tyr Gln Gln Gln Lys Met Glu Lys Val Leu Ser Leu Pro Lys Pro				
389	394	399	404	
acc att att ctc agt gcc tac cag cga aag tgc att cag tcc atc ctg				2203
Thr Ile Ile Leu Ser Ala Tyr Gln Arg Lys Cys Ile Gln Ser Ile Leu				
405	410	415	420	

tta agc cca aca caa cat cat gta gca ctt ata gga ata aaa gga ctt	441
Leu Ser Pro Thr Gln His His Val Ala Leu Ile Gly Ile Lys Gly Leu	
116 121 126 131	
atg gta tta gaa tta cct aaa aga tgg ggg aag aat tct gaa ttt gaa	489
Met Val Leu Glu Leu Pro Lys Arg Trp Gly Lys Asn Ser Glu Phe Glu	
132 137 142 147	
ggg gga aaa tca aca gtg aat tgt agt acc act cca gtt gcg gag aga	537
Gly Gly Lys Ser Thr Val Asn Cys Ser Thr Thr Pro Val Ala Glu Arg	
148 153 158 163	
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Phe Phe Thr Ser Ser Thr Ser Leu Thr Leu Lys His Ala Ala Trp Tyr	
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Pro Ser Glu Ile Leu Asp Pro His Val Val Leu Leu Thr Ser Asp Asn	
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Val Ile Arg Ile Tyr Ser Leu Arg Glu Pro Gln Thr Pro Thr Asn Val	
196 201 206 211	
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Ile Ile Leu Ser Glu Ala Glu Glu Glu Ser Leu Val Leu Asn Lys Gly	
212 217 222 227	
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Arg Ala Tyr Thr Ala Ser Leu Gly Glu Thr Ala Val Ala Phe Asp Phe	
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Gly Pro Leu Ala Ala Val Pro Lys Thr Leu Phe Gly Gln Asn Gly Lys	
244 249 254 259	
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Asp Glu Val Val Ala Tyr Pro Leu Tyr Ile Leu Tyr Glu Asn Gly Glu	
260 265 270 275	
act ttc ctg aca tac atc agt ctg tta cac agc cct gga aat att tgg	921
Thr Phe Leu Thr Tyr Ile Ser Leu Leu His Ser Pro Gly Asn Ile Trp	
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Lys Ala Val Gly Ser Ile Ala His Ala Ser Cys Gly *	
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gaggggaaccc gagcgctcatg ttaggggtgaa gcagaggacc tcagtgctga ac	atg Met 1	175
cta agg agg ttg gac aaa atc agg ttc aga ggt cac aag aga gat gac Leu Arg Arg Leu Asp Lys Ile Arg Phe Arg Gly His Lys Arg Asp Asp 2 7 12 17		223
ttc ctc gat cta gcg gag tct cca aat gcc tcg gac acc gaa tgc agc Phe Leu Asp Leu Ala Glu Ser Pro Asn Ala Ser Asp Thr Glu Cys Ser 18 23 28 33		271
gac gaa atc ccc ctg aag gta ccg cgg acc tcg ccc cgg gac agc gag Asp Glu Ile Pro Leu Lys Val Pro Arg Thr Ser Pro Arg Asp Ser Glu 34 39 44 49		319
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gtc cag gac ttt aac cgg aca gag ttt gat cga ctg aat gag atc aaa Val Gln Asp Phe Asn Arg Thr Glu Phe Asp Arg Leu Asn Glu Ile Lys 66 71 76 81		415
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ctc cgg aag ctg cga gaa gaa acc aac gcg gag atg ctg cgg cag gag Leu Arg Lys Leu Arg Glu Glu Thr Asn Ala Glu Met Leu Arg Gln Glu 98 103 108 113		511
ctg gac cgc gag cgg cag cgg cgg atg gag ctg gag cag aag gtg cag Leu Asp Arg Glu Arg Gln Arg Arg Met Glu Leu Glu Gln Lys Val Gln 114 119 124 129		559
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cgc ggt gcc aag ccg gtc act aac ttt gtg aag aac ctc tct gcc tta		847

Arg Gly Ala Lys Pro Val Thr Asn Phe Val Lys Asn Leu Ser Ala Leu	
210 215 220 225	
tcc gac tgg tac tcc gtc tac acg tct gcc att gcc ttc acc gtg tac	895
Ser Asp Trp Tyr Ser Val Tyr Thr Ser Ala Ile Ala Phe Thr Val Tyr	
226 231 236 241	
atg aat gcc gtg tgg cat ggc tgg gcc atc cca ttg ttc tta ttt cta	943
Met Asn Ala Val Trp His Gly Trp Ala Ile Pro Leu Phe Leu Phe Leu	
242 247 252 257	
gca att ctg agg tta tcc ctc aat tac ctc atc gcc agg ggg tgg cgg	991
Ala Ile Leu Arg Leu Ser Leu Asn Tyr Leu Ile Ala Arg Gly Trp Arg	
258 263 268 273	
ata cag tgg agc atc gtg ccc gaa gtg tct gag ccc gtg gaa cct cca	1039
Ile Gln Trp Ser Ile Val Pro Glu Val Ser Glu Pro Val Glu Pro Pro	
274 279 284 289	
aag gaa gac ctg act gtg tct gag aag ttc cag ctg gtg ctg gac gtc	1087
Lys Glu Asp Leu Thr Val Ser Glu Lys Phe Gln Leu Val Leu Asp Val	
290 295 300 305	
gcc cag aaa gcc cag aac ctt ttc ggg aag atg gct gac atc ctg gag	1135
Ala Gln Lys Ala Gln Asn Leu Phe Gly Lys Met Ala Asp Ile Leu Glu	
306 311 316 321	
aag atc aag aac ttg ttc atg tgg gtc cag ccg gag atc aca cag aag	1183
Lys Ile Lys Asn Leu Phe Met Trp Val Gln Pro Glu Ile Thr Gln Lys	
322 327 332 337	
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Leu Tyr Val Ala Leu Trp Ala Ala Phe Leu Ala Ser Cys Phe Phe Pro	
338 343 348 353	
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Tyr Arg Leu Val Gly Leu Ala Val Gly Leu Tyr Ala Gly Ile Lys Phe	
354 359 364 369	
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Phe Leu Ile Asp Phe Ile Phe Lys Arg Cys Pro Arg Leu Arg Ala Lys	
370 375 380 385	
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Tyr Asp Thr Pro Tyr Ile Ile Trp Arg Ser Leu Pro Thr Asp Pro Gln	
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ctc aag gag cgc tcc agc gcc gca gtc tca cgc agg ctg cag acg acc	1423
Leu Lys Glu Arg Ser Ser Ala Ala Val Ser Arg Arg Leu Gln Thr Thr	
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tcg tca cgg agc tac gta ccc agc gca ccg gcc ggc ctg ggt aaa gag	1471
Ser Ser Arg Ser Tyr Val Pro Ser Ala Pro Ala Gly Leu Gly Lys Glu	
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Glu Asp Ala Gly Arg Phe His Ser Thr Lys Lys Gly Asn Phe His Glu	

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Ile Phe Asn Leu Thr Glu Asn Glu Arg Pro Leu Ala Val Cys Glu Asn				
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ggc tgg cgc tgc tgc ctc atc aac agg gac cgg aag atg ccc acg gac				1615
Gly Trp Arg Cys Cys Leu Ile Asn Arg Asp Arg Lys Met Pro Thr Asp				
466	471	476	481	
tac atc agg aac ggg gtg ctc tac gtc acg gag aat tac ttg tgc ttc				1663
Tyr Ile Arg Asn Gly Val Leu Tyr Val Thr Glu Asn Tyr Leu Cys Phe				
482	487	492	497	
gaa agc tcc aaa tct ggg tcc tca aag agg aac aaa gtc atc aag cta				1711
Glu Ser Ser Lys Ser Gly Ser Ser Lys Arg Asn Lys Val Ile Lys Leu				
498	503	508	513	
gtg gac atc acg gac atc cag aag tac aag gtc ctg tct gtc ctc cca				1759
Val Asp Ile Thr Asp Ile Gln Lys Tyr Lys Val Leu Ser Val Leu Pro				
514	519	524	529	
ggc tca ggc atg ggg att gcc gtg tcg acg cca tcc acc cag aaa ccg				1807
Gly Ser Gly Met Gly Ile Ala Val Ser Thr Pro Ser Thr Gln Lys Pro				
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ctc gtg ttt ggt gcc atg gtg cac agg gat gag gcc ttc gag acc att				1855
Leu Val Phe Gly Ala Met Val His Arg Asp Glu Ala Phe Glu Thr Ile				
546	551	556	561	
ctc agc cag tac atc aag atc acc tca gcg gca gcg tct ggc ggg gac				1903
Leu Ser Gln Tyr Ile Lys Ile Thr Ser Ala Ala Ala Ser Gly Gly Asp				
562	567	572	577	
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Ser *				
578				
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Met Glu
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Ser Arg Lys Asp Ile Thr Asn Gln Glu Glu Leu Trp Lys Met Lys Pro
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Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp Thr Gly Glu
19 24 29 34
acc agc atg cta aaa aga cct gtg ctt ttg cat ttg cac caa aca gcc 319
Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln Thr Ala
35 40 45 50
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His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr Gln Glu
51 56 61 66
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Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala Ile Ile Ala
67 72 77 82
tct ctg act ttt ctt tac act ctt ctg agg gaa gta att cac cct tta 463
Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Ile His Pro Leu
83 88 93 98
gca act tcc cat caa caa tat ttt tat aaa att cca atc ctg gtc atc 511
Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Pro Ile Leu Val Ile
99 104 109 114

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Asn Lys Val Leu Pro Met Val Ser Ile Thr Leu Leu Ala Leu Val Tyr	
115 120 125 130	
ctg cca ggt gtg ata gca gca att gtc caa ctt cat aat gga acc aag	607
Leu Pro Gly Val Ile Ala Ala Ile Val Gln Leu His Asn Gly Thr Lys	
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Tyr Lys Lys Phe Pro His Trp Leu Asp Lys Trp Met Leu Thr Arg Lys	
147 152 157 162	
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Gln Phe Gly Leu Leu Ser Phe Phe Phe Ala Val Leu His Ala Ile Tyr	
163 168 173 178	
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Ser Leu Ser Tyr Pro Met Arg Arg Ser Tyr Arg Tyr Lys Leu Leu Asn	
179 184 189 194	
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Trp Ala Tyr Gln Gln Val Gln Gln Asn Lys Glu Asp Ala Trp Ile Glu	
195 200 205 210	
cat gat gtt tgg aga atg gag att tat gtg tct ctg gga att gtg gga	847
His Asp Val Trp Arg Met Glu Ile Tyr Val Ser Leu Gly Ile Val Gly	
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Leu Ala Ile Leu Ala Leu Leu Ala Val Thr Ser Ile Pro Ser Val Ser	
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Asp Ser Leu Thr Trp Arg Glu Phe His Tyr Ile Gln Ser Lys Leu Gly	
243 248 253 258	
att gtt tcc ctt cta ctg ggc aca ata cac gca ttg att ttt gcc tgg	991
Ile Val Ser Leu Leu Leu Gly Thr Ile His Ala Leu Ile Phe Ala Trp	
259 264 269 274	
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Asn Lys Trp Ile Asp Ile Lys Gln Phe Val Trp Tyr Thr Pro Pro Thr	
275 280 285 290	
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Phe Met Ile Ala Val Phe Leu Pro Ile Val Val Leu Ile Phe Lys Ser	
291 296 301 306	
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Ile Leu Phe Leu Pro Cys Leu Arg Lys Lys Ile Leu Lys Ile Arg His	
307 312 317 322	
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Gly Trp Glu Asp Val Thr Lys Ile Asn Lys Thr Glu Ile Cys Ser Gln	
323 328 333 338	
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Leu *
339

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cctgaggaac aagctgcgtg agctctgcgt caagctt atg ttc ctg cac cca gtg 355
Met Phe Leu His Pro Val
1

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Asp Tyr Gly Arg Lys Ala Glu Glu Leu Leu Trp Arg Lys Val Tyr Tyr
7 12 17 22

gaa gtt atc cag ctt atc aag act aac aaa aag cac atc cac agc cgg 451
Glu Val Ile Gln Leu Ile Lys Thr Asn Lys Lys His Ile His Ser Arg
23 28 33 38

agc act ttg gaa tgt gcc tac agg acg cac ctg gtt gct ggt att ggc 499
Ser Thr Leu Glu Cys Ala Tyr Arg Thr His Leu Val Ala Gly Ile Gly
39 44 49 54

ttc tac cag cat ctc ctt ctc tat atc cag tcc cac tac cag ctg gaa 547
Phe Tyr Gln His Leu Leu Leu Tyr Ile Gln Ser His Tyr Gln Leu Glu
55 60 65 70

ctg cag tgc tgc atc gac tgg acc cat gtc act gac ccc ctc ata gga 595
Leu Gln Cys Cys Ile Asp Trp Thr His Val Thr Asp Pro Leu Ile Gly
71 76 81 86

tgc aag aag cca gtg tct gcc tca ggg aag gag atg gat tgg gca cag 643
Cys Lys Lys Pro Val Ser Ala Ser Gly Lys Glu Met Asp Trp Ala Gln
87 92 97 102

atg gca tgt cac cga tgt ctg gtg tat ctg ggg gat ttg tcc cga tat 691

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cag	aat	gaa	tta	gct	ggc	gta	gat	acc	gag	ctg	cta	gcc	gag	aga	ttt	739
Gln	Asn	Glu	Leu	Ala	Gly	Val	Asp	Thr	Glu	Leu	Leu	Ala	Glu	Arg	Phe	
119					124					129					134	
tac	tac	caa	gcc	ctg	tca	gta	gct	cct	cag	att	gga	atg	ccc	ttc	aat	787
Tyr	Tyr	Gln	Ala	Leu	Ser	Val	Ala	Pro	Gln	Ile	Gly	Met	Pro	Phe	Asn	
135					140					145					150	
cag	ctg	ggc	acc	ctg	gca	ggc	agc	aag	tac	tat	aat	gtg	gaa	gcc	atg	835
Gln	Leu	Gly	Thr	Leu	Ala	Gly	Ser	Lys	Tyr	Tyr	Asn	Val	Glu	Ala	Met	
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Tyr	Cys	Tyr	Leu	Arg	Cys	Ile	Gln	Ser	Glu	Val	Ser	Phe	Glu	Gly	Ala	
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Tyr	Gly	Asn	Leu	Lys	Arg	Leu	Tyr	Asp	Lys	Ala	Ala	Lys	Met	Tyr	His	
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caa	ctg	aag	aag	tgt	gag	act	cgg	aaa	ctg	tct	cct	ggc	aaa	aag	cga	979
Gln	Leu	Lys	Lys	Cys	Glu	Thr	Arg	Lys	Leu	Ser	Pro	Gly	Lys	Lys	Arg	
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Cys	Lys	Asp	Ile	Lys	Arg	Leu	Leu	Val	Asn	Phe	Met	Tyr	Leu	Gln	Ser	
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ctc	cta	cag	ccc	aaa	agc	agc	tcc	gtg	gac	tca	gag	ctg	acc	tca	ctt	1075
Leu	Leu	Gln	Pro	Lys	Ser	Ser	Ser	Val	Asp	Ser	Glu	Leu	Thr	Ser	Leu	
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Cys	Gln	Ser	Val	Leu	Glu	Asp	Phe	Asn	Leu	Cys	Leu	Phe	Tyr	Leu	Pro	
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Ser	Ser	Pro	Asn	Leu	Ser	Leu	Ala	Ser	Glu	Asp	Glu	Glu	Glu	Tyr	Glu	
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Ser	Gly	Tyr	Ala	Phe	Leu	Pro	Asp	Leu	Leu	Ile	Phe	Gln	Met	Val	Ile	
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atc	tgc	ctt	atg	tgt	gtg	cac	agc	ttg	gag	aga	gca	gga	tcc	aag	cag	1267
Ile	Cys	Leu	Met	Cys	Val	His	Ser	Leu	Glu	Arg	Ala	Gly	Ser	Lys	Gln	
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Tyr	Ser	Ala	Ala	Ile	Ala	Phe	Thr	Leu	Ala	Leu	Phe	Ser	His	Leu	Val	
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Asn	His	Val	Asn	Ile	Arg	Leu	Gln	Ala	Glu	Leu	Glu	Glu	Gly	Glu	Asn	

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Pro Val Pro Ala Phe Gln Ser Asp Gly Thr Asp Glu Pro Glu Ser Lys				
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Glu Pro Val Glu Lys Glu Glu Glu Pro Asp Pro Glu Pro Pro Pro Val				
359	364	369	374	
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Thr Pro Gln Val Gly Glu Gly Arg Lys Ser Arg Lys Phe Ser Arg Leu				
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Ser Cys Leu Arg Arg Arg Arg His Pro Pro Lys Val Gly Asp Asp Ser				
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gac ctg agt gaa ggc ttt gaa tcg gac tca agc cat gac tca gcc cgg				1603
Asp Leu Ser Glu Gly Phe Glu Ser Asp Ser Ser His Asp Ser Ala Arg				
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Ala Ser Glu Gly Ser Asp Ser Gly Ser Asp Lys Ser Leu Glu Gly Gly				
423	428	433	438	
gga acg gcc ttt gat gct gaa aca gac tcg gaa atg aat agc cag gag				1699
Gly Thr Ala Phe Asp Ala Glu Thr Asp Ser Glu Met Asn Ser Gln Glu				
439	444	449	454	
tcc cga tca gac ttg gaa gat atg gag gaa gag gag ggg aca cgg tca				1747
Ser Arg Ser Asp Leu Glu Asp Met Glu Glu Glu Glu Gly Thr Arg Ser				
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Pro Thr Leu Glu Pro Pro Arg Gly Arg Ser Glu Ala Pro Asp Ser Leu				
471	476	481	486	
aat ggc cca ctg ggc ccc agt gag gct agc att gcc agc aat cta caa				1843
Asn Gly Pro Leu Gly Pro Ser Glu Ala Ser Ile Ala Ser Asn Leu Gln				
487	492	497	502	
gcc atg tcc acc cag atg ttc cag act aag cgc tgc ttc cga ctg gcc				1891
Ala Met Ser Thr Gln Met Phe Gln Thr Lys Arg Cys Phe Arg Leu Ala				
503	508	513	518	
ccc acc ttt agc aac ctg ctc ctc cag ccc acc acc aac cct cat acc				1939
Pro Thr Phe Ser Asn Leu Leu Leu Gln Pro Thr Thr Asn Pro His Thr				
519	524	529	534	
tcg gcc agc cac agg cct tgc gtc aat ggg gat gta gac aag cct tca				1987
Ser Ala Ser His Arg Pro Cys Val Asn Gly Asp Val Asp Lys Pro Ser				
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Glu Ser Val Val Arg Ile Cys Cys Ile Arg Ser Phe Gly His Phe Ile	
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Gln Ala Gln Phe Arg Met Ala Gln Glu Glu Ala Arg Arg Asn Arg Leu	
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Glu Gly Ser Leu Gln Gln Pro Lys Ala Gln Ser Ala Met Ser Pro Tyr	
775 780 785 790	

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Gln Leu Ala Thr Ser Gly Arg Phe Ile Val Ile Ile Pro Arg Thr Val	
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Ile Asp Gly Leu Asp Leu Leu Lys Lys Glu His Pro Gly Ala Arg Asp	
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 Met Val Phe Gly Thr Lys Phe Pro Glu Ser Lys Ile Val Leu
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 gcc tta aga act aaa cgg gaa ggc cct ggg gaa gtt agg att caa gtt 277

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tat	gcc	tta	agg	ata	ggg	gag	aat	gag	aac	aca	gac	aga	gaa	aga	gac	325	
Tyr	Ala	Leu	Arg	Ile	Gly	Glu	Asn	Glu	Asn	Thr	Asp	Arg	Glu	Arg	Asp		
31					36					41					46		
cca	act	ccc	acc	ccc	tgt	ccc	cag	gga	cac	cgg	atg	atg	acg	gag	cct	373	
Pro	Thr	Pro	Thr	Pro	Cys	Pro	Gln	Gly	His	Arg	Met	Met	Thr	Glu	Pro		
47					52					57					62		
agg	gag	agg	aga	ggg	tac	agt	gta	cca	cct	aga	cca	gag	gtc	cgg	acc	421	
Arg	Glu	Arg	Arg	Gly	Tyr	Ser	Val	Pro	Pro	Arg	Pro	Glu	Val	Arg	Thr		
63					68					73					78		
cag	gcc	acg	gag	tgg	aga	gta	gaa	gaa	tct	aac	ttc	aac	aag	atc	ttc	469	
Gln	Ala	Thr	Glu	Trp	Arg	Val	Glu	Glu	Ser	Asn	Phe	Asn	Lys	Ile	Phe		
79					84					89					94		
ctg	aaa	aaa	gac	gct	gag	ctt	gga	cgg	tcc	aac	cac	ctc	cct	acc	tgg	517	
Leu	Lys	Lys	Asp	Ala	Glu	Leu	Gly	Arg	Ser	Asn	His	Leu	Pro	Thr	Trp		
95					100					105					110		
gat	aag	ccg	gag	gat	gct	tct	tgg	ctt	ccc	caa	agc	tgt	ctt	ggg	ggg	565	
Asp	Lys	Pro	Glu	Asp	Ala	Ser	Trp	Leu	Pro	Gln	Ser	Cys	Leu	Gly	Gly		
111					116					121					126		
gat	gct	gtg	gca	acc	aca	ggg	gag	att	cac	gag	gag	aaa	gcc	tgg	aag	613	
Asp	Ala	Val	Ala	Thr	Thr	Gly	Glu	Ile	His	Glu	Glu	Lys	Ala	Trp	Lys		
127					132					137					142		
acc	aga	gcc	ctg	gaa	gtg	ggg	cag	cca	gcc	cag	cgg	gac	att	cgt	agg	661	
Thr	Arg	Ala	Leu	Glu	Val	Gly	Gln	Pro	Ala	Gln	Arg	Asp	Ile	Arg	Arg		
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Thr	Leu	Glu	Asp	Leu	Ser	Ser	Leu	Glu	Arg	Thr	Leu	Val	Val	Ser	Glu		
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Ser	Ser	Pro	Leu	Gly	Gly	Asp	Cys	Gln	Glu	Val	Thr	Thr	Leu	Thr	Val		
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Lys	Tyr	Gln	Val	Ser	Glu	Glu	Val	Pro	Ser	Gly	Thr	Val	Ile	Gly	Lys		
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Leu	Ser	Gln	Glu	Leu	Gly	Arg	Glu	Glu	Arg	Arg	Arg	Gln	Ala	Gly	Ala		
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Ser Glu Glu Gly Leu Leu Ser Thr Gly Arg Arg Leu Asp Arg Glu Gln				
255	260	265	270	
ctg tgc cga cag tgg gat ccc tgc ctg gtt tcc ttt gat gtg ctt gcc				1045
Leu Cys Arg Gln Trp Asp Pro Cys Leu Val Ser Phe Asp Val Leu Ala				
271	276	281	286	
aca ggg gat ttg gct ctg atc cat gtg gag atc caa gtg ctg gac atc				1093
Thr Gly Asp Leu Ala Leu Ile His Val Glu Ile Gln Val Leu Asp Ile				
287	292	297	302	
aat gac cac cag cca cgg ttt ccc aaa ggc gag cag gag ctg gaa atc				1141
Asn Asp His Gln Pro Arg Phe Pro Lys Gly Glu Gln Glu Leu Glu Ile				
303	308	313	318	
tct gag agc gcc tct ctg cga acc cgg atc ccc ctg gac aga gct ctt				1189
Ser Glu Ser Ala Ser Leu Arg Thr Arg Ile Pro Leu Asp Arg Ala Leu				
319	324	329	334	
gac cca gac aca ggc cct aac acc ctg cac acc tac act ctg tct ccc				1237
Asp Pro Asp Thr Gly Pro Asn Thr Leu His Thr Tyr Thr Leu Ser Pro				
335	340	345	350	
agt gag cac ttt gcc ttg gat gtc att gtg ggc cct gat gag acc aaa				1285
Ser Glu His Phe Ala Leu Asp Val Ile Val Gly Pro Asp Glu Thr Lys				
351	356	361	366	
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His Ala Glu Leu Ile Val Val Lys Glu Leu Asp Arg Glu Ile His Ser				
367	372	377	382	
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Phe Phe Asp Leu Val Leu Thr Ala Tyr Asp Asn Gly Asn Pro Pro Lys				
383	388	393	398	
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Ser Gly Thr Ser Leu Val Lys Val Asn Val Leu Asp Ser Asn Asp Asn				
399	404	409	414	
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Ser Pro Ala Phe Ala Glu Ser Ser Leu Ala Leu Glu Ile Gln Glu Asp				
415	420	425	430	
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Ala Ala Pro Gly Thr Leu Leu Ile Lys Leu Thr Ala Thr Asp Pro Asp				
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caa ggc ccc aat ggg gag gtg gag ttc ttc ctc agt aag cac atg cct				1573
Gln Gly Pro Asn Gly Glu Val Glu Phe Phe Leu Ser Lys His Met Pro				
447	452	457	462	
cca gag gtg ctg gac acc ttc agt att gat gcc aag aca ggc cag gtc				1621
Pro Glu Val Leu Asp Thr Phe Ser Ile Asp Ala Lys Thr Gly Gln Val				
463	468	473	478	

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Asp Val Gln Ala Arg Asp Leu Gly Pro Asn Pro Ile Pro Ala His Cys	
495 500 505 510	
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Lys Val Leu Ile Lys Val Leu Asp Val Asn Asp Asn Ile Pro Ser Ile	
511 516 521 526	
cac gtc aca tgg gcc tcc cag cca tca ctg gtg tca gaa gct ctt ccc	1813
His Val Thr Trp Ala Ser Gln Pro Ser Leu Val Ser Glu Ala Leu Pro	
527 532 537 542	
aag gac agt ttt att gct ctt gtc atg gca gat gac ttg gat tca gga	1861
Lys Asp Ser Phe Ile Ala Leu Val Met Ala Asp Asp Leu Asp Ser Gly	
543 548 553 558	
cac aat ggt ttg gtc cac tgc tgg ctg agc caa gag ctg ggc cac ttc	1909
His Asn Gly Leu Val His Cys Trp Leu Ser Gln Glu Leu Gly His Phe	
559 564 569 574	
agg ctg aaa aga act aat ggc aac aca tac atg ttg cta acc aat gcc	1957
Arg Leu Lys Arg Thr Asn Gly Asn Thr Tyr Met Leu Leu Thr Asn Ala	
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aca ctg gac aga gag cag tgg ccc aaa tat acc ctc act ctg tta gcc	2005
Thr Leu Asp Arg Glu Gln Trp Pro Lys Tyr Thr Leu Thr Leu Leu Ala	
591 596 601 606	
caa gac caa gga ctc cag ccc tta tca gcc aag aaa cag ctc agc att	2053
Gln Asp Gln Gly Leu Gln Pro Leu Ser Ala Lys Lys Gln Leu Ser Ile	
607 612 617 622	
cag atc agt gac atc aac gac aat gca cct gtg ttt gag aaa agc agg	2101
Gln Ile Ser Asp Ile Asn Asp Asn Ala Pro Val Phe Glu Lys Ser Arg	
623 628 633 638	
tat gaa gtc tcc acg cgg gaa aac aac tta ccc tct ctt cac ctc att	2149
Tyr Glu Val Ser Thr Arg Glu Asn Asn Leu Pro Ser Leu His Leu Ile	
639 644 649 654	
acc atc aag gct cat gat gca gac ttg ggc att aat gga aaa gtc tca	2197
Thr Ile Lys Ala His Asp Ala Asp Leu Gly Ile Asn Gly Lys Val Ser	
655 660 665 670	
tac cgc atc cag gac tcc cca gtt gct cac tta gta gct att gac tcc	2245
Tyr Arg Ile Gln Asp Ser Pro Val Ala His Leu Val Ala Ile Asp Ser	
671 676 681 686	
aac aca gga gag gtc act gct cag agg tca ctg aac tat gaa gag atg	2293
Asn Thr Gly Glu Val Thr Ala Gln Arg Ser Leu Asn Tyr Glu Glu Met	
687 692 697 702	

gcc ggc ttt gag ttc cag gtg atc gca gag gac agc ggg caa ccc atg Ala Gly Phe Glu Phe Gln Val Ile Ala Glu Asp Ser Gly Gln Pro Met 703 708 713 718	2341
ctt gca tcc agt gtc tct gtg tgg gtc agc ctc ttg gat gcc aat gat Leu Ala Ser Ser Val Ser Val Trp Val Ser Leu Leu Asp Ala Asn Asp 719 724 729 734	2389
aat gcc cca gag gtg gtc cag cct gtg ctc agc gat gga aaa gcc agc Asn Ala Pro Glu Val Val Gln Pro Val Leu Ser Asp Gly Lys Ala Ser 735 740 745 750	2437
ctc tcc gtg ctt gtg aat gcc tcc aca ggc cac ctg ctg gtg ccc atc Leu Ser Val Leu Val Asn Ala Ser Thr Gly His Leu Leu Val Pro Ile 751 756 761 766	2485
gag act ccc aat ggc ttg ggc cca gcg ggc act gac aca cct cca ctg Glu Thr Pro Asn Gly Leu Gly Pro Ala Gly Thr Asp Thr Pro Pro Leu 767 772 777 782	2533
gcc act cac agc tcc cgg cca ttc ctt ttg aca acc att gtg gca aga Ala Thr His Ser Ser Arg Pro Phe Leu Leu Thr Thr Ile Val Ala Arg 783 788 793 798	2581
gat gca gac tcg ggg gca aat gga gag ccc ctc tac agc atc cgc agt Asp Ala Asp Ser Gly Ala Asn Gly Glu Pro Leu Tyr Ser Ile Arg Ser 799 804 809 814	2629
gga aat gaa gcc cac ctc ttc atc ctc aac cct cat acg ggg cag ctg Gly Asn Glu Ala His Leu Phe Ile Leu Asn Pro His Thr Gly Gln Leu 815 820 825 830	2677
ttc gtc aat gtc acc aat gcc agc agc ctc att ggg agt gag tgg gag Phe Val Asn Val Thr Asn Ala Ser Ser Leu Ile Gly Ser Glu Trp Glu 831 836 841 846	2725
ctg gag ata gta gta gag gac cag gga agc ccc ccc tta cag acc cga Leu Glu Ile Val Val Glu Asp Gln Gly Ser Pro Pro Leu Gln Thr Arg 847 852 857 862	2773
gcc ctg ttg agg gtc atg ttt gtc acc agt gtg gac cac ctg agg gac Ala Leu Leu Arg Val Met Phe Val Thr Ser Val Asp His Leu Arg Asp 863 868 873 878	2821
tca gcc cgc aag cct ggg gcc ttg agc atg tcg atg ctg acg gtg atc Ser Ala Arg Lys Pro Gly Ala Leu Ser Met Ser Met Leu Thr Val Ile 879 884 889 894	2869
tgc ctg gct gta ctg ttg ggc atc ttc ggg ttg atc ctg gct ttg ttc Cys Leu Ala Val Leu Leu Gly Ile Phe Gly Leu Ile Leu Ala Leu Phe 895 900 905 910	2917
atg tcc atc tgc cgg aca gaa aag aag gac aac agg gcc tac aac tgt Met Ser Ile Cys Arg Thr Glu Lys Lys Asp Asn Arg Ala Tyr Asn Cys 911 916 921 926	2965
cgg gag gcc gag tcc acc tac cgc cag cag ccc aag agg ccc cag aaa	3013

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His	Ile	Gln	Lys	Ala	Asp	Ile	His	Leu	Val	Pro	Val	Leu	Arg	Gly	Gln	
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Ala	Gly	Glu	Pro	Cys	Glu	Val	Gly	Gln	Ser	His	Lys	Asp	Val	Asp	Lys	
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gag	gcg	atg	atg	gaa	gca	ggc	tgg	gac	ccc	tgc	ctg	cag	gcc	ccc	ttc	3157
Glu	Ala	Met	Met	Glu	Ala	Gly	Trp	Asp	Pro	Cys	Leu	Gln	Ala	Pro	Phe	
975					980					985					990	
cac	ctc	acc	ccg	acc	ctg	tac	agg	acg	ctg	cgt	aat	caa	ggc	aac	cag	3205
His	Leu	Thr	Pro	Thr	Leu	Tyr	Arg	Thr	Leu	Arg	Asn	Gln	Gly	Asn	Gln	
991					996					1001					1006	
gga	gca	ccg	gcg	gag	agc	cga	gag	gtg	ctg	caa	gac	acg	gtc	aac	ctc	3253
Gly	Ala	Pro	Ala	Glu	Ser	Arg	Glu	Val	Leu	Gln	Asp	Thr	Val	Asn	Leu	
1007					1012					1017					1022	
ctt	ttc	aac	cat	ccc	agg	cag	agg	aat	gcc	tcc	cgg	gag	aac	ctg	aac	3301
Leu	Phe	Asn	His	Pro	Arg	Gln	Arg	Asn	Ala	Ser	Arg	Glu	Asn	Leu	Asn	
1023					1028					1033					1038	
ctt	ccc	gag	ccc	cag	cct	gcc	aca	ggc	cag	cca	cgt	tcc	agg	cct	ctg	3349
Leu	Pro	Glu	Pro	Gln	Pro	Ala	Thr	Gly	Gln	Pro	Arg	Ser	Arg	Pro	Leu	
1039					1044					1049					1054	
aag	gtt	gca	ggc	agc	ccc	aca	ggg	agg	ctg	gct	gga	gac	cag	ggc	agt	3397
Lys	Val	Ala	Gly	Ser	Pro	Thr	Gly	Arg	Leu	Ala	Gly	Asp	Gln	Gly	Ser	
1055					1060					1065					1070	
gag	gaa	gcc	cca	cag	agg	cca	cca	gcc	tcc	tct	gca	acc	ctg	aga	cgg	3445
Glu	Glu	Ala	Pro	Gln	Arg	Pro	Pro	Ala	Ser	Ser	Ala	Thr	Leu	Arg	Arg	
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cag	cga	cat	ctc	aat	ggc	aaa	gtg	tcc	cct	gag	aaa	gaa	tca	ggg	ccc	3493
Gln	Arg	His	Leu	Asn	Gly	Lys	Val	Ser	Pro	Glu	Lys	Glu	Ser	Gly	Pro	
1087					1092					1097					1102	
cgt	cag	atc	ctg	cgg	agc	ctg	gtc	cgg	ctg	tct	gtg	gct	gcc	ttc	gcc	3541
Arg	Gln	Ile	Leu	Arg	Ser	Leu	Val	Arg	Leu	Ser	Val	Ala	Ala	Phe	Ala	
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gag	cgg	aac	ccc	gtg	gag	gag	ctc	act	gtg	gat	tct	cct	cct	gtt	cag	3589
Glu	Arg	Asn	Pro	Val	Glu	Glu	Leu	Thr	Val	Asp	Ser	Pro	Pro	Val	Gln	
1119					1124					1129					1134	
caa	atc	tcc	cag	ctg	ctg	tcc	ttg	ctg	cat	cag	ggc	caa	ttc	cag	ccc	3637
Gln	Ile	Ser	Gln	Leu	Leu	Ser	Leu	Leu	His	Gln	Gly	Gln	Phe	Gln	Pro	
1135					1140					1145					1150	
aaa	cca	aac	cac	cga	gga	aat	aag	tac	ttg	gcc	aag	cca	gga	ggc	agc	3685
Lys	Pro	Asn	His	Arg	Gly	Asn	Lys	Tyr	Leu	Ala	Lys	Pro	Gly	Gly	Ser	

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agg agt gca atc cca gac aca gat ggc cca agt gca agg gct gga ggc				3733
Arg Ser Ala Ile Pro Asp Thr Asp Gly Pro Ser Ala Arg Ala Gly Gly				
1167	1172	1177	1182	
cag aca gac cca gaa cag gag gaa ggg cct ttg gat cct gaa gag gac				3781
Gln Thr Asp Pro Glu Gln Glu Glu Gly Pro Leu Asp Pro Glu Glu Asp				
1183	1188	1193	1198	
ctc tct gtg aag caa ctg cta gaa gaa gag ctg tca agt ctg ctg gac				3829
Leu Ser Val Lys Gln Leu Leu Glu Glu Glu Leu Ser Ser Leu Leu Asp				
1199	1204	1209	1214	
ccc agc aca ggt ctg gcc ctg gac cgg ctg agc gcc cct gac ccg gcc				3877
Pro Ser Thr Gly Leu Ala Leu Asp Arg Leu Ser Ala Pro Asp Pro Ala				
1215	1220	1225	1230	
tgg atg gcg aga ctc tct ttg ccc ctc acc acc aac tac cgt gac aat				3925
Trp Met Ala Arg Leu Ser Leu Pro Leu Thr Thr Asn Tyr Arg Asp Asn				
1231	1236	1241	1246	
gtg atc tcc ccg gat gct gca gcc acg gag gag cca agg acc ttc cag				3973
Val Ile Ser Pro Asp Ala Ala Ala Thr Glu Glu Pro Arg Thr Phe Gln				
1247	1252	1257	1262	
acg ttc ggc aag gca gag gca cca gag ctg agc cca aca ggc acg agg				4021
Thr Phe Gly Lys Ala Glu Ala Pro Glu Leu Ser Pro Thr Gly Thr Arg				
1263	1268	1273	1278	
ctg gcc agc acc ttt gtc tcg gag atg agc tca ctg ctg gag atg ctg				4069
Leu Ala Ser Thr Phe Val Ser Glu Met Ser Ser Leu Leu Glu Met Leu				
1279	1284	1289	1294	
ctg gaa cag cgc tcc agc atg ccc gtg gag gcc gcc tcc gag gcg ctg				4117
Leu Glu Gln Arg Ser Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu				
1295	1300	1305	1310	
cgg cgg ctc tcg gtc tgc ggg agg acc ctc agt tta gac ttg gcc acc				4165
Arg Arg Leu Ser Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr				
1311	1316	1321	1326	
agt gca gcc tca ggc atg aaa gtg caa ggg gac cca ggt gga aag acg				4213
Ser Ala Ala Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr				
1327	1332	1337	1342	
ggg act gag ggc aag agc aga ggc agc agc agc agc agc agc agg tgc ctg				4261
Gly Thr Glu Gly Lys Ser Arg Gly Ser Ser Ser Ser Ser Ser Arg Cys Leu				
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tga				4264
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 Met Glu Phe Ser Gly Arg Lys Arg
 1 5
 agg aag ctg agg ttg gca ggt gac cag agg aat gct tcc tac cct cat 159
 Arg Lys Leu Arg Leu Ala Gly Asp Gln Arg Asn Ala Ser Tyr Pro His
 9 14 19 24
 tgc ctt cag ttt tac ttg cag cca cct tct gaa aac ata tct tta aca 207
 Cys Leu Gln Phe Tyr Leu Gln Pro Pro Ser Glu Asn Ile Ser Leu Thr
 25 30 35 40
 gaa ttt gaa aac ttg gct att gat aga gtt aaa ttg tta aaa tca gtt 255
 Glu Phe Glu Asn Leu Ala Ile Asp Arg Val Lys Leu Leu Lys Ser Val
 41 46 51 56
 gaa aat ctt gga gtg agc tat gtg aaa gga act gaa caa tac cag agt 303
 Glu Asn Leu Gly Val Ser Tyr Val Lys Gly Thr Glu Gln Tyr Gln Ser
 57 62 67 72
 aag ttg gag agt gag ctt cgg aag ctc aag ttt tcc tac aga gag aag 351
 Lys Leu Glu Ser Glu Leu Arg Lys Leu Lys Phe Ser Tyr Arg Glu Lys
 73 78 83 88
 cta gaa gat gaa tat gaa cca cga aga aga gat cat att tct cat ttt 399
 Leu Glu Asp Glu Tyr Glu Pro Arg Arg Arg Asp His Ile Ser His Phe
 89 94 99 104
 att ttg cgg ctt gct tat tgc cag tct gaa gaa ctt aga cgc tgg ttc 447
 Ile Leu Arg Leu Ala Tyr Cys Gln Ser Glu Glu Leu Arg Arg Trp Phe
 105 110 115 120
 att caa caa gaa atg gat ctc ctt cga ttt aga ttt agt att tta ccc 495
 Ile Gln Gln Glu Met Asp Leu Leu Arg Phe Arg Phe Ser Ile Leu Pro
 121 126 131 136
 aag gat aaa att cag gat ttc tta aag gat agc caa ttg cag ttt gag 543
 Lys Asp Lys Ile Gln Asp Phe Leu Lys Asp Ser Gln Leu Gln Phe Glu
 137 142 147 152
 gct ata agt gat gaa gag aag act ctt cga gaa cag gag att gtt gcc 591
 Ala Ile Ser Asp Glu Glu Lys Thr Leu Arg Glu Gln Glu Ile Val Ala
 153 158 163 168

tca tca cca agt tta agt gga ctt aag ttg ggg ttc gag tcc att tat	639
Ser Ser Pro Ser Leu Ser Gly Leu Lys Leu Gly Phe Glu Ser Ile Tyr	
169 174 179 184	
aag atc cct ttt gct gat gct ctg gat ttg ttt cga gga agg aaa gtc	687
Lys Ile Pro Phe Ala Asp Ala Leu Asp Leu Phe Arg Gly Arg Lys Val	
185 190 195 200	
tat ttg gaa gat ggc ttt gct tac gta cca ctt aag gac att gtg gca	735
Tyr Leu Glu Asp Gly Phe Ala Tyr Val Pro Leu Lys Asp Ile Val Ala	
201 206 211 216	
atc atc ctg aat gaa ttt aga gcc aaa ctg tcc aag gct ttg gca tta	783
Ile Ile Leu Asn Glu Phe Arg Ala Lys Leu Ser Lys Ala Leu Ala Leu	
217 222 227 232	
aca gcc agg tcc ttg cct gct gtg cag tct gat gaa aga ctt cag cct	831
Thr Ala Arg Ser Leu Pro Ala Val Gln Ser Asp Glu Arg Leu Gln Pro	
233 238 243 248	
ctg ctc aat cac ctc agt cat tcc tac act ggc caa gat tac agt acc	879
Leu Leu Asn His Leu Ser His Ser Tyr Thr Gly Gln Asp Tyr Ser Thr	
249 254 259 264	
cag gga aat gtt ggg aag att tct tta gat cag att gat ttg ctt tct	927
Gln Gly Asn Val Gly Lys Ile Ser Leu Asp Gln Ile Asp Leu Leu Ser	
265 270 275 280	
acc aaa tcc ttc cca cct tgc atg cgt cag tta cat aaa gcc ttg cgg	975
Thr Lys Ser Phe Pro Pro Cys Met Arg Gln Leu His Lys Ala Leu Arg	
281 286 291 296	
gaa aat cac cat ctt cgt cat gga ggc cga atg cag tat ggc cta ttt	1023
Glu Asn His His Leu Arg His Gly Gly Arg Met Gln Tyr Gly Leu Phe	
297 302 307 312	
ctg aag ggc att ggt tta act ttg gaa cag gca ttg cag ttc tgg aag	1071
Leu Lys Gly Ile Gly Leu Thr Leu Glu Gln Ala Leu Gln Phe Trp Lys	
313 318 323 328	
caa gaa ttt atc aaa gga aag atg ggt tcc aga caa gtt tga taaaggt	1120
Gln Glu Phe Ile Lys Gly Lys Met Gly Ser Arg Gln Val *	
329 334 339	
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taatcagtac ttttgtgaga gccaacgtat tctaaatggt ggtaaagaca taaagaagga	1480
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 aaaa 2324

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 aagggtgacg cgagctctgc cctttaaccg gaaacgtctc cctgctcacc ccacccccgc 180
 gcagacgcag tgctgagcac acagctaccg gacaaagagt gacgcccgga gctggagtt 239
 atg gcg gct acg gag ccg atc ttg gcg gcc act ggg agt ccc gcg gcg 287
 Met Ala Ala Thr Glu Pro Ile Leu Ala Ala Thr Gly Ser Pro Ala Ala
 1 5 10 15

gtg cac cgg aga aac tgg aag gag ccg gtt cga gct cag ccc ctg agc	335
Val His Arg Arg Asn Trp Lys Glu Pro Val Arg Ala Gln Pro Leu Ser	
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Val Thr Val Trp Ala Pro Arg Cys Gln Arg Pro His Arg Leu Pro Leu	
33 38 43 48	
agc ctt cca gtc cca acg ccg cgg tcc ctg aag cca tcc cta cgc ccc	431
Ser Leu Pro Val Pro Thr Pro Arg Ser Leu Lys Pro Ser Leu Arg Pro	
49 54 59 64	
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Glu Leu Arg Pro Pro Arg Pro Trp Ser Cys Leu Ser Gly Pro His Pro	
65 70 75 80	
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gagcgggtgga gctgcggggc gccagggccg ggcgctctgt gcggactggg gccatgatcg	836
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aaaaaaaaaa aa	908

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gcgggtctcg gtcgcggggc ccgtttgcag agccccgcggc gccgggagga ctttgttctt	180
cttcagaaga gaaaactgaa gaaggagga atg gct gtg ggg ctt tgt aaa gcc	233
Met Ala Val Gly Leu Cys Lys Ala	
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Met Ser Gln Gly Leu Val Thr Phe Arg Asp Val Ala Leu Asp Phe Ser	
9 14 19 24	
caa gaa gag tgg gaa tgg ctg aag cca tct cag aag gat tta tac aga	329
Gln Glu Glu Trp Glu Trp Leu Lys Pro Ser Gln Lys Asp Leu Tyr Arg	
25 30 35 40	
gat gtc atg ttg gag aac tac agg aac ttg gta tgg ctt gga ctc tcc	377
Asp Val Met Leu Glu Asn Tyr Arg Asn Leu Val Trp Leu Gly Leu Ser	
41 46 51 56	
att tct aag ccc aac atg atc tcc tta ctg gag caa ggg aag gaa ccg	425
Ile Ser Lys Pro Asn Met Ile Ser Leu Leu Glu Gln Gly Lys Glu Pro	
57 62 67 72	
tgg atg gtg gag aga aag atg tca cag ggt cac tgt gca gac tgg gag	473
Trp Met Val Glu Arg Lys Met Ser Gln Gly His Cys Ala Asp Trp Glu	
73 78 83 88	
tct tgg tgt gaa att gag gaa tta tct cca aaa tgg ttc att gat gaa	521
Ser Trp Cys Glu Ile Glu Glu Leu Ser Pro Lys Trp Phe Ile Asp Glu	
89 94 99 104	
gat gaa ata tcc cag gag atg gta atg gaa agg cta gca agt cat ggc	569
Asp Glu Ile Ser Gln Glu Met Val Met Glu Arg Leu Ala Ser His Gly	
105 110 115 120	
ctt gaa tgc tcc agt ttc aga gaa gcc tgg aaa tat aag ggt gaa ttt	617
Leu Glu Cys Ser Ser Phe Arg Glu Ala Trp Lys Tyr Lys Gly Glu Phe	
121 126 131 136	
gag cta cat cag gga aat gcg gag agg cat ttc atg caa gtg aca gct	665
Glu Leu His Gln Gly Asn Ala Glu Arg His Phe Met Gln Val Thr Ala	
137 142 147 152	
gtt aag gaa atc tct act ggg aaa aga gac aat gaa ttt agt aat tct	713
Val Lys Glu Ile Ser Thr Gly Lys Arg Asp Asn Glu Phe Ser Asn Ser	
153 158 163 168	
ggg aga agc ata ccc ctg aaa tca gta ttt tta aca caa cag aaa gtt	761
Gly Arg Ser Ile Pro Leu Lys Ser Val Phe Leu Thr Gln Gln Lys Val	
169 174 179 184	
cct acc ata cag caa gta cat aaa ttt gat att tat gat aaa ctc ttc	809
Pro Thr Ile Gln Gln Val His Lys Phe Asp Ile Tyr Asp Lys Leu Phe	
185 190 195 200	
ccc caa aat tca gtc ata att gaa tat aaa aga ctc cat gct gag aag	857
Pro Gln Asn Ser Val Ile Ile Glu Tyr Lys Arg Leu His Ala Glu Lys	
201 206 211 216	
gaa tct ttg ata ggt aat gaa tgt gaa gaa ttc aac cag agt acg tac	905
Glu Ser Leu Ile Gly Asn Glu Cys Glu Glu Phe Asn Gln Ser Thr Tyr	
217 222 227 232	

ctt agt aaa gat ata gga att cct cct ggg gag aaa cct tat gaa agt	953
Leu Ser Lys Asp Ile Gly Ile Pro Pro Gly Glu Lys Pro Tyr Glu Ser	
233 238 243 248	
cat gat ttt tca aag ctc tta agt ttc cac tca tta ttt act caa cat	1001
His Asp Phe Ser Lys Leu Leu Ser Phe His Ser Leu Phe Thr Gln His	
249 254 259 264	
cag acc act cat ttt gga aaa tta ccc cat gga tac gat gaa tgt ggt	1049
Gln Thr Thr His Phe Gly Lys Leu Pro His Gly Tyr Asp Glu Cys Gly	
265 270 275 280	
gat gcc ttt agc tgt tac tca ttc ttt act caa cct cag aga att cac	1097
Asp Ala Phe Ser Cys Tyr Ser Phe Phe Thr Gln Pro Gln Arg Ile His	
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Ser Gly Glu Lys Pro Tyr Ala Cys Asn Asp Cys Gly Lys Ala Phe Ser	
297 302 307 312	
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His Asp Phe Phe Leu Ser Glu His Gln Arg Thr His Ile Gly Glu Lys	
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Pro Tyr Glu Cys Lys Glu Cys Asn Lys Ala Phe Arg Gln Ser Ala His	
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Leu Ala Gln His Gln Arg Ile His Thr Gly Glu Lys Pro Phe Ala Cys	
345 350 355 360	
aat gaa tgt ggg aag gcc ttt agc cgt tat gcc ttc ctt gtt gaa cat	1337
Asn Glu Cys Gly Lys Ala Phe Ser Arg Tyr Ala Phe Leu Val Glu His	
361 366 371 376	
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Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys Asn	
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Lys Ala Phe Arg Gln Ser Ala His Leu Asn Gln His Gln Arg Ile His	
393 398 403 408	
act gga gag aaa ccc tat gaa tgt aat cag tgt gga aaa gcc ttc agc	1481
Thr Gly Glu Lys Pro Tyr Glu Cys Asn Gln Cys Gly Lys Ala Phe Ser	
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Pro Phe Lys Cys Ser Glu Cys Gly Lys Thr Phe Gly Tyr Arg Ser His	
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Leu Asn Gln His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys	
457 462 467 472	
atc aaa tgt ggg aag ttt ttt agg act gac tca caa ctt aat cga cat	1673
Ile Lys Cys Gly Lys Phe Phe Arg Thr Asp Ser Gln Leu Asn Arg His	
473 478 483 488	
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His Arg Ile His Thr Gly Glu Arg Pro Phe Glu Cys Ser Lys Cys Gly	
489 494 499 504	
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Lys Ala Phe Ser Asp Ala Leu Val Leu Ile His His Lys Arg Ser His	
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gca gga gag aaa ccc tat gaa tgt aac aaa tgt gga aag gcc ttc agt	1817
Ala Gly Glu Lys Pro Tyr Glu Cys Asn Lys Cys Gly Lys Ala Phe Ser	
521 526 531 536	
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Cys Gly Ser Tyr Leu Asn Gln His Gln Arg Ile His Thr Gly Glu Lys	
537 542 547 552	
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Pro Tyr Glu Cys Ser Glu Cys Gly Lys Ala Phe His Gln Ile Leu Ser	
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Ala Lys Val Ala Glu Pro Ala Arg Ala Gly Thr Glu Ala Ala Leu Arg	
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Pro Ala Leu Ser Val Ala Glu Ser Ala Thr Ser Leu Gly Pro Leu His	
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Gln Gly Arg Arg Phe Pro Glu Ala Pro Ala Ala His Pro Gly Gly Thr	
649 654 659 664	
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Gly Phe Thr Val Cys Ala Ser *	
665 670	
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Ala Leu Gly Pro Pro Leu Ala Pro Gly Val Arg Gly Ser Glu Ala Glu
12 17 22 27

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Gly Arg Leu Arg Glu Lys Leu Phe Ser Gly Tyr Asp Ser Ser Val Arg
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cca gcg cgg gag gtg gga gac cgt gtc agg gtc agc gtt ggt ctc atc 193
Pro Ala Arg Glu Val Gly Asp Arg Val Arg Val Ser Val Gly Leu Ile
44 49 54 59

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Leu Ala Gln Leu Ile Ser Leu Asn Glu Lys Asp Glu Glu Met Ser Thr
60 65 70 75

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Lys Val Tyr Leu Asp Leu Glu Trp Thr Asp Tyr Arg Leu Ser Trp Asp
76 81 86 91

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Pro Ala Glu His Asp Gly Ile Asp Ser Leu Arg Ile Thr Ala Glu Ser
92 97 102 107

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Val Trp Leu Pro Asp Val Val Leu Leu Asn Asn Asn Asp Gly Asn Phe
108 113 118 123

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124 129 134 139

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Arg Trp Gln Pro Pro Gly Ile Tyr Arg Ser Ser Cys Ser Ile Gln Val
140 145 150 155

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Thr Tyr Phe Pro Phe Asp Trp Gln Asn Cys Thr Met Val Phe Ser Ser	
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Tyr Ser Tyr Asp Ser Ser Glu Val Ser Leu Gln Thr Gly Leu Gly Pro	
172 177 182 187	
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Asp Gly Gln Gly His Gln Glu Ile His Ile His Glu Gly Thr Phe Ile	
188 193 198 203	
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Glu Asn Gly Gln Trp Glu Asn Ile His Lys Pro Ser Arg Leu Ile Gln	
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Glu Thr Ser Leu Ser Val Pro Ile Ile Ile Lys Tyr Leu Met Phe Thr	
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Met Val Leu Val Thr Phe Ser Val Ile Leu Ser Val Val Val Leu Asn	
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Leu His His Arg Ser Pro His Thr His Gln Met Pro Leu Trp Val Arg	
332 337 342 347	
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Gln Ile Phe Ile His Lys Leu Pro Leu Tyr Leu Arg Leu Lys Arg Pro	
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Lys Pro Glu Arg Asp Leu Met Pro Glu Pro Pro His Cys Ser Ser Pro	
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cca	agt	gat	ttt	ctc	ttc	ccc	aaa	ccc	aat	agg	ttc	cag	cct	gaa	ctg	1249
Pro	Ser	Asp	Phe	Leu	Phe	Pro	Lys	Pro	Asn	Arg	Phe	Gln	Pro	Glu	Leu	
396					401					406					411	
tct	gcc	cct	gat	ctg	cgg	cga	ttt	atc	gat	ggg	cca	aac	cgg	gct	gtg	1297
Ser	Ala	Pro	Asp	Leu	Arg	Arg	Phe	Ile	Asp	Gly	Pro	Asn	Arg	Ala	Val	
412					417					422					427	
gcc	ctg	ctt	cgg	gag	cta	cgg	gag	gtc	gtc	tcc	tct	atc	agc	tac	atc	1345
Ala	Leu	Leu	Pro	Glu	Leu	Arg	Glu	Val	Val	Ser	Ser	Ile	Ser	Tyr	Ile	
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Ala	Arg	Gln	Leu	Gln	Glu	Gln	Glu	Asp	His	Asp	Ala	Leu	Lys	Glu	Asp	
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Trp	Gln	Phe	Val	Ala	Met	Val	Val	Asp	Arg	Leu	Phe	Leu	Trp	Thr	Phe	
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atc	atc	ttc	acc	agc	gtt	ggg	acc	cta	gtc	atc	ttc	ctg	gac	gcc	acg	1489
Ile	Ile	Phe	Thr	Ser	Val	Gly	Thr	Leu	Val	Ile	Phe	Leu	Asp	Ala	Thr	
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tac	cac	ttg	ccc	cct	cca	gac	ccc	ttt	cct	tga	agactgga	gggttgagac				1540
Tyr	His	Leu	Pro	Pro	Pro	Asp	Pro	Phe	Pro	*						
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Met Val Arg Ala	
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Arg Arg Leu Asp Ser Ser Leu Ala Ser Ala Val Gly Leu Leu His Pro	
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Pro Pro Asp Arg Arg Gly Ala Arg Thr Gly Ala Thr Ala Ser Cys Arg	
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Leu Pro Pro Asp Ser Pro Arg Glu Leu Val Pro Lys Gln Ala Pro Cys	
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Ser Pro Ser Asp Pro Ala Leu Pro Trp Thr Leu Gly His Gly Asn Gln	
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ccc cct gct gtg gtt ccc gaa ccc caa ggc ccg atg ggt ccc gcg ggg	895
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Val Ala Ala Arg Pro Gly Arg Phe Phe Gly Val Tyr Leu Leu Tyr Cys	
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Leu Asn Pro Arg Tyr Arg Gly Arg Val Tyr Val Gly Phe Thr Val Asn	
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Gln His Pro His Ala Ser Arg Arg Leu Ala His Val Gly Pro Arg Leu	
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Arg Gly Glu Thr Ala Phe Ala Phe His Leu Arg Val Leu Ala His Met	
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Arg Pro Asp Leu Arg Gln Asp Leu Cys Leu Pro Pro Pro Pro His Val	
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Pro Leu Ala Phe Gly Pro Pro Pro Pro Gln Ala Pro Ala Pro Arg Arg	
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 Pro Leu Arg Gly Gly Ala Gly Pro Ser Pro Ala Ser His Gly Pro Thr
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 His Gly Pro Ser Asp Pro Arg Thr Cys Leu Pro Gly Arg Gly Ala Gly
 42 47 52 57
 ggc atg cgg cca cac gga agg ggc gcg ctg ggc tgc tgc ggc ctc tgc 544
 Gly Met Arg Pro His Gly Arg Gly Ala Leu Gly Cys Cys Gly Leu Cys
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 Ser Phe Tyr Thr Cys His Gly Ala Ala Gly Asp Glu Ile Met His Gln
 74 79 84 89

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Arg Phe Ala Tyr Leu Ser Gly Gly Arg Gly Gln Asp Gly Ser Pro Val	
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Ile Thr Phe Pro Asp Tyr Pro Ala Phe Ser Glu Ile Pro Asp Lys Glu	
122 127 132 137	
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Phe Gln Asn Val Met Thr Tyr Leu Thr Ser Ile Pro Ser Leu Gln Asp	
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Ala Gly Ile Gly Phe Ile Leu Val Ile Asp Arg Arg Arg Asp Lys Trp	
154 159 164 169	
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Thr Ser Val Lys Ala Ser Val Leu Arg Ile Ala Ala Ser Phe Pro Ala	
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Lys Val Pro Val Ile Met Leu Ser Ser Val Pro Asp Leu His Gly Tyr	
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atg	gct	acg	ctg	agg	aac	acg	aac	ccc	aac	ttt	gtc	cgc	tgc	atc	atc	2253
Met	Ala	Thr	Leu	Arg	Asn	Thr	Asn	Pro	Asn	Phe	Val	Arg	Cys	Ile	Ile	
658					663					668					673	
ccc	aac	cac	gag	aag	aag	gcc	ggc	aag	ctg	gac	ccg	cat	ctc	gtg	ctg	2301
Pro	Asn	His	Glu	Lys	Lys	Ala	Gly	Lys	Leu	Asp	Pro	His	Leu	Val	Leu	
674					679					684					689	
gac	cag	ctg	cgc	tgc	aac	ggc	gtt	ctc	gag	ggc	atc	cgt	atc	tgc	cgc	2349
Asp	Gln	Leu	Arg	Cys	Asn	Gly	Val	Leu	Glu	Gly	Ile	Arg	Ile	Cys	Arg	
690					695					700					705	
cag	ggc	ttc	ccc	aac	agg	gtg	gtc	ttc	cag	gag	ttt	cgg	cag	aga	tat	2397
Gln	Gly	Phe	Pro	Asn	Arg	Val	Val	Phe	Gln	Glu	Phe	Arg	Gln	Arg	Tyr	
706					711					716					721	
gag	atc	ctg	act	cca	aac	tcc	att	ccc	aag	ggc	ttc	atg	gac	ggg	aag	2445
Glu	Ile	Leu	Thr	Pro	Asn	Ser	Ile	Pro	Lys	Gly	Phe	Met	Asp	Gly	Lys	
722					727					732					737	
cag	gcg	tgc	gtg	ctc	atg	ata	aaa	gcc	ctg	gag	ctc	gac	agc	aat	ctg	2493
Gln	Ala	Cys	Val	Leu	Met	Ile	Lys	Ala	Leu	Glu	Leu	Asp	Ser	Asn	Leu	
738					743					748					753	
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Tyr	Arg	Ile	Gly	Gln	Ser	Lys	Val	Phe	Phe	Arg	Ala	Gly	Val	Leu	Ala	
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cac	ctg	gag	gag	gag	cga	gac	ctg	aag	atc	acc	gac	gtc	atc	ata	ggg	2589
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Ala	Tyr	Leu	Lys	Leu	Arg	Asn	Trp	Gln	Trp	Trp	Arg	Leu	Phe	Thr	Lys	
818					823					828					833	
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Val	Lys	Pro	Leu	Leu	Gln	Val	Ser	Arg	Gln	Glu	Glu	Glu	Met	Met	Ala	
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Lys	Glu	Glu	Glu	Leu	Val	Lys	Val	Arg	Glu	Lys	Gln	Leu	Ala	Ala	Glu	
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Asn	Arg	Leu	Thr	Glu	Met	Glu	Thr	Leu	Gln	Ser	Gln	Leu	Met	Ala	Glu	

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Glu Ala Glu Glu Leu Arg Ala Arg Leu Thr Ala Lys Lys Gln Glu Leu				
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Glu Glu Ile Cys His Asp Leu Glu Ala Arg Val Glu Glu Glu Glu Glu				
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Arg Cys Gln His Leu Gln Ala Glu Lys Lys Lys Met Gln Gln Asn Ile				
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Gln Glu Leu Glu Glu Gln Leu Glu Glu Glu Glu Ser Ala Arg Gln Lys				
946	951	956	961	
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Leu Gln Leu Glu Lys Val Thr Thr Glu Ala Lys Leu Lys Lys Leu Glu				
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Glu Glu Gln Ile Ile Leu Glu Asp Gln Asn Cys Lys Leu Ala Lys Glu				
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Lys Lys Leu Leu Glu Asp Arg Ile Ala Glu Phe Thr Thr Asn Leu Thr				
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Gln Arg Gln Glu Leu Glu Lys Thr Arg Arg Lys Leu Glu Gly Asp Ser				
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Thr Asp Leu Ser Asp Gln Ile Ala Glu Leu Gln Ala Gln Ile Ala Glu				
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Leu Lys Met Gln Leu Ala Lys Lys Glu Glu Glu Leu Gln Ala Ala Leu				
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tcc aca gct gcc cag cag gag ctc agg tca aaa cgt gag cag gag gtg Ser Thr Ala Ala Gln Gln Glu Leu Arg Ser Lys Arg Glu Gln Glu Val 1154 1159 1164 1169	3741
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247 252 257 262	
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Trp Ser Asp Ser Arg His Ser Arg Gln Val Leu Leu Leu Gln Asp Ser	
263 268 273 278	
ttt atg aat tgc tct gac agc atc atc aat ggt tcc ttt cgt gcg ctt	1096
Phe Met Asn Cys Ser Asp Ser Ile Ile Asn Gly Ser Phe Arg Ala Leu	
279 284 289 294	
ggc ttt att cat gag gct cag gtc ggg gaa aga ctg atg gtc cac tgt	1144
Gly Phe Ile His Glu Ala Gln Val Gly Glu Arg Leu Met Val His Cys	
295 300 305 310	
gac agc aag aca ggt aat gca aat acg gat ttc atc tgg gtg ggt cca	1192
Asp Ser Lys Thr Gly Asn Ala Asn Thr Asp Phe Ile Trp Val Gly Pro	
311 316 321 326	
gat aac aga ctg cta gag ccg gat aaa gag atg gaa aac ttt tac gtg	1240
Asp Asn Arg Leu Leu Glu Pro Asp Lys Glu Met Glu Asn Phe Tyr Val	
327 332 337 342	
ttt cac aat gga agt ctg gtt ata gaa agc cct cgt ttt gag gat gct	1288
Phe His Asn Gly Ser Leu Val Ile Glu Ser Pro Arg Phe Glu Asp Ala	
343 348 353 358	
gga gtg tat tct tgt atc gca atg aat aag caa cgc ctg tta aat gaa	1336
Gly Val Tyr Ser Cys Ile Ala Met Asn Lys Gln Arg Leu Leu Asn Glu	
359 364 369 374	
act gtg gac gtc aca ata aat gtg agc aat ttc act gta agc aga tcc	1384
Thr Val Asp Val Thr Ile Asn Val Ser Asn Phe Thr Val Ser Arg Ser	
375 380 385 390	
cat gct cat gag gca ttt aac aca gct ttt acc act ctt gct gct tgc	1432
His Ala His Glu Ala Phe Asn Thr Ala Phe Thr Thr Leu Ala Ala Cys	
391 396 401 406	
gtg gcc agt atc gtt ttg gta ctt ttg tac ctc tat ctg act cca tgc	1480
Val Ala Ser Ile Val Leu Val Leu Leu Tyr Leu Tyr Leu Thr Pro Cys	
407 412 417 422	
ccc tgc aag tgt aaa acc aag aga cag aaa aat atg cta cac caa agc	1528
Pro Cys Lys Cys Lys Thr Lys Arg Gln Lys Asn Met Leu His Gln Ser	
423 428 433 438	
aat gcc cat tca tcg att ctc agt cct ggc ccc gct agt gat gcc tcc	1576
Asn Ala His Ser Ser Ile Leu Ser Pro Gly Pro Ala Ser Asp Ala Ser	
439 444 449 454	
gct gat gaa cgg aag gca ggt gca ggt aaa aga gtg gtg ttt ttg gaa	1624

Ala Asp Glu Arg Lys	Ala Gly Ala Gly Lys	Arg Val Val Phe Leu Glu	
455	460	465	470
ccc ctg aag gat act	gca gca ggg cag aac	ggg aaa gtc agg ctc ttt	1672
Pro Leu Lys Asp Thr	Ala Ala Gly Gln Asn	Gly Lys Val Arg Leu Phe	
471	476	481	486
ccc agc gag gca gtg	ata gct gag ggc atc	cta aag tcc acg agg ggg	1720
Pro Ser Glu Ala Val	Ile Ala Glu Gly Ile	Leu Lys Ser Thr Arg Gly	
487	492	497	502
aaa tct gac tca gat	tca gtc aat tca gtg	ttt tct gac aca cct ttt	1768
Lys Ser Asp Ser Asp	Ser Val Asn Ser Val	Phe Ser Asp Thr Pro Phe	
503	508	513	518
gtg gcg tcc act taa	tttgtgccta tatttgtatg	atgtcataat ttaattctgtt	1823
Val Ala Ser Thr *			
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		Met Pro Glu	
		1	
gat gta cga gaa aaa	aag gaa aat ctt cta	ctc aat tct gag aga tct	165
Asp Val Arg Glu Lys	Lys Glu Asn Leu Leu	Leu Asn Ser Glu Arg Ser	
4	9	14	19
act agg ctc tta aca	aag acc agt cat tca	caa gga ggg gat caa gct	213
Thr Arg Leu Leu Thr	Lys Thr Ser His Ser	Gln Gly Gly Asp Gln Ala	
20	25	30	35
tta agt aag tcc aca	ggg tca cca aca gag	aag ttg att gaa aaa cgt	261
Leu Ser Lys Ser Thr	Gly Ser Pro Thr Glu	Lys Leu Ile Glu Lys Arg	
36	41	46	51
caa gga gct aag act	gtt ttt aac aag ttc	agc aac atg aat tgg cca	309
Gln Gly Ala Lys Thr	Val Phe Asn Lys Phe	Ser Asn Met Asn Trp Pro	
52	57	62	67
gtg gac att cac cct	tta aac aaa agt tta	gtc aaa gat aat aaa tgg	357

Val	Asp	Ile	His	Pro	Leu	Asn	Lys	Ser	Leu	Val	Lys	Asp	Asn	Lys	Trp	
68					73					78					83	
aag	aaa	act	gag	gag	acc	caa	gag	aaa	cga	agg	tct	ttc	ctt	cag	gag	405
Lys	Lys	Thr	Glu	Glu	Thr	Gln	Glu	Lys	Arg	Arg	Ser	Phe	Leu	Gln	Glu	
84					89					94					99	
ttt	tgc	aag	aaa	tac	ggg	ggg	gtg	agt	cat	cat	cag	tca	cat	ctt	ttt	453
Phe	Cys	Lys	Lys	Tyr	Gly	Gly	Val	Ser	His	His	Gln	Ser	His	Leu	Phe	
100					105					110					115	
cat	aca	gta	tcc	aga	atc	tat	gta	gaa	gat	aaa	cac	aaa	atc	tta	tat	501
His	Thr	Val	Ser	Arg	Ile	Tyr	Val	Glu	Asp	Lys	His	Lys	Ile	Leu	Tyr	
116					121					126					131	
tgt	gag	gta	cct	aag	gct	ggc	tgt	tcc	aat	tgg	aaa	aga	att	ctg	atg	549
Cys	Glu	Val	Pro	Lys	Ala	Gly	Cys	Ser	Asn	Trp	Lys	Arg	Ile	Leu	Met	
132					137					142					147	
gta	cta	aat	gga	ttg	gct	tcc	tct	gca	tac	aac	atc	tcc	cac	aat	gct	597
Val	Leu	Asn	Gly	Leu	Ala	Ser	Ser	Ala	Tyr	Asn	Ile	Ser	His	Asn	Ala	
148					153					158					163	
gtc	cac	tac	ggg	aag	cat	ttg	aag	aag	cta	gat	agc	ttt	gac	cta	aaa	645
Val	His	Tyr	Gly	Lys	His	Leu	Lys	Lys	Leu	Asp	Ser	Phe	Asp	Leu	Lys	
164					169					174					179	
ggg	ata	tat	acc	cgc	tta	aat	act	tac	acc	aaa	gct	gtg	ttt	gtt	cgt	693
Gly	Ile	Tyr	Thr	Arg	Leu	Asn	Thr	Tyr	Thr	Lys	Ala	Val	Phe	Val	Arg	
180					185					190					195	
gat	ccc	atg	gaa	aga	tta	gta	tca	gcc	ttt	agg	gac	aaa	ttt	gaa	cac	741
Asp	Pro	Met	Glu	Arg	Leu	Val	Ser	Ala	Phe	Arg	Asp	Lys	Phe	Glu	His	
196					201					206					211	
ccc	aat	agt	tat	tac	cat	cca	gta	ttc	gga	aag	gca	att	atc	aag	aaa	789
Pro	Asn	Ser	Tyr	Tyr	His	Pro	Val	Phe	Gly	Lys	Ala	Ile	Ile	Lys	Lys	
212					217					222					227	
tat	cga	cca	aat	gcc	tgt	gaa	gaa	gca	tta	att	aat	gga	tct	gga	gtc	837
Tyr	Arg	Pro	Asn	Ala	Cys	Glu	Glu	Ala	Leu	Ile	Asn	Gly	Ser	Gly	Val	
228					233					238					243	
aag	ttc	aaa	gag	ttt	atc	cac	tac	ttg	ctg	gat	tcc	cac	cgt	cca	gta	885
Lys	Phe	Lys	Glu	Phe	Ile	His	Tyr	Leu	Leu	Asp	Ser	His	Arg	Pro	Val	
244					249					254					259	
gga	atg	gac	att	cac	tgg	gaa	aag	gtc	agc	aaa	ctc	tgc	tat	ccg	tgt	933
Gly	Met	Asp	Ile	His	Trp	Glu	Lys	Val	Ser	Lys	Leu	Cys	Tyr	Pro	Cys	
260					265					270					275	
ttg	atc	aac	tat	gat	ttt	gta	ggg	aaa	ttt	gag	act	ttg	gaa	gaa	gat	981
Leu	Ile	Asn	Tyr	Asp	Phe	Val	Gly	Lys	Phe	Glu	Thr	Leu	Glu	Glu	Asp	
276					281					286					291	
gcc	aat	tac	ttt	tta	cag	atg	atc	ggg	gct	cca	aag	gag	ctg	aaa	ttt	1029
Ala	Asn	Tyr	Phe	Leu	Gln	Met	Ile	Gly	Ala	Pro	Lys	Glu	Leu	Lys	Phe	

292	297	302	307	
ccc aac ttt aag gat	agg cac tct tcc gat	gaa aga acc aat gct	caa	1077
Pro Asn Phe Lys Asp	Arg His Ser Ser Asp	Glu Arg Thr Asn Ala	Gln	
308	313	318	323	
gtc gtg aga cag tat	tta aag gat ctg act	aga act gag aga	caa tta	1125
Val Val Arg Gln Tyr	Leu Lys Asp Leu Thr	Arg Thr Glu Arg	Gln Leu	
324	329	334	339	
atc tat gac ttt tat	tac ttg gac tat tta	atg ttt aat tat	aca act	1173
Ile Tyr Asp Phe Tyr	Tyr Leu Asp Tyr Leu	Met Phe Asn Tyr	Thr Thr	
340	345	350	355	
cca ttt ttg tag ttt	gcattcattt tctaaaaccc	tgtatatact	taatgatgat	1228
Pro Phe Leu *				
356				
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aaa				1291

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aacttgaaat ttcttgaaca cacagtttac ttgttcatat	ctttaactat gctgttctct 120
tttatctaca atgccatcta tctcttccac tgaaaacttc	catttattcc tcaaaatcct 180
gctcaggtgc tagcatatct gtgaagcgtt ctctgacctg	ttcctgaagt caaacattcc 240
ctcctcggta atatttccat acttttaaact tactattatt	gatggactcc aaaaaaatcc 300
tctttattgt tgtgtctagc cctatgatcc tgatttcaag	atcctgaaag acaagtttct 360
atccettaca aataccacag gacctggcac atagaagaca	catttattga ctcagtgttt 420
tcttcatggt tacattcttc aagtacacag ctgtctatgc	agtgaaaaat gtgctctaca 480
agtagaaaaa gaaatatgtg aagtgcacaa tagacaatcc	tcaattccca taatgcagat 540
gtgcatgagc aattattagc agttcaaagt tgtttcatta	cggtaagtac tattctaaca 600
aactaactgc cccaaccaat tttgtctagg aagcatatat	ggttttaaag tgttgattta 660

ccc gcc cca ctt gcc cct ctt gaa ccg gat tct ggt acc agc tct gct	2088
Pro Ala Pro Leu Ala Pro Leu Glu Pro Asp Ser Gly Thr Ser Ser Ala	
79 84 89 94	
gct gat ggt cct tgg aca cag aga ggg gag gag gag gca gag gcc	2136
Ala Asp Gly Pro Trp Thr Gln Arg Gly Glu Glu Glu Glu Ala Glu Ala	
95 100 105 110	
aga gcc aag ctg gcc cca ggg agg gag ccc cct agt ccc tgc cac tca	2184
Arg Ala Lys Leu Ala Pro Gly Arg Glu Pro Pro Ser Pro Cys His Ser	
111 116 121 126	
gag gac agc ctt ggg ctg ggg gca gca ccc ctt ggc agc gaa cca ccc	2232
Glu Asp Ser Leu Gly Leu Gly Ala Ala Pro Leu Gly Ser Glu Pro Pro	
127 132 137 142	
ctg agc cag ctg gtg tcc gac tca gac tca gag ctg gac agc aca gag	2280
Leu Ser Gln Leu Val Ser Asp Ser Asp Ser Glu Leu Asp Ser Thr Glu	
143 148 153 158	
cgg ctg gcc ctg gga agc aca gac acc ttg tcc aat ggg cag aaa gcg	2328
Arg Leu Ala Leu Gly Ser Thr Asp Thr Leu Ser Asn Gly Gln Lys Ala	
159 164 169 174	
gac ctg gag gct gcg cag cgc ctg gcc aag agg ctg tac cga cta gat	2376
Asp Leu Glu Ala Ala Gln Arg Leu Ala Lys Arg Leu Tyr Arg Leu Asp	
175 180 185 190	
ggc ttc agg aag gcc gat gtg gcc cgg cac ctg ggc aag aac aat gac	2424
Gly Phe Arg Lys Ala Asp Val Ala Arg His Leu Gly Lys Asn Asn Asp	
191 196 201 206	
ttc agc aaa ctg gtg gct ggg gag tac ctc aag ttc ttt gtc ttc acg	2472
Phe Ser Lys Leu Val Ala Gly Glu Tyr Leu Lys Phe Phe Val Phe Thr	
207 212 217 222	
ggc atg act ctg gac caa gct ctc agg gtg ttt ctg aag gag ctg gcc	2520
Gly Met Thr Leu Asp Gln Ala Leu Arg Val Phe Leu Lys Glu Leu Ala	
223 228 233 238	
tta atg ggt gag acc cag gaa cga gag cgc gtg ctg gcc cac ttc tcc	2568
Leu Met Gly Glu Thr Gln Glu Arg Glu Arg Val Leu Ala His Phe Ser	
239 244 249 254	
cag cga tac ttc cag tgc aat cct gaa gcc ctg tcc tca gag gac ggc	2616
Gln Arg Tyr Phe Gln Cys Asn Pro Glu Ala Leu Ser Ser Glu Asp Gly	
255 260 265 270	
gcc cac acg ctg acc tgt gcg ctc atg ctg ctc aac acg gat ctc cac	2664
Ala His Thr Leu Thr Cys Ala Leu Met Leu Leu Asn Thr Asp Leu His	
271 276 281 286	
ggc cat aac atc ggg aag cgc atg acc tgc ggg gag ttc atc ggg aac	2712
Gly His Asn Ile Gly Lys Arg Met Thr Cys Gly Asp Phe Ile Gly Asn	
287 292 297 302	

ctg gag ggc ctc aat gat ggc ggc gac ttc cct agg gag ctg ctc aag	2760
Leu Glu Gly Leu Asn Asp Gly Gly Asp Phe Pro Arg Glu Leu Leu Lys	
303 308 313 318	
gcc ttg tac agc tcc atc aag aat gag aag ctg cag tgg gcc ata gac	2808
Ala Leu Tyr Ser Ser Ile Lys Asn Glu Lys Leu Gln Trp Ala Ile Asp	
319 324 329 334	
gag gag gag ctg aga cgc tct ctg tct gag ttg gcc gac ccc aac ccc	2856
Glu Glu Glu Leu Arg Arg Ser Leu Ser Glu Leu Ala Asp Pro Asn Pro	
335 340 345 350	
aag gtc atc aag cgg atc agc ggg ggc agt ggc agt ggc tcc agc cct	2904
Lys Val Ile Lys Arg Ile Ser Gly Gly Ser Gly Ser Gly Ser Ser Pro	
351 356 361 366	
ttc ctg gac ctg act ccc gag cct ggg gct gcc gtc tac aag cac ggg	2952
Phe Leu Asp Leu Thr Pro Glu Pro Gly Ala Ala Val Tyr Lys His Gly	
367 372 377 382	
gcc ctg gtg cga aag gtg cac gca gac cct gac tgc agg aag aca cct	3000
Ala Leu Val Arg Lys Val His Ala Asp Pro Asp Cys Arg Lys Thr Pro	
383 388 393 398	
cgg ggc aag cgg ggc tgg aag agc ttc cac ggg atc ctc aag ggc atg	3048
Arg Gly Lys Arg Gly Trp Lys Ser Phe His Gly Ile Leu Lys Gly Met	
399 404 409 414	
atc ctc tac ctg cag aag gag gag tac aag cct ggg aag gcc ctt tca	3096
Ile Leu Tyr Leu Gln Lys Glu Glu Tyr Lys Pro Gly Lys Ala Leu Ser	
415 420 425 430	
gag acg gag ctc aag aat gcc atc agc atc cac cat gcc ctg gcc act	3144
Glu Thr Glu Leu Lys Asn Ala Ile Ser Ile His His Ala Leu Ala Thr	
431 436 441 446	
cgt gcc agt gac tac agc aag agg ccc cac gtc ttc tac ctg cgc aca	3192
Arg Ala Ser Asp Tyr Ser Lys Arg Pro His Val Phe Tyr Leu Arg Thr	
447 452 457 462	
gct gac tgg cgg gtc ttc ctc ttc cag gcc ccg agc ctg gag cag atg	3240
Ala Asp Trp Arg Val Phe Leu Phe Gln Ala Pro Ser Leu Glu Gln Met	
463 468 473 478	
cag tcc tgg atc act cgc atc aat gta gta gcc gct atg ttc tct gcg	3288
Gln Ser Trp Ile Thr Arg Ile Asn Val Val Ala Ala Met Phe Ser Ala	
479 484 489 494	
ccc ccc ttc cca gct gct gtt agc tcc caa aag aag ttc agc cgc cct	3336
Pro Pro Phe Pro Ala Ala Val Ser Ser Gln Lys Lys Phe Ser Arg Pro	
495 500 505 510	
ctc ctg ccc agc gct gcc acc cgc ctc tcc cag gag gag cag gtg cgg	3384
Leu Leu Pro Ser Ala Ala Thr Arg Leu Ser Gln Glu Glu Gln Val Arg	
511 516 521 526	
acc cac gag gcc aag ctg aag gcc atg gca agt gag ctg cgg gag cac	3432

Thr	His	Glu	Ala	Lys	Leu	Lys	Ala	Met	Ala	Ser	Glu	Leu	Arg	Glu	His	
527					532					537					542	
cgg	gcc	gcc	cag	ctg	ggc	aag	aag	ggc	cgg	ggc	aag	aag	gct	gaa	gag	3480
Arg	Ala	Ala	Gln	Leu	Gly	Lys	Lys	Gly	Arg	Gly	Lys	Lys	Ala	Glu	Glu	
543					548					553					558	
cag	cgg	cag	aag	gag	gcc	tac	ctg	gag	ttt	gag	aaa	tcc	cgc	tac	agc	3528
Gln	Arg	Gln	Lys	Glu	Ala	Tyr	Leu	Glu	Phe	Glu	Lys	Ser	Arg	Tyr	Ser	
559					564					569					574	
acc	tat	gca	gcg	ctg	ctt	cgg	gtc	aag	ctg	aag	gca	ggc	agt	gag	gag	3576
Thr	Tyr	Ala	Ala	Leu	Leu	Arg	Val	Lys	Leu	Lys	Ala	Gly	Ser	Glu	Glu	
575					580					585					590	
ctg	gat	gca	gtg	gag	gca	gca	ctg	gcc	cag	gcc	ggg	agc	aca	gag	gat	3624
Leu	Asp	Ala	Val	Glu	Ala	Ala	Leu	Ala	Gln	Ala	Gly	Ser	Thr	Glu	Asp	
591					596					601					606	
gga	ctc	cct	cct	tct	cac	tcc	agt	ccc	tcc	ctg	cag	ccc	aaa	ccc	tcc	3672
Gly	Leu	Pro	Pro	Ser	His	Ser	Ser	Pro	Ser	Leu	Gln	Pro	Lys	Pro	Ser	
607					612					617					622	
agc	cag	ccc	cgg	gct	cag	cgt	cac	agc	tca	gag	cct	cgg	cca	ggg	gca	3720
Ser	Gln	Pro	Arg	Ala	Gln	Arg	His	Ser	Ser	Glu	Pro	Arg	Pro	Gly	Ala	
623					628					633					638	
ggc	agt	ggg	cgg	cgg	aag	ccc	tga	gatgaggttt								3754
Gly	Ser	Gly	Arg	Arg	Lys	Pro	*									
639					644											

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gtcccggggc ccgggggtccc gtctggcggc ccgggattac cgtgacgtca cattgagcct	180
ctggccacct tggactggga cacctccgga gcctcacagc cccgcgccgc gccgcgcctc	240
acctcgccac cagcgcctt tgggaacccg catcttcttc cttcccctgc ccatccatgg	300
gcccttctgt cttccggacc ccacgggccg gaggggccc ttccggagcg cagggtcgg	360

cagccgggct gccctcggt ctgctccac tggggccaac caggcgaagg aaccggcgct	420
gggcatccgc agcgggtgtaa ggaactgaga cacctcactg ctggggggcgc ggaacagctg	480
ggctgagacg ggaactcgac aggggaagaga gagacggggc agggacagcc acc atg Met 1	536
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gcg tcg gca agt tcc agc acc aca tgc tgc gaa tct acc caa cgc tct Ala Ser Ala Ser Ser Ser Thr Thr Cys Cys Glu Ser Thr Gln Arg Ser 18 23 28 33	632
gtc tca gat gtg gca tca ggc tcc acc cca gcg ccc gct ctc tgc tgc Val Ser Asp Val Ala Ser Gly Ser Thr Pro Ala Pro Ala Leu Cys Cys 34 39 44 49	680
gca ccc tac gat agt cga ctg ctg ggc agt gcg cga ccg gag ctg ggc Ala Pro Tyr Asp Ser Arg Leu Leu Gly Ser Ala Arg Pro Glu Leu Gly 50 55 60 65	728
gcc gcc ttg ggc atc tat gga gca ccc tat gcg gcc gct gca gct gcc Ala Ala Leu Gly Ile Tyr Gly Ala Pro Tyr Ala Ala Ala Ala Ala Ala 66 71 76 81	776
cag agc tac cct ggc tac ctg ccc tat agc cca gag ccc ccc tca ctg Gln Ser Tyr Pro Gly Tyr Leu Pro Tyr Ser Pro Glu Pro Pro Ser Leu 82 87 92 97	824
tat ggg gca ctg aat cca cag tat gaa ttt aag gag gct gca ggg agt Tyr Gly Ala Leu Asn Pro Gln Tyr Glu Phe Lys Glu Ala Ala Gly Ser 98 103 108 113	872
ttt aca tcc agc ctg gca caa cca gga gcc tat tat ccc tat gag cgg Phe Thr Ser Ser Leu Ala Gln Pro Gly Ala Tyr Tyr Pro Tyr Glu Arg 114 119 124 129	920
act ctg ggg cag tac caa tat gaa cgg tat ggc gca gtg gaa ttg agt Thr Leu Gly Gln Tyr Gln Tyr Glu Arg Tyr Gly Ala Val Glu Leu Ser 130 135 140 145	968
ggc gcc ggt cgc cga aag aac gcg acc cgg gag acc acc agt aca ctc Gly Ala Gly Arg Arg Lys Asn Ala Thr Arg Glu Thr Thr Ser Thr Leu 146 151 156 161	1016
aag gcc tgg ctc aac gag cac cgc aaa aac ccc tac ccc act aag ggt Lys Ala Trp Leu Asn Glu His Arg Lys Asn Pro Tyr Pro Thr Lys Gly 162 167 172 177	1064
gag aag atc atg ctg gcc atc atc acc aag atg acc ctc acc cag gtg Glu Lys Ile Met Leu Ala Ile Ile Thr Lys Met Thr Leu Thr Gln Val 178 183 188 193	1112
tcc acc tgg ttc gcc aac gca cgc cgg cgc ctc aag aaa gag aac aaa	1160

Ser	Thr	Trp	Phe	Ala	Asn	Ala	Arg	Arg	Arg	Leu	Lys	Lys	Glu	Asn	Lys		
194					199					204					209		
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Met	Thr	Trp	Ala	Pro	Lys	Asn	Lys	Gly	Gly	Glu	Glu	Arg	Lys	Ala	Glu		
210					215					220					225		
gga	gga	gag	gag	gac	tca	cta	ggc	tgc	cta	act	gct	gac	acc	aaa	gaa		1256
Gly	Gly	Glu	Glu	Asp	Ser	Leu	Gly	Cys	Leu	Thr	Ala	Asp	Thr	Lys	Glu		
226					231					236					241		
gtt	act	gct	agc	cag	gag	gcc	cgg	ggg	ctc	cgg	ctg	agt	gac	ctg	gaa		1304
Val	Thr	Ala	Ser	Gln	Glu	Ala	Arg	Gly	Leu	Arg	Leu	Ser	Asp	Leu	Glu		
242					247					252					257		
gac	ctg	gag	gaa	gag	gag	gag	gag	gag	gag	gaa	gct	gaa	gac	gag	gag		1352
Asp	Leu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Ala	Glu	Asp	Glu	Glu		
258					263					268					273		
gta	gtg	gcc	aca	gct	ggg	gac	agg	ctg	acg	gag	ttc	cga	aag	ggc	gcg		1400
Val	Val	Ala	Thr	Ala	Gly	Asp	Arg	Leu	Thr	Glu	Phe	Arg	Lys	Gly	Ala		
274					279					284					289		
cag	tca	ctg	cct	ggg	ccg	tgc	gct	gca	gct	cga	gag	ggc	cga	ttg	gag		1448
Gln	Ser	Leu	Pro	Gly	Pro	Cys	Ala	Ala	Ala	Arg	Glu	Gly	Arg	Leu	Glu		
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Arg	Arg	Glu	Cys	Gly	Leu	Ala	Ala	Pro	Arg	Phe	Ser	Phe	Asn	Asp	Pro		
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Ser	Gly	Ser	Glu	Glu	Ala	Asp	Phe	Leu	Ser	Ala	Glu	Thr	Gly	Ser	Pro		
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Arg	Leu	Thr	Met	His	Tyr	Pro	Cys	Leu	Glu	Lys	Pro	Arg	Ile	Trp	Ser		
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Leu	Ala	His	Thr	Ala	Thr	Ala	Ser	Ala	Val	Glu	Gly	Ala	Pro	Pro	Ala		
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Arg	Pro	Arg	Pro	Arg	Ser	Pro	Glu	Cys	Arg	Met	Ile	Pro	Gly	Gln	Pro		
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Pro	Ala	Ser	Ala	Arg	Arg	Leu	Ser	Val	Pro	Arg	Asp	Ser	Ala	Cys	Asp		
386					391					396					401		
gag	tct	tcc	tgc	ata	ccc	aaa	gcc	ttt	gga	aac	ccc	aag	ttt	gcc	ctg		1784
Glu	Ser	Ser	Cys	Ile	Pro	Lys	Ala	Phe	Gly	Asn	Pro	Lys	Phe	Ala	Leu		
402					407					412					417		
cag	gga	cta	ccg	ctg	aac	tgt	gcg	ccg	tgc	ccg	cgg	agg	agc	gag	cct		1832
Gln	Gly	Leu	Pro	Leu	Asn	Cys	Ala	Pro	Cys	Pro	Arg	Arg	Ser	Glu	Pro		

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gta gtg cag tgc cag tac ccg tct gga gca gaa ggt agt ggg ccc cca				1880
Val Val Gln Cys Gln Tyr Pro Ser Gly Ala Glu Gly Ser Gly Pro Pro				
434	439	444	449	
gcg gcg ctg gga gta tct atg caa aag aca ccc acc tac cgc ccc gcc				1928
Ala Ala Leu Gly Val Ser Met Gln Lys Thr Pro Thr Tyr Arg Pro Ala				
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cgg caa ttg cac acc ctc tgc cat tcc agt ctg ccc aga gga gac tcg				1976
Arg Gln Leu His Thr Leu Cys His Ser Ser Leu Pro Arg Gly Asp Ser				
466	471	476	481	
ctg gtc cct gct gtg ctg ctc aga gag ttt act agg gtt ggg cag gca				2024
Leu Val Pro Ala Val Leu Leu Arg Glu Phe Thr Arg Val Gly Gln Ala				
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cca ggg ctt tta gag aag tct aag act gtg ggc cag acg cac acc aca				2072
Pro Gly Leu Leu Glu Lys Ser Lys Thr Val Gly Gln Thr His Thr Thr				
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gagacgtggt gggcggtcct tcctgtgaca cgacccttga gtgacagttc tatttgattg	420
cctccggtac tgtgaggaaa ggacacgact ct atg gtg agg act gat gga cat	473
Met Val Arg Thr Asp Gly His	

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Thr Leu Ser Glu Lys Arg Asn Tyr Gln Val	Thr Asn Ser Met Phe Gly	
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Ala Ser Arg Lys Lys Phe Val Glu Gly Val	Asp Ser Asp Tyr His Asp	
24 29 34 39		
gaa aac atg tac tac agc cag tct tct atg	ttt cca cat cgg tca gaa	617
Glu Asn Met Tyr Tyr Ser Gln Ser Ser Met	Phe Pro His Arg Ser Glu	
40 45 50 55		
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Lys Asp Met Leu Ala Ser Pro Ser Thr Ser	Gly Gln Leu Ser Gln Phe	
56 61 66 71		
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Gly Ala Ser Leu Tyr Gly Gln Gln Ser Ala	Leu Gly Leu Pro Met Arg	
72 77 82 87		
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Gly Met Ser Asn Asn Thr Pro Gln Leu Asn	Arg Ser Leu Ser Gln Gly	
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Thr Gln Leu Pro Ser His Val Thr Pro Thr	Thr Gly Val Pro Thr Met	
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Ser Leu His Thr Pro Pro Ser Pro Ser Arg	Gly Ile Leu Pro Met Asn	
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Pro Arg Asn Met Met Asn His Ser Gln Val	Gly Gln Gly Ile Gly Ile	
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Pro Ser Arg Thr Asn Ser Met Ser Ser Ser	Gly Leu Gly Ser Pro Asn	
152 157 162 167		
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Arg Ser Ser Pro Ser Ile Ile Cys Met Pro	Lys Gln Gln Pro Ser Arg	
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Gln Pro Phe Thr Val Asn Ser Met Ser Gly	Phe Gly Met Asn Arg Asn	
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Thr Asp Gly Ser Glu Asn Val Thr Gly Leu	Asp Leu Ser Asp Phe Pro	
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Ala Leu Ala Asp Arg Asn Arg Arg Glu Gly Ser Gly Asn Pro Thr Pro	
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Leu Ile Asn Pro Leu Ala Gly Arg Ala Pro Tyr Val Gly Met Val Thr	
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Phe Pro Ala Leu Pro Gly Ser Ser Tyr Lys Asp Pro Thr Ser Ser Asn	
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Asp Asp Ser Lys Ser Asn Leu Asn Thr Ser Gly Lys Thr Thr Ser Ser	
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Thr Asp Gly Pro Lys Phe Pro Gly Asp Lys Ser Ser Thr Thr Gln Asn	
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Asn Asn Gln Gln Lys Lys Gly Ile Gln Val Leu Pro Asp Gly Arg Val	
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Pro Glu Asn Leu Tyr Pro Lys Phe Ala Ser Pro Trp Ala Ser Ser Pro	
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Cys Arg Pro Gln Asp Ile Asp Phe His Val Pro Ser Glu Tyr Leu Thr	
408 413 418 423	
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Asn Ile His Ile Arg Asp Lys Leu Phe Phe Phe Phe Ser Trp Leu Gln	
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440	

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Met Ala Thr Ser Gln Tyr Phe Asp Phe Ala Gln Gly Gly Gly Pro
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Gln Tyr Ser Thr Gln Ala Pro Thr Leu Pro Leu Pro Thr Val Gly Ala
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Ser Tyr Thr Gly Gln Pro Thr Pro Gly Met Asp Pro Ala Val Asn Pro
32 37 42 47
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Ala Phe Pro Pro Ala Ala Pro Ala Gly Tyr Gly Gly Tyr Gln Pro His
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Ser Gly Gln Asp Phe Ala Tyr Gly Ser Arg Pro Gln Glu Pro Val Pro
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acg gcc acc acc atg gct acc tac cag gac agt tac agc tac gga cag 349
Thr Ala Thr Thr Met Ala Thr Tyr Gln Asp Ser Tyr Ser Tyr Gly Gln
80 85 90 95
tca gca gct gcc agg agc tat gag gac agg ccg tac ttc cag tct gct 397
Ser Ala Ala Ala Arg Ser Tyr Glu Asp Arg Pro Tyr Phe Gln Ser Ala
96 101 106 111
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Ala Leu Gln Ser Gly Arg Met Thr Ala Ala Asp Ser Gly Gln Pro Gly
112 117 122 127

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Thr Gln Glu Ala Cys Gly Gln Pro Ser Pro His Gly Ser His Ser His	
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Pro Glu Ser Ser Ala Ser Ile Val Thr Ser Tyr Pro Pro Pro Ser Tyr	
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Asn Pro Thr Cys Thr Ala Tyr Thr Ala Pro Ser Tyr Pro Asn Tyr Asp	
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Ala Ser Val Tyr Ser Ala Ala Ser Pro Phe Tyr Pro Pro Ala Gln Pro	
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Ser Lys Leu Pro Arg Pro Lys Ala Gly Pro Arg Gln Leu Gln Leu His	
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Glu His Leu Gly Gly Gln Lys His Arg Lys Lys Glu Ala Ala Gln Lys	
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Thr Gly Val Gln Pro Asn Gly Ser Pro Arg Gly Val Gln Ala Gln Leu	
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His Cys Asp Leu Cys Ala Val Ser Cys Thr Gly Ala Asp Ala Tyr Ala	
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Pro	Asp	Trp	Ala	Gln	Pro	Leu	Leu	Met	Gly	Arg	Pro	Glu	Ser	Pro	Ala	
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agc	gcc	cca	ctc	cag	ccc	ggg	cgg	cgg	ccg	gcg	tcc	agc	gac	gac	cgg	1837
Ser	Ala	Pro	Leu	Gln	Pro	Gly	Arg	Arg	Pro	Ala	Ser	Ser	Asp	Asp	Arg	

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Val Ser Asp Thr Leu	Ala Glu Glu Asp Arg	Gly Arg Arg Glu Glu	Glu	
624	629	634	639	
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Arg Asn Val Arg Leu	Ala Leu Leu Cys Ser	Glu Lys Pro Thr His	Ser	
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atc tcc tcc tgt gag	gag gcc agg atg cag	gtc acc ata tct gtc	acc	2269
Ile Ser Ser Cys Glu	Glu Pro Arg Met Gln	Val Thr Ile Ser Val	Thr	
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Pro Gln Ala Asp Ala	Gly Asp Val Leu Ser	Pro Lys Lys Cys Leu	Glu	
752	757	762	767	
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cgg cgt gtg ccc acc	tgg ggg gcc ctg cca	gcc tgg gcc atg gag	ctg	2509
Arg Arg Val Pro Thr	Trp Gly Ala Leu Pro	Ala Trp Ala Met Glu	Leu	
800	805	810	815	

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Asp Ala Val Arg Arg Val Leu Glu Cys Val Ala Thr Gly Thr Leu Leu	
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Pro Glu Phe Ala Asn Pro Asp Phe Met Glu Ser Ile Ser Asp Val Val	
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Val Gln Val Val Thr His His Met Gln Arg Tyr Ala Val Trp Phe Gly	
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Gly Ser Met Leu Ala Ser Thr Pro Glu Phe Phe Gln Val Cys His Thr	
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 Glu Glu Ser Pro Ala Pro Ser Arg Ala Pro Ala Ser Ala Ser Leu Trp
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 Ala Ala Gln Ala Ala Ala Ala Gln Ala Ala Gln Ala Glu Ala Ala Asp
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 Ser Trp Tyr Leu Ala Leu Leu Gly Phe Ala Glu His Phe Arg Thr Ser
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 Ser Pro Pro Lys Ile Arg Leu Cys Val His Cys Leu Gln Ala Val Phe
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Pro Phe Lys Pro Pro Gln Arg Ile Glu Ala Arg Thr His Leu Gln Leu	
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His Leu Glu Lys Ala Trp Leu Ile Ser Gln Gln Ile Pro Gln Phe Glu	
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Leu Gly Val Gly Ala Glu Tyr Ala Arg Val Val Gly Ser Glu Tyr Thr	
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Leu	Leu	Glu	Arg	Ile	Asn	Pro	Asp	His	Ser	Phe	Pro	Val	Ser	Ser	His		
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Cys	Leu	Arg	Ala	Ala	Ala	Phe	Tyr	Val	Arg	Gly	Leu	Phe	Ser	Phe	Phe		
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Ser Val Gln Leu Trp Ser Ser Ala Leu Leu Arg Asp Leu Asn Lys Ala				
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Cys Gly Asn Ala Met Asp Ala His Glu Ala Ala Gln Met His Gln Asn				
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Ala Glu Glu Val Arg Tyr Phe Leu Lys Asn Lys Val Ser Pro Asp Leu	
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Cys Asn Glu Asp Gly Leu Thr Ala Leu His Gln Cys Cys Ile Asp Asn	
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ccc	ctc	ctg	cgc	aca	ggc	cgg	ctg	gat	cct	gca	ggc	agc	tgt	agc	cgt	3736	
Pro	Leu	Leu	Arg	Thr	Gly	Arg	Leu	Asp	Pro	Ala	Gly	Ser	Cys	Ser	Arg		
681					686					691					696		
tcc	ctg	gcc	agc	cgg	gca	gtg	cag	cgc	agc	ctg	gcc	atc	atc	cgg	cag	3784	
Ser	Leu	Ala	Ser	Arg	Ala	Val	Gln	Arg	Ser	Leu	Ala	Ile	Ile	Arg	Gln		
697					702					707					712		
gcg	cgg	cag	cgc	agg	gag	aag	agg	aag	gag	tac	tgc	atg	tac	tac	aac	3832	
Ala	Arg	Gln	Arg	Arg	Glu	Lys	Arg	Lys	Glu	Tyr	Cys	Met	Tyr	Tyr	Asn		
713					718					723					728		
cgc	ttc	ggc	agg	tgc	aac	cgt	ggc	gag	cgc	tgc	ccc	tac	atc	cac	gat	3880	
Arg	Phe	Gly	Arg	Cys	Asn	Arg	Gly	Glu	Arg	Cys	Pro	Tyr	Ile	His	Asp		
729					734					739					744		
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Pro	Glu	Lys	Val	Ala	Val	Cys	Thr	Arg	Phe	Val	Arg	Gly	Thr	Cys	Lys		
745					750					755					760		
aaa	acg	gat	ggg	acc	tgc	ccc	ttc	tcc	cac	cat	gtg	tcc	aag	gag	aag	3976	
Lys	Thr	Asp	Gly	Thr	Cys	Pro	Phe	Ser	His	His	Val	Ser	Lys	Glu	Lys		
761					766					771					776		
atg	ccg	gtg	tgc	tcc	tac	ttc	ctg	aag	ggc	atc	tgc	agc	aac	agc	aac	4024	
Met	Pro	Val	Cys	Ser	Tyr	Phe	Leu	Lys	Gly	Ile	Cys	Ser	Asn	Ser	Asn		
777					782					787					792		
tgt	ccc	tat	agc	cac	gtg	tac	gtg	tcc	cgc	aag	gcc	gag	gtc	tgc	agc	4072	
Cys	Pro	Tyr	Ser	His	Val	Tyr	Val	Ser	Arg	Lys	Ala	Glu	Val	Cys	Ser		

4120 4168 4216 4264 4312 4360 4408 4456 4504 4552 4600 4648 4708 4768 4828 4888

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Asp Phe Leu Lys Gly Tyr Cys Pro Leu Gly Ala Lys Cys Lys Lys Lys				
809	814	819	824	
cac acg ctg ctg tgc ccc gac ttt gcc cgc agg ggg gcg tgt ccc cgc				4168
His Thr Leu Leu Cys Pro Asp Phe Ala Arg Arg Gly Ala Cys Pro Arg				
825	830	835	840	
ggc gcc cag tgc cag ctg ctc cac cgt acc cag aaa cgc cac agt cgg				4216
Gly Ala Gln Cys Gln Leu Leu His Arg Thr Gln Lys Arg His Ser Arg				
841	846	851	856	
cgg gca gcc acg tcc ccc gcc cca ggg ccc agc gac gca acc gcc agg				4264
Arg Ala Ala Thr Ser Pro Ala Pro Gly Pro Ser Asp Ala Thr Ala Arg				
857	862	867	872	
agc agg gtc tcg gcc agc cac ggg ccc agg aag cct tca gca tcc cag				4312
Ser Arg Val Ser Ala Ser His Gly Pro Arg Lys Pro Ser Ala Ser Gln				
873	878	883	888	
cgc ccc acc agg cag acg ccc agc tcg gct gcc ctc act gcg gct gcc				4360
Arg Pro Thr Arg Gln Thr Pro Ser Ser Ala Ala Leu Thr Ala Ala Ala				
889	894	899	904	
gtg gct gca cct ccc cac tgc cca ggg ggg tca gcc tct ccc tca tcc				4408
Val Ala Ala Pro Pro His Cys Pro Gly Gly Ser Ala Ser Pro Ser Ser				
905	910	915	920	
tcg aag gct tcc tcc tcc tcc tcc tcc tcc tca tcc cct ccc gct tcc				4456
Ser Lys Ala Ser Ser Ser Ser Ser Ser Ser Ser Ser Pro Pro Ala Ser				
921	926	931	936	
ttg gac cac gag gca cca tct ctc cag gag gct gcc tta gca gca gcg				4504
Leu Asp His Glu Ala Pro Ser Leu Gln Glu Ala Ala Leu Ala Ala Ala				
937	942	947	952	
tgc tcc aac agg ctc tgc aag ctg cct tcc ttc atc tcc ctg cag tcc				4552
Cys Ser Asn Arg Leu Cys Lys Leu Pro Ser Phe Ile Ser Leu Gln Ser				
953	958	963	968	
tcg ccg agc cca gga gcc cag ccc agg gtc cgg gcc cct agg gcc ccc				4600
Ser Pro Ser Pro Gly Ala Gln Pro Arg Val Arg Ala Pro Arg Ala Pro				
969	974	979	984	
ctc acc aag gac tca ggg aag cct ctg cac atc aaa cca cgt ctg tga				4648
Leu Thr Lys Asp Ser Gly Lys Pro Leu His Ile Lys Pro Arg Leu *				
985	990	995	1000	
ggaccccagg gaccggcctg cacctacctc agaccctcat ccttgagag gaaagaggct				4708
ctgtccacca ctctaccca caggagggcc gcccgccacc aagcctcacc tgggggccac				4768
agggacactg ctctgcctgc ctggccctca accttccatg accagcgtgt gcgcagggcc				4828
tggtcttcct cccccaagcc agggccctgt cccaccccca ccaccttcca gggtgccagg				4888

Gly	Leu	Ile	Leu	Asn	Pro	Ile	Phe	Arg	Gln	Asn	Leu	Arg	Ile	Ala	Leu		
107					112					117					122		
ctg	ggt	ggg	ggg	aag	gcc	tgg	tct	gat	gac	aca	agt	cag	ctg	gga	cca	676	
Leu	Gly	Gly	Gly	Lys	Ala	Trp	Ser	Asp	Asp	Thr	Ser	Gln	Leu	Gly	Pro		
123					128					133					138		
gac	aag	cat	gcc	cgg	gac	gtt	ccc	tcc	ctt	gac	aag	tac	gcc	gag	gag	724	
Asp	Lys	His	Ala	Arg	Asp	Val	Pro	Ser	Leu	Asp	Lys	Tyr	Ala	Glu	Glu		
139					144					149					154		
cga	tgg	gag	gtg	gtc	ttg	cac	ttc	atg	gtg	ggc	tcc	ccc	agt	gca	gct	772	
Arg	Trp	Glu	Val	Val	Leu	His	Phe	Met	Val	Gly	Ser	Pro	Ser	Ala	Ala		
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Val	Ser	Gln	Asp	Leu	Ala	Gln	Leu	Leu	Ser	Gln	Ala	Gly	Leu	Met	Lys		
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Ser	Thr	Glu	Pro	Gly	Glu	Pro	Pro	Cys	Ile	Thr	Ser	Ala	Gly	Phe	Gln		
187					192					197					202		
ttc	ctg	ttg	ctg	gac	acc	ccg	gct	cag	ctc	tgg	tac	ttt	atg	ttg	cag	916	
Phe	Leu	Leu	Leu	Asp	Thr	Pro	Ala	Gln	Leu	Trp	Tyr	Phe	Met	Leu	Gln		
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Tyr	Leu	Gln	Thr	Ala	Gln	Ser	Arg	Gly	Met	Asp	Leu	Val	Glu	Ile	Leu		
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Ser	Phe	Leu	Phe	Gln	Leu	Ser	Phe	Ser	Thr	Leu	Gly	Lys	Asp	Tyr	Ser		
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Val	Glu	Gly	Met	Ser	Asp	Ser	Leu	Leu	Asn	Phe	Leu	Gln	His	Leu	Arg		
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gag	ttt	ggg	ctt	gtt	ttc	cag	agg	aag	agg	aaa	tct	cgg	cgt	tac	tac	1108	
Glu	Phe	Gly	Leu	Val	Phe	Gln	Arg	Lys	Arg	Lys	Ser	Arg	Arg	Tyr	Tyr		
267					272					277					282		
ccc	aca	cgc	ctg	gcc	atc	aat	ctc	tca	tca	ggt	gtc	tct	gga	gct	ggg	1156	
Pro	Thr	Arg	Leu	Ala	Ile	Asn	Leu	Ser	Ser	Gly	Val	Ser	Gly	Ala	Gly		
283					288					293					298		
ggc	act	gtg	cat	cag	cca	ggt	ttc	att	gtc	gtg	gaa	acc	aat	tac	cga	1204	
Gly	Thr	Val	His	Gln	Pro	Gly	Phe	Ile	Val	Val	Glu	Thr	Asn	Tyr	Arg		
299					304					309					314		
ctg	tat	gcc	tac	acg	gag	tcg	gag	ctg	cag	att	gcc	ctc	att	gcc	ctc	1252	
Leu	Tyr	Ala	Tyr	Thr	Glu	Ser	Glu	Leu	Gln	Ile	Ala	Leu	Ile	Ala	Leu		
315					320					325					330		
ttc	tct	gag	atg	ctc	tat	cgg	ttc	ccc	aac	atg	gtg	gtg	gcg	cag	gtg	1300	
Phe	Ser	Glu	Met	Leu	Tyr	Arg	Phe	Pro	Asn	Met	Val	Val	Ala	Gln	Val		

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acc cgg gag agt gtg cag cag gca atc gcc agt ggc atc aca gcc cag				1348
Thr Arg Glu Ser Val Gln Gln Ala Ile Ala Ser Gly Ile Thr Ala Gln				
347	352	357	362	
cag ata atc cat ttc cta agg aca aga gcc cac cca gtg atg ctc aaa				1396
Gln Ile Ile His Phe Leu Arg Thr Arg Ala His Pro Val Met Leu Lys				
363	368	373	378	
cag aca cct gtg ctg ccc ccc acc atc acc gac cag atc cgg ctc tgg				1444
Gln Thr Pro Val Leu Pro Pro Thr Ile Thr Asp Gln Ile Arg Leu Trp				
379	384	389	394	
gag ctg gaa agg gac aga ctc cgg ttc act gag ggt gtc ctg tat aac				1492
Glu Leu Glu Arg Asp Arg Leu Arg Phe Thr Glu Gly Val Leu Tyr Asn				
395	400	405	410	
cag ttc ctg tcg caa gtg gac ttt gag ctg ctg ctg gcc cac gcg cgg				1540
Gln Phe Leu Ser Gln Val Asp Phe Glu Leu Leu Leu Ala His Ala Arg				
411	416	421	426	
gag ctg ggc gtg ctc gtg ttc gag aac tcg gcc aag cgg ctc atg gtg				1588
Glu Leu Gly Val Leu Val Phe Glu Asn Ser Ala Lys Arg Leu Met Val				
427	432	437	442	
gtg acc ccg gcc ggg cac agc gac gtc aag cgc ttt tgg aag cgg cag				1636
Val Thr Pro Ala Gly His Ser Asp Val Lys Arg Phe Trp Lys Arg Gln				
443	448	453	458	
aaa cat agc tcc tga gagcgcggga cttggacacg gacctcggcg ggcgggactg				1691
Lys His Ser Ser *				
459				
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ggcggcgcgg ctgctatcct gaactagctt ggtaagtgtt gtgtcccgaa ccagcgtaga	180

gagacctcgg accagccgcc ttg	atg aca gca tcc gcg tcc tcc ttt tca	230
	Met Thr Ala Ser Ala Ser Ser Phe Ser	
	1 5	
tca tct cag ggt gtc cag cag ccc tcc atc tac agc ttc tcc caa ata	278	
Ser Ser Gln Gly Val Gln Gln Pro Ser Ile Tyr Ser Phe Ser Gln Ile		
10 15 20 25		
acc aga agc ttg ttt ctc agc aat ggt gtg gcc gcc aac gac aaa ctc	326	
Thr Arg Ser Leu Phe Leu Ser Asn Gly Val Ala Ala Asn Asp Lys Leu		
26 31 36 41		
ctt ctg tcc agc aat cgc atc acc gcc att gtc aat gcc tcg gtg gaa	374	
Leu Leu Ser Ser Asn Arg Ile Thr Ala Ile Val Asn Ala Ser Val Glu		
42 47 52 57		
gtg gtc aac gta ttc ttc gag ggc att cag tac ata aag gtg cct gtt	422	
Val Val Asn Val Phe Phe Glu Gly Ile Gln Tyr Ile Lys Val Pro Val		
58 63 68 73		
acc gat gct cgt gac tcg cgt ctc tac gac ttt ttt gac ccc att gct	470	
Thr Asp Ala Arg Asp Ser Arg Leu Tyr Asp Phe Phe Asp Pro Ile Ala		
74 79 84 89		
gat ctt atc cac acc atc gat atg agg cag ggc cgt acg ctg ctg cac	518	
Asp Leu Ile His Thr Ile Asp Met Arg Gln Gly Arg Thr Leu Leu His		
90 95 100 105		
tgc atg gct gga gtg agc cgt tcc gcc tca ctg tgc ctt gcg tac ctc	566	
Cys Met Ala Gly Val Ser Arg Ser Ala Ser Leu Cys Leu Ala Tyr Leu		
106 111 116 121		
atg aaa tac cac tcc atg tcg ctg ctg gac gcc cat aca tgg acc aag	614	
Met Lys Tyr His Ser Met Ser Leu Leu Asp Ala His Thr Trp Thr Lys		
122 127 132 137		
tcg cgc cgc ccc atc atc cgg ccc aac aac ggc ttt tgg gaa cag ctc	662	
Ser Arg Arg Pro Ile Ile Arg Pro Asn Asn Gly Phe Trp Glu Gln Leu		
138 143 148 153		
atc aat tac gaa ttc aag ctg ttt aat aac aac acc gtg cgc atg atc	710	
Ile Asn Tyr Glu Phe Lys Leu Phe Asn Asn Asn Thr Val Arg Met Ile		
154 159 164 169		
aac tcg ccg gta ggt aac atc cct gac atc tat gag aag gac cta cgt	758	
Asn Ser Pro Val Gly Asn Ile Pro Asp Ile Tyr Glu Lys Asp Leu Arg		
170 175 180 185		
acg atg ata tca atg taa gccatc ccggccagcc cctgacatct gccatcgatc	812	
Thr Met Ile Ser Met *		
186 191		
ttgcaccaag actgaacttg aacactgaca ttttgtagt aaagaaaacc ggatgggtgcc	872	
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                                Met Gln Arg Leu Leu Thr Pro Val Lys
                                1                      5

cgc att ctg caa ctg aca aga gcg gtg cag gaa acc tcc ctc aca cct      159
Arg Ile Leu Gln Leu Thr Arg Ala Val Gln Glu Thr Ser Leu Thr Pro
10                      15                      20                      25

gct cgc ctg ctc cca gta gcc cac caa agg ttt tct aca gcc tct gct      207
Ala Arg Leu Leu Pro Val Ala His Gln Arg Phe Ser Thr Ala Ser Ala
26                      31                      36                      41

gtc ccc ctg gcc aaa aca gat act tgg cca aag gac gtg ggc atc ctg      255
Val Pro Leu Ala Lys Thr Asp Thr Trp Pro Lys Asp Val Gly Ile Leu
42                      47                      52                      57

gcc ctg gag gtc tac ttc cca gcc caa tat gtg gac caa act gac ctg      303
Ala Leu Glu Val Tyr Phe Pro Ala Gln Tyr Val Asp Gln Thr Asp Leu
58                      63                      68                      73

gag aag tat aac aat gtg gaa gca gga aag tat aca gtg ggc ttg ggc      351
Glu Lys Tyr Asn Asn Val Glu Ala Gly Lys Tyr Thr Val Gly Leu Gly
74                      79                      84                      89

cag acc cgt atg ggc ttc tgc tca gtc caa gag gac atc aac tcc ctg      399
Gln Thr Arg Met Gly Phe Cys Ser Val Gln Glu Asp Ile Asn Ser Leu
90                      95                      100                      105

tgc ctg acg gtg gtg caa cgg ctg atg gag cgc ata cag ctc cca tgg      447
Cys Leu Thr Val Val Gln Arg Leu Met Glu Arg Ile Gln Leu Pro Trp
106                      111                      116                      121

gac tct gtg ggc agg ctg gaa gta ggc act gag acc atc att gac aag      495
Asp Ser Val Gly Arg Leu Glu Val Gly Thr Glu Thr Ile Ile Asp Lys
122                      127                      132                      137

tcc aaa gct gtc aaa aca gtg ctc atg gaa ctc ttc cag gat tca ggc      543
Ser Lys Ala Val Lys Thr Val Leu Met Glu Leu Phe Gln Asp Ser Gly
138                      143                      148                      153

aat act gat att gag ggc ata gat acc acc aat gcc tgc tac ggt ggt      591

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Asn Thr Asp Ile Glu Gly Ile Asp Thr Thr Asn Ala Cys Tyr Gly Gly	
154 159 164 169	
act gcc tcc ctc ttc aat gct gcc aac tgg atg gag tcc agt tcc tgg	639
Thr Ala Ser Leu Phe Asn Ala Ala Asn Trp Met Glu Ser Ser Ser Trp	
170 175 180 185	
gat ggt cgt tat gcc atg gtg gtc tgt gga gac att gcc gtc tat ccc	687
Asp Gly Arg Tyr Ala Met Val Val Cys Gly Asp Ile Ala Val Tyr Pro	
186 191 196 201	
agt ggt aat gct cgt ccc aca ggt ggg gcc gga gct gtg gct atg ctg	735
Ser Gly Asn Ala Arg Pro Thr Gly Gly Ala Gly Ala Val Ala Met Leu	
202 207 212 217	
att ggg ccc aag gcc cct ctg gcc ctg gag cga ggg ctg agg gga acc	783
Ile Gly Pro Lys Ala Pro Leu Ala Leu Glu Arg Gly Leu Arg Gly Thr	
218 223 228 233	
cat atg gag aat gtg tat gac ttc tac aaa cca aat ttg gcc tcg gag	831
His Met Glu Asn Val Tyr Asp Phe Tyr Lys Pro Asn Leu Ala Ser Glu	
234 239 244 249	
tac cca ata gtg gat ggg aag ctt tcc atc cag tgc tac ttg cgg gcc	879
Tyr Pro Ile Val Asp Gly Lys Leu Ser Ile Gln Cys Tyr Leu Arg Ala	
250 255 260 265	
ttg gat cga tgt tac aca tca tac cgt aaa aaa atc cag aat cag tgg	927
Leu Asp Arg Cys Tyr Thr Ser Tyr Arg Lys Lys Ile Gln Asn Gln Trp	
266 271 276 281	
aag caa gct ggc agc gat cga ccc ttc acc ctt gac gat tta cag tac	975
Lys Gln Ala Gly Ser Asp Arg Pro Phe Thr Leu Asp Asp Leu Gln Tyr	
282 287 292 297	
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Met Ile Phe His Thr Pro Phe Cys Lys Met Val Gln Lys Ser Leu Ala	
298 303 308 313	
cgc ctg atg ttc aat gac ttc ctg tca gcc agc agt gac aca caa acc	1071
Arg Leu Met Phe Asn Asp Phe Leu Ser Ala Ser Ser Asp Thr Gln Thr	
314 319 324 329	
agc tta tat aag ggg ctg gag gct ttc ggg ggg cta aag ctg gaa gac	1119
Ser Leu Tyr Lys Gly Leu Glu Ala Phe Gly Gly Leu Lys Leu Glu Asp	
330 335 340 345	
acc tac acc aac aag gac ctg gat aaa gca ctt cta aag gcc tct cag	1167
Thr Tyr Thr Asn Lys Asp Leu Asp Lys Ala Leu Leu Lys Ala Ser Gln	
346 351 356 361	
gac atg ttc gac aag aaa acc aag gct tcc ctt tac ctc tcc act cac	1215
Asp Met Phe Asp Lys Lys Thr Lys Ala Ser Leu Tyr Leu Ser Thr His	
362 367 372 377	
aat ggg aac atg tac acc tca tcc ctg tac ggg tgc ctg gcc tcg ctt	1263
Asn Gly Asn Met Tyr Thr Ser Ser Leu Tyr Gly Cys Leu Ala Ser Leu	

378	383	388	393	
ctg tcc cac cac tct gcc caa gaa ctg gct ggc tcc agg att ggt gcc				1311
Leu Ser His His Ser Ala Gln Glu Leu Ala Gly Ser Arg Ile Gly Ala				
394	399	404	409	
ttc tct tat ggc tct ggt tta gca gca agt ttt ttt tca ttt cga gta				1359
Phe Ser Tyr Gly Ser Gly Leu Ala Ala Ser Phe Phe Ser Phe Arg Val				
410	415	420	425	
tcc cag gat gct gct cca ggc tct ccc ctg gac aag ttg gtg tcc agc				1407
Ser Gln Asp Ala Ala Pro Gly Ser Pro Leu Asp Lys Leu Val Ser Ser				
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aca tca gac ctg cca aaa cgc cta gcc tcc cga aag tgt gtg tct cct				1455
Thr Ser Asp Leu Pro Lys Arg Leu Ala Ser Arg Lys Cys Val Ser Pro				
442	447	452	457	
gag gag ttc aca gaa ata atg aac caa aga gag caa ttc tac cat aag				1503
Glu Glu Phe Thr Glu Ile Met Asn Gln Arg Glu Gln Phe Tyr His Lys				
458	463	468	473	
gtg aat ttc tcc cca cct ggt gac aca aac agc ctt ttc cca ggt act				1551
Val Asn Phe Ser Pro Pro Gly Asp Thr Asn Ser Leu Phe Pro Gly Thr				
474	479	484	489	
tgg tac ctg gag cga gtg gac gag cag cat cgc cga aag tat gcc cgg				1599
Trp Tyr Leu Glu Arg Val Asp Glu Gln His Arg Arg Lys Tyr Ala Arg				
490	495	500	505	
cgt ccc gtc taa agg tggtctgcag atccatggaa agcttctctgg gaaacgtatg				1654
Arg Pro Val *				
506				
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ccggggccagc cctgcccagg agaccagca accaggtcca tgtctcagcc atg ctc	236
	Met Leu
	1
ccc acg gag gtc ccc caa tcc cac ccg ggc ccc tca gcg ttg ctt ctg	284
Pro Thr Glu Val Pro Gln Ser His Pro Gly Pro Ser Ala Leu Leu Leu	
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ctg cag ctg ttg ctg ccc ccc aca tct gcc ttc ttc ccc aac atc tgg	332
Leu Gln Leu Leu Leu Pro Thr Ser Ala Phe Phe Pro Asn Ile Trp	
19 24 29 34	
agc ctg ctg gct gcc cct ggc tcc atc acc cac caa gac cta act gag	380
Ser Leu Leu Ala Ala Pro Gly Ser Ile Thr His Gln Asp Leu Thr Glu	
35 40 45 50	
gag gca gcg ctc aac gtc acc ctg cag ctc ttc ctg gag cag cca ccc	428
Glu Ala Ala Leu Asn Val Thr Leu Gln Leu Phe Leu Glu Gln Pro Pro	
51 56 61 66	
cca ggc cgc ccc cct ctt cgt ctt gag gac ttc ctg ggt cga aca ctc	476
Pro Gly Arg Pro Pro Leu Arg Leu Glu Asp Phe Leu Gly Arg Thr Leu	
67 72 77 82	
ctt gct gat gac ctc ttt gcc gcc tac ttt gga cct ggt tct tct cgg	524
Leu Ala Asp Asp Leu Phe Ala Ala Tyr Phe Gly Pro Gly Ser Ser Arg	
83 88 93 98	
cgg ttc cga gca gcc tta ggt gag gtg tct cgt gcc aat gca gcc cag	572
Arg Phe Arg Ala Ala Leu Gly Glu Val Ser Arg Ala Asn Ala Ala Gln	
99 104 109 114	
gac ttc ctg cca act tcc agg aat gac ccc gac ctg cac ttt gat gct	620
Asp Phe Leu Pro Thr Ser Arg Asn Asp Pro Asp Leu His Phe Asp Ala	
115 120 125 130	
gag cga ctg ggt cag gga cgc gcg cgc ctg gta ggg gct ctg cgg gag	668
Glu Arg Leu Gly Gln Gly Arg Ala Arg Leu Val Gly Ala Leu Arg Glu	
131 136 141 146	
acc gtg gtg gca gcc agg gcc ctt gac cac acc ctg gct cgc cag cgc	716
Thr Val Val Ala Ala Arg Ala Leu Asp His Thr Leu Ala Arg Gln Arg	
147 152 157 162	
ctc ggg gct gca ctt cat gcc ctg cag gat ttc tac agt cat agc aac	764

Leu Gly Ala Ala Leu His Ala Leu Gln Asp Phe Tyr Ser His Ser Asn	
163 168 173 178	
tgg gtg gag ctg ggc gag cag cag cca cac cct cac ctc ctc tgg cca	812
Trp Val Glu Leu Gly Glu Gln Gln Pro His Pro His Leu Leu Trp Pro	
179 184 189 194	
agg cag gag ctc cag aac ctg gca caa gtg gcc gat cct acc tgc tcc	860
Arg Gln Glu Leu Gln Asn Leu Ala Gln Val Ala Asp Pro Thr Cys Ser	
195 200 205 210	
gat tgc gag gag ttg agc tgc ccc agg aat tgg ctg ggc ttc aca ctc	908
Asp Cys Glu Glu Leu Ser Cys Pro Arg Asn Trp Leu Gly Phe Thr Leu	
211 216 221 226	
ctc acc tct ggc tac ttt gga act cat ccc ccg aaa cct cca ggg aaa	956
Leu Thr Ser Gly Tyr Phe Gly Thr His Pro Pro Lys Pro Pro Gly Lys	
227 232 237 242	
tgt agc cac ggg ggc cat ttt gac cgg agc agc tcc cag cca ccg agg	1004
Cys Ser His Gly Gly His Phe Asp Arg Ser Ser Ser Gln Pro Pro Arg	
243 248 253 258	
gga ggc atc aac aag gac agc aca tcc cca ggc ttc tcc cct cac cac	1052
Gly Gly Ile Asn Lys Asp Ser Thr Ser Pro Gly Phe Ser Pro His His	
259 264 269 274	
atg ctg cac ctc cag gct gca aaa ctg gcc ctt cta gcc tcc atc cag	1100
Met Leu His Leu Gln Ala Ala Lys Leu Ala Leu Leu Ala Ser Ile Gln	
275 280 285 290	
gcc ttc agc ctt ctg cga agc cgc ctg gga gac agg gat ttc tcc agg	1148
Ala Phe Ser Leu Leu Arg Ser Arg Leu Gly Asp Arg Asp Phe Ser Arg	
291 296 301 306	
ctg ctg gac atc acc cca gcc tcc agc ctg agc ttt gtc ctg gac acc	1196
Leu Leu Asp Ile Thr Pro Ala Ser Ser Leu Ser Phe Val Leu Asp Thr	
307 312 317 322	
acg ggc agc atg ggt gag gag atc aac gct gcc aaa atc cag gct cgc	1244
Thr Gly Ser Met Gly Glu Glu Ile Asn Ala Ala Lys Ile Gln Ala Arg	
323 328 333 338	
cac ctt gtg gag cag cgg aga ggc agc ccc atg gag cct gtc cac tat	1292
His Leu Val Glu Gln Arg Arg Gly Ser Pro Met Glu Pro Val His Tyr	
339 344 349 354	
gtc ctg gtg cct ttt cat gac cca ggg ttc gcc cct gtc ttt aca acc	1340
Val Leu Val Pro Phe His Asp Pro Gly Phe Gly Pro Val Phe Thr Thr	
355 360 365 370	
agt gac cct gac agc ttc tgg caa cag ctt aat gag atc cat gcc ttg	1388
Ser Asp Pro Asp Ser Phe Trp Gln Gln Leu Asn Glu Ile His Ala Leu	
371 376 381 386	
ggg ggt gga gac gag cct gag atg tgc ctg tca gcc ctg cag ctg gcc	1436
Gly Gly Gly Asp Glu Pro Glu Met Cys Leu Ser Ala Leu Gln Leu Ala	

387	392	397	402	
ctg ctg cac aca cct cca ctc tca gat atc ttt gtc ttc acg gat gcc				1484
Leu Leu His Thr Pro Pro Leu Ser Asp Ile Phe Val Phe Thr Asp Ala				
403	408	413	418	
tcc ccc aag gat gcc ttt ctc acc aac cag gtg gaa tcc ctg act cag				1532
Ser Pro Lys Asp Ala Phe Leu Thr Asn Gln Val Glu Ser Leu Thr Gln				
419	424	429	434	
gag cgg cgc tgc cgg gta aca ttc ctg gtg act gaa gat aca tca agg				1580
Glu Arg Arg Cys Arg Val Thr Phe Leu Val Thr Glu Asp Thr Ser Arg				
435	440	445	450	
gtt cag ggt cga gct cgg cgt gag atc ttg tcc cct ctg cgt ttt gag				1628
Val Gln Gly Arg Ala Arg Arg Glu Ile Leu Ser Pro Leu Arg Phe Glu				
451	456	461	466	
cca tac aaa gca gtg gcc ctg gcc tca gga gga gag gtg atc ttc acc				1676
Pro Tyr Lys Ala Val Ala Leu Ala Ser Gly Gly Glu Val Ile Phe Thr				
467	472	477	482	
aaa gac cag cac att cga gac gtg gca gcc att gtt ggg gag agc atg				1724
Lys Asp Gln His Ile Arg Asp Val Ala Ala Ile Val Gly Glu Ser Met				
483	488	493	498	
gct gcc ctg gtg act ctt ccc ctg gac cct cct gtt gtg gtg cct ggg				1772
Ala Ala Leu Val Thr Leu Pro Leu Asp Pro Pro Val Val Val Pro Gly				
499	504	509	514	
cag cca ctt gtg ttc agc gtg gat ggg ctg ctc cag aag atc aca gtc				1820
Gln Pro Leu Val Phe Ser Val Asp Gly Leu Leu Gln Lys Ile Thr Val				
515	520	525	530	
cgg atc cac gga gac atc agc agc ttc tgg atc aag aac cct gca ggg				1868
Arg Ile His Gly Asp Ile Ser Ser Phe Trp Ile Lys Asn Pro Ala Gly				
531	536	541	546	
gtc tcc cag ggc cag gag gaa ggc ggg ggt cct cta ggt cac act cgc				1916
Val Ser Gln Gly Gln Glu Glu Gly Gly Gly Pro Leu Gly His Thr Arg				
547	552	557	562	
cgc ttt ggg cag ttc tgg atg gtg acc atg gat gac cct cca cag aca				1964
Arg Phe Gly Gln Phe Trp Met Val Thr Met Asp Asp Pro Pro Gln Thr				
563	568	573	578	
gga acc tgg gag atc cag gtc aca gct gag gac acc cct ggg gtg aga				2012
Gly Thr Trp Glu Ile Gln Val Thr Ala Glu Asp Thr Pro Gly Val Arg				
579	584	589	594	
gtg caa gcc cag acc tcc ctg gac ttc ctc ttc cac ttt ggg atc ccc				2060
Val Gln Ala Gln Thr Ser Leu Asp Phe Leu Phe His Phe Gly Ile Pro				
595	600	605	610	
atg gag gat gga ccc cac cct ggc ctc tac ccc ctg act cag cca gtt				2108
Met Glu Asp Gly Pro His Pro Gly Leu Tyr Pro Leu Thr Gln Pro Val				
611	616	621	626	

gca ggt ctt cag acc cag ctg ctg gta gaa gtg aca ggg ttg ggt tcc	2156
Ala Gly Leu Gln Thr Gln Leu Leu Val Glu Val Thr Gly Leu Gly Ser	
627 632 637 642	
aga gcc aat cct ggg gat cct cag ccg cat ttc tcc cac gtc atc ctt	2204
Arg Ala Asn Pro Gly Asp Pro Gln Pro His Phe Ser His Val Ile Leu	
643 648 653 658	
cga ggg gtc cca gag ggt gcc gaa cta ggc cag gtg ccc ttg gag ccc	2252
Arg Gly Val Pro Glu Gly Ala Glu Leu Gly Gln Val Pro Leu Glu Pro	
659 664 669 674	
gtg gga cct ccg gag cga ggt ctc ctc gca gcc tcg ctg tcg ccc acg	2300
Val Gly Pro Pro Glu Arg Gly Leu Leu Ala Ala Ser Leu Ser Pro Thr	
675 680 685 690	
ctg ctg tcc acc cct aga ccc ttc tcc ctg gag ctg att ggc cag gac	2348
Leu Leu Ser Thr Pro Arg Pro Phe Ser Leu Glu Leu Ile Gly Gln Asp	
691 696 701 706	
gca gcg ggt cgg cgc ctg cac agg gct gcc cct cag cct agc act gta	2396
Ala Ala Gly Arg Arg Leu His Arg Ala Ala Pro Gln Pro Ser Thr Val	
707 712 717 722	
gtc cct gtc ctt ctg gag ctt agt ggc ccc tcg ggt ttc ttg gcc ccg	2444
Val Pro Val Leu Leu Glu Leu Ser Gly Pro Ser Gly Phe Leu Ala Pro	
723 728 733 738	
ggc agc aaa gtc ccg ctc agt ctc cgc atc gcc agc ttc tcg ggc cct	2492
Gly Ser Lys Val Pro Leu Ser Leu Arg Ile Ala Ser Phe Ser Gly Pro	
739 744 749 754	
cag gat ctt gac ctt agg act ttc gtc aac ccc agc ttc tcc ctc acc	2540
Gln Asp Leu Asp Leu Arg Thr Phe Val Asn Pro Ser Phe Ser Leu Thr	
755 760 765 770	
tcc aac ctc tcc agg gct cac ctg gaa ctg aat gag tcg gcc tgg ggc	2588
Ser Asn Leu Ser Arg Ala His Leu Glu Leu Asn Glu Ser Ala Trp Gly	
771 776 781 786	
cgc ctg tgg ctg gag gtc cca gat tca gcg gcc ccg gat tcc gtg gtg	2636
Arg Leu Trp Leu Glu Val Pro Asp Ser Ala Ala Pro Asp Ser Val Val	
787 792 797 802	
atg gtg act gtg act gca ggg gga cga gaa gcc aac cca gta ccc ccg	2684
Met Val Thr Val Thr Ala Gly Gly Arg Glu Ala Asn Pro Val Pro Pro	
803 808 813 818	
act cat gct ttc ctc cgg ctc ctg gta tcg gcc cca gcc ccg cag gac	2732
Thr His Ala Phe Leu Arg Leu Leu Val Ser Ala Pro Ala Pro Gln Asp	
819 824 829 834	
cgg cac acc acc cct acc ggc tca tct gac ccg atc ctc acc acg gcc	2780
Arg His Thr Thr Pro Thr Gly Ser Ser Asp Pro Ile Leu Thr Thr Ala	
835 840 845 850	

gtg aag ctg gac gat gag ccg ccc aac agc ggc ggg gga agc ccg tgc	423
Val Lys Leu Asp Asp Glu Pro Pro Asn Ser Gly Gly Gly Ser Pro Cys	
56 61 66 71	
gag gcg ggc gag gag ggc gag ggc ggg gtg tgc ctc aac gga ggt gtg	471
Glu Ala Gly Glu Glu Gly Glu Gly Gly Val Cys Leu Asn Gly Gly Val	
72 77 82 87	
tgc tcc gtg gtg gac gac cag gcc gtg tgc gac tgc tcg cga acc ggc	519
Cys Ser Val Val Asp Asp Gln Ala Val Cys Asp Cys Ser Arg Thr Gly	
88 93 98 103	
ttc cgc ggc aag gac tgc agc caa gaa gac aac aat gtg gaa ggt ctg	567
Phe Arg Gly Lys Asp Cys Ser Gln Glu Asp Asn Asn Val Glu Gly Leu	
104 109 114 119	
gcg cac ctg atg atg ggc gac caa gga aaa gaa gaa tat att gcc acg	615
Ala His Leu Met Met Gly Asp Gln Gly Lys Glu Glu Tyr Ile Ala Thr	
120 125 130 135	
ttc aaa gga tct gaa tac ttc tgc tac gac ttg tct caa aac ccc att	663
Phe Lys Gly Ser Glu Tyr Phe Cys Tyr Asp Leu Ser Gln Asn Pro Ile	
136 141 146 151	
caa agc agc agt gat gaa ata act ctg tca ttt aaa acc ctt cag agg	711
Gln Ser Ser Ser Asp Glu Ile Thr Leu Ser Phe Lys Thr Leu Gln Arg	
152 157 162 167	
aat gga ctg atg ctt cac act ggg aaa tcg gct gat tat gtc aat ctt	759
Asn Gly Leu Met Leu His Thr Gly Lys Ser Ala Asp Tyr Val Asn Leu	
168 173 178 183	
gcc ctg aaa aat gga gct gtc tct ctg gtc att aat ttg gga tca ggc	807
Ala Leu Lys Asn Gly Ala Val Ser Leu Val Ile Asn Leu Gly Ser Gly	
184 189 194 199	
gcc ttt gaa gca cta gtg gag cct gtg aat gga aag ttt aat gat aat	855
Ala Phe Glu Ala Leu Val Glu Pro Val Asn Gly Lys Phe Asn Asp Asn	
200 205 210 215	
gcc tgg cat gat gtg aaa gtc acc agg aat ctg cgt cag cac tca ggc	903
Ala Trp His Asp Val Lys Val Thr Arg Asn Leu Arg Gln His Ser Gly	
216 221 226 231	
att gga cac gct atg gtg aca ata tca gtg gat ggg att ctt acc aca	951
Ile Gly His Ala Met Val Thr Ile Ser Val Asp Gly Ile Leu Thr Thr	
232 237 242 247	
acg ggc tac acg caa gaa gat tat acc atg ctg ggg tct gat gac ttt	999
Thr Gly Tyr Thr Gln Glu Asp Tyr Thr Met Leu Gly Ser Asp Asp Phe	
248 253 258 263	
ttc tat gtt gga ggc agt ccc agc aca gcc gac ctt cca ggg tca cca	1047
Phe Tyr Val Gly Gly Ser Pro Ser Thr Ala Asp Leu Pro Gly Ser Pro	
264 269 274 279	
gtc agt aac aac ttt atg ggc tgt ctc aaa gag gtt gta tat aaa aat	1095

Val Ser Asn Asn Phe Met Gly Cys Leu Lys Glu Val Val Tyr Lys Asn	
280 285 290 295	
aat gat gtg agg ctg gaa tta tct cga ctt gcc aag caa gga gat cct	1143
Asn Asp Val Arg Leu Glu Leu Ser Arg Leu Ala Lys Gln Gly Asp Pro	
296 301 306 311	
aag atg aag atc cat gga gtg gtg gca ttt aaa tgt gag aat gtt gca	1191
Lys Met Lys Ile His Gly Val Val Ala Phe Lys Cys Glu Asn Val Ala	
312 317 322 327	
act tta gac cca atc acc ttt gaa acc cca gag tct ttc atc tct ttg	1239
Thr Leu Asp Pro Ile Thr Phe Glu Thr Pro Glu Ser Phe Ile Ser Leu	
328 333 338 343	
cct aaa tgg aat gca aag aaa act ggc tcc ata tca ttt gat ttc cgt	1287
Pro Lys Trp Asn Ala Lys Lys Thr Gly Ser Ile Ser Phe Asp Phe Arg	
344 349 354 359	
aca aca gag cca aat ggc ctc atc tta ttt agc cat ggc aag cca aga	1335
Thr Thr Glu Pro Asn Gly Leu Ile Leu Phe Ser His Gly Lys Pro Arg	
360 365 370 375	
cat cag aaa gat gcc aag cac cca cag atg ata aag gtg gac ttc ttt	1383
His Gln Lys Asp Ala Lys His Pro Gln Met Ile Lys Val Asp Phe Phe	
376 381 386 391	
gct att gag atg cta gat ggc cac ctc tac ctc ctc ctg gac atg ggg	1431
Ala Ile Glu Met Leu Asp Gly His Leu Tyr Leu Leu Leu Asp Met Gly	
392 397 402 407	
tca ggt act ata aaa ata aaa gcc ctg ttg aag aaa gtg aat gat gga	1479
Ser Gly Thr Ile Lys Ile Lys Ala Leu Leu Lys Lys Val Asn Asp Gly	
408 413 418 423	
gaa tgg tat cat gtg gac ttc cag aga gac gga cgg tca ggt acc att	1527
Glu Trp Tyr His Val Asp Phe Gln Arg Asp Gly Arg Ser Gly Thr Ile	
424 429 434 439	
tct gtc aac acg ttg cgt act ccc tac act gct cct ggt gag agt gag	1575
Ser Val Asn Thr Leu Arg Thr Pro Tyr Thr Ala Pro Gly Glu Ser Glu	
440 445 450 455	
att ctg gac ctg gat gat gag ttg tac ctg ggg ggg ctg cca gaa aat	1623
Ile Leu Asp Leu Asp Asp Glu Leu Tyr Leu Gly Gly Leu Pro Glu Asn	
456 461 466 471	
aaa gct ggc ctt gtc ttc ccc acc gag gtg tgg act gct ctg ctc aac	1671
Lys Ala Gly Leu Val Phe Pro Thr Glu Val Trp Thr Ala Leu Leu Asn	
472 477 482 487	
tat ggc tac gtg ggc tgc atc agg gat ttg ttc atc gat ggc caa agc	1719
Tyr Gly Tyr Val Gly Cys Ile Arg Asp Leu Phe Ile Asp Gly Gln Ser	
488 493 498 503	
aaa gat atc cgg caa atg gct gaa gtt caa agt act gct gga gtg aag	1767
Lys Asp Ile Arg Gln Met Ala Glu Val Gln Ser Thr Ala Gly Val Lys	

504	509	514	519	
cct tcc tgc tca aag	gaa aca gca aaa ccg	tgc ctt agc aac cct	tgc	1815
Pro Ser Cys Ser Lys	Glu Thr Ala Lys Pro	Cys Leu Ser Asn Pro	Cys	
520	525	530	535	
aaa aac aat ggc atg	tgc agg gat ggg tgg	aac aga tat gtc tgt	gat	1863
Lys Asn Asn Gly Met	Cys Arg Asp Gly Trp	Asn Arg Tyr Val Cys	Asp	
536	541	546	551	
tgt tcc gga aca ggc	tat ctt ggc agg tcc	tgt gag aga gag gca	acg	1911
Cys Ser Gly Thr Gly	Tyr Leu Gly Arg Ser	Cys Glu Arg Glu Ala	Thr	
552	557	562	567	
gtt ttg agc tat gat	ggg agc atg ttt atg	aaa att cag ctc ccc	gta	1959
Val Leu Ser Tyr Asp	Gly Ser Met Phe Met	Lys Ile Gln Leu Pro	Val	
568	573	578	583	
gtc atg cat acg gag	gct gag gat gtt tcc	tta cgg ttc cga tcc	cag	2007
Val Met His Thr Glu	Ala Glu Asp Val Ser	Leu Arg Phe Arg Ser	Gln	
584	589	594	599	
cgt gca tat ggc att	ctg atg gca acc act	tct aga gac tct gct	gac	2055
Arg Ala Tyr Gly Ile	Leu Met Ala Thr Thr	Ser Arg Asp Ser Ala	Asp	
600	605	610	615	
acc ctc cgc ctg gag	cta gac gca gga cgt	gtg aaa ctg acg gtc	aat	2103
Thr Leu Arg Leu Glu	Leu Asp Ala Gly Arg	Val Lys Leu Thr Val	Asn	
616	621	626	631	
cta gat tgt atc agg	att aac tgt aat tcc	agc aaa ggt ccc gag	act	2151
Leu Asp Cys Ile Arg	Ile Asn Cys Asn Ser	Ser Lys Gly Pro Glu	Thr	
632	637	642	647	
ctt ttt gct ggc tat	aac ctc aat gat aac	gag tgg cac aca gtg	cgt	2199
Leu Phe Ala Gly Tyr	Asn Leu Asn Asp Asn	Glu Trp His Thr Val	Arg	
648	653	658	663	
gta gtt cgg cgt gga	aaa agt tta aag tta	aca gtg cat gac caa	cag	2247
Val Val Arg Arg Gly	Lys Ser Leu Lys Leu	Thr Val His Asp Gln	Gln	
664	669	674	679	
gcc atg aca ggt caa	atg gca ggt gat cat	act agg ctg gag ttc	cat	2295
Ala Met Thr Gly Gln	Met Ala Gly Asp His	Thr Arg Leu Glu Phe	His	
680	685	690	695	
aac ata gag act ggc	atc atc aca gaa cga	cgg tat ctt tct tct	gtc	2343
Asn Ile Glu Thr Gly	Ile Ile Thr Glu Arg	Arg Tyr Leu Ser Ser	Val	
696	701	706	711	
ccc tcc aac ttc att	gga cac ctg cag agc	ttg aca ttt aat gga	atg	2391
Pro Ser Asn Phe Ile	Gly His Leu Gln Ser	Leu Thr Phe Asn Gly	Met	
712	717	722	727	
gca tac att gac ctg	tgt aaa aat ggc gac	ata gat tac tgt gag	ctt	2439
Ala Tyr Ile Asp Leu	Cys Lys Asn Gly Asp	Ile Asp Tyr Cys Glu	Leu	
728	733	738	743	

aat gcc aga ttt ggc ttc agg aac atc ata gca gat cct gtc acc ttc	2487
Asn Ala Arg Phe Gly Phe Arg Asn Ile Ile Ala Asp Pro Val Thr Phe	
744 749 754 759	
aag acc aaa tcg agc tat gtt gcc tta gct acc ttg caa gcc tac act	2535
Lys Thr Lys Ser Ser Tyr Val Ala Leu Ala Thr Leu Gln Ala Tyr Thr	
760 765 770 775	
tct atg cat ctt ttt ttc cag ttc aag aca aca tcc cta gat gga tta	2583
Ser Met His Leu Phe Phe Gln Phe Lys Thr Thr Ser Leu Asp Gly Leu	
776 781 786 791	
att cta tat aac agt ggg gat gga aat gac ttt att gtg gtt gaa tta	2631
Ile Leu Tyr Asn Ser Gly Asp Gly Asn Asp Phe Ile Val Val Glu Leu	
792 797 802 807	
gtt aaa ggg tac tta cat tac gtg ttt gat ttg gga aat ggt gct aac	2679
Val Lys Gly Tyr Leu His Tyr Val Phe Asp Leu Gly Asn Gly Ala Asn	
808 813 818 823	
ctc atc aaa gga agc tca aat aaa cct ctc aat gac aat cag tgg cac	2727
Leu Ile Lys Gly Ser Ser Asn Lys Pro Leu Asn Asp Asn Gln Trp His	
824 829 834 839	
aac gtg atg ata tca agg gac acc agc aac ctc cac act gta aag att	2775
Asn Val Met Ile Ser Arg Asp Thr Ser Asn Leu His Thr Val Lys Ile	
840 845 850 855	
gac aca aaa atc aca acg caa atc acc gcc gga gcc agg aac tta gac	2823
Asp Thr Lys Ile Thr Thr Gln Ile Thr Ala Gly Ala Arg Asn Leu Asp	
856 861 866 871	
ctc aag agt gac tta tat ata gga gga gta gct aaa gaa aca tac aaa	2871
Leu Lys Ser Asp Leu Tyr Ile Gly Gly Val Ala Lys Glu Thr Tyr Lys	
872 877 882 887	
tcc tta cca aaa ctt gta cat gcc aaa gaa ggc ttt caa ggc tgc ctg	2919
Ser Leu Pro Lys Leu Val His Ala Lys Glu Gly Phe Gln Gly Cys Leu	
888 893 898 903	
gca tca gtt gat tta aat gga cgg ctt ccg gac ctc atc tcc gat gct	2967
Ala Ser Val Asp Leu Asn Gly Arg Leu Pro Asp Leu Ile Ser Asp Ala	
904 909 914 919	
ctt ttc tgc aac gga cag atc gag aga gga tgt gaa ggg ccc agc aca	3015
Leu Phe Cys Asn Gly Gln Ile Glu Arg Gly Cys Glu Gly Pro Ser Thr	
920 925 930 935	
acc tgc caa gag gac tca tgt tcc aat caa ggt gtg tgc ttg caa caa	3063
Thr Cys Gln Glu Asp Ser Cys Ser Asn Gln Gly Val Cys Leu Gln Gln	
936 941 946 951	
tgg gat ggc ttc agc tgt gac tgt agt atg act tcc ttc agt gga cca	3111
Trp Asp Gly Phe Ser Cys Asp Cys Ser Met Thr Ser Phe Ser Gly Pro	
952 957 962 967	

ctc tgc aat gac cct ggg acg aca tat atc ttt agc aaa ggt ggt gga Leu Cys Asn Asp Pro Gly Thr Thr Tyr Ile Phe Ser Lys Gly Gly Gly 968 973 978 983	3159
caa atc acg tat aag tgg cct cct aat gac cga ccc agt acg cga gca Gln Ile Thr Tyr Lys Trp Pro Pro Asn Asp Arg Pro Ser Thr Arg Ala 984 989 994 999	3207
gac aga ctg gcc ata ggt ttt agc act gtt cag aaa gaa gct gta ttg Asp Arg Leu Ala Ile Gly Phe Ser Thr Val Gln Lys Glu Ala Val Leu 1000 1005 1010 1015	3255
gtg cga gtg gac agt tct tca ggc ttg ggt gac tac cta gaa ctg cat Val Arg Val Asp Ser Ser Ser Gly Leu Gly Asp Tyr Leu Glu Leu His 1016 1021 1026 1031	3303
ata cac cag gga aaa att gga gtt aag ttt aat gtt ggg aca gat gac Ile His Gln Gly Lys Ile Gly Val Lys Phe Asn Val Gly Thr Asp Asp 1032 1037 1042 1047	3351
atc gcc att gaa gaa tcc aat gca atc att aat gat ggg aaa tac cat Ile Ala Ile Glu Glu Ser Asn Ala Ile Ile Asn Asp Gly Lys Tyr His 1048 1053 1058 1063	3399
gta gtt cgt ttc acg agg agt ggt ggc aat gcc acg ttg cag gtg gac Val Val Arg Phe Thr Arg Ser Gly Gly Asn Ala Thr Leu Gln Val Asp 1064 1069 1074 1079	3447
agc tgg cca gtg atc gag cgc tac cct gca ggg cgt cag ctc aca atc Ser Trp Pro Val Ile Glu Arg Tyr Pro Ala Gly Arg Gln Leu Thr Ile 1080 1085 1090 1095	3495
ttc aat agc caa gca acc ata ata att ggc ggg aaa gag cag ggc cag Phe Asn Ser Gln Ala Thr Ile Ile Ile Gly Gly Lys Glu Gln Gly Gln 1096 1101 1106 1111	3543
ccc ttc cag ggc cag ctc tct ggg ctg tac tac aat ggc ttg aaa gtt Pro Phe Gln Gly Gln Leu Ser Gly Leu Tyr Tyr Asn Gly Leu Lys Val 1112 1117 1122 1127	3591
ctg aat atg gca gcc gaa aac gat gcc aac atc gcc ata gtg gga aat Leu Asn Met Ala Ala Glu Asn Asp Ala Asn Ile Ala Ile Val Gly Asn 1128 1133 1138 1143	3639
gtg aga ctg gtt ggt gaa gtg cct tcc tct atg aca act gag tca aca Val Arg Leu Val Gly Glu Val Pro Ser Ser Met Thr Thr Glu Ser Thr 1144 1149 1154 1159	3687
gcc act gcc atg caa tca gag atg tcc aca tca att atg gag act acc Ala Thr Ala Met Gln Ser Glu Met Ser Thr Ser Ile Met Glu Thr Thr 1160 1165 1170 1175	3735
acg acc ctg gct act agc aca gcc aga aga gga aag ccc ccg aca aaa Thr Thr Leu Ala Thr Ser Thr Ala Arg Arg Gly Lys Pro Pro Thr Lys 1176 1181 1186 1191	3783
gaa ccc att agc cag acc aca gat gac atc ctt gtg gcc tca gca gag	3831

Glu Pro Ile Ser Gln Thr Thr Asp Asp Ile Leu Val Ala Ser Ala Glu	
1192	1197 1202 1207
tgt ccc agc gat gat gag gac att gac ccc tgt gag ccg agc tca ggt	3879
Cys Pro Ser Asp Asp Glu Asp Ile Asp Pro Cys Glu Pro Ser Ser Gly	
1208	1213 1218 1223
ggg tta gcc aac cca acc cga gca ggc ggc aga gag ccg tat cca ggc	3927
Gly Leu Ala Asn Pro Thr Arg Ala Gly Gly Arg Glu Pro Tyr Pro Gly	
1224	1229 1234 1239
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Gly Ile Val Ala Ala Ala Ala Leu Cys Ile Leu Ile Leu Leu Tyr Ala	
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Met Tyr Lys Tyr Arg Asn Arg Asp Glu Gly Ser Tyr His Val Asp Glu	
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agt cga aac tac atc agt aac tca gca cag tcc aat ggg gct gtt gta	4119
Ser Arg Asn Tyr Ile Ser Asn Ser Ala Gln Ser Asn Gly Ala Val Val	
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Lys Glu Lys Gln Pro Ser Ser Ala Lys Ser Ser Asn Lys Asn Lys Lys	
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1 5 10 15	
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Ala Ser Leu Ser Tyr Arg Gly Asp Gln Gln Asp Tyr Phe Leu Asn Leu	
17 22 27 32	
ccc ctc caa aac cag aga cca ggc cta aga agg acc ctg caa atc aga	202
Pro Leu Gln Asn Gln Arg Pro Gly Leu Arg Arg Thr Leu Gln Ile Arg	
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Asp Arg Ser Cys Leu Lys *	
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atctccctgg gccggaggcc actgtcttct ctctctctc caccgagtcg tgctctcgcc	180
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Met Glu Val Ala Glu Val Glu
1 5

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Ser Pro Leu Asn Pro Ser Cys Lys Ile Met Thr Phe Arg Pro Ser Met	
8 13 18 23	
gag gag ttc cgg gag ttc aac aaa tac ctt gca tac atg gag tct aaa	330
Glu Glu Phe Arg Glu Phe Asn Lys Tyr Leu Ala Tyr Met Glu Ser Lys	
24 29 34 39	
gga gcc cat cgt gcg ggt ctt gca aag gtg att cct cct aag gag tgg	378
Gly Ala His Arg Ala Gly Leu Ala Lys Val Ile Pro Pro Lys Glu Trp	
40 45 50 55	
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Lys Pro Arg Gln Cys Tyr Asp Asp Ile Asp Asn Leu Leu Ile Pro Ala	
56 61 66 71	
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Pro Ile Gln Gln Met Val Thr Gly Gln Ser Gly Leu Phe Thr Gln Tyr	
72 77 82 87	
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Asn Ile Gln Lys Lys Ala Met Thr Val Lys Glu Phe Arg Gln Leu Ala	
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Ala Asp Ile Asn Gly Ser Ile Tyr Asp Glu Gly Val Asp Glu Trp Asn	
136 141 146 151	
ata gct cgc ctc aat aca gtc ttg gat gtg gtt gaa gaa gag tgt ggc	714
Ile Ala Arg Leu Asn Thr Val Leu Asp Val Glu Glu Glu Cys Gly	
152 157 162 167	
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Ile Ser Ile Glu Gly Val Asn Thr Pro Tyr Leu Tyr Phe Gly Met Trp	
168 173 178 183	
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Lys Thr Thr Phe Ala Trp His Thr Glu Asp Met Asp Leu Tyr Ser Ile	
184 189 194 199	
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Asn Tyr Leu His Phe Gly Glu Pro Lys Ser Trp Tyr Ala Ile Pro Pro	
200 205 210 215	
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Glu His Gly Lys Arg Leu Glu Arg Leu Ala Gln Gly Phe Phe Pro Ser	

216	221	226	231	
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Ser Ser Gln Gly Cys Asp Ala Phe Leu Arg His Lys Met Thr Leu Ile				
232	237	242	247	
tct cca tca gta ttg aag aaa tat ggt att ccc ttt gac aag ata acc				1002
Ser Pro Ser Val Leu Lys Lys Tyr Gly Ile Pro Phe Asp Lys Ile Thr				
248	253	258	263	
cag gag gct gga gaa ttc atg atc act ttc cca tat ggc tac cat gct				1050
Gln Glu Ala Gly Glu Phe Met Ile Thr Phe Pro Tyr Gly Tyr His Ala				
264	269	274	279	
ggc ttt aat cat ggt ttc aac tgt gca gaa tct aca aat ttt gct act				1098
Gly Phe Asn His Gly Phe Asn Cys Ala Glu Ser Thr Asn Phe Ala Thr				
280	285	290	295	
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Val Arg Trp Ile Asp Tyr Gly Lys Val Ala Lys Leu Cys Thr Cys Arg				
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Lys Asp Met Val Lys Ile Ser Met Asp Ile Phe Val Arg Lys Phe Gln				
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Pro Asp Arg Tyr Gln Leu Trp Lys Gln Gly Lys Asp Ile Tyr Thr Ile				
328	333	338	343	
gat cac acg aag cct act cca gca tcc acc cct gaa gta aaa gca tgg				1290
Asp His Thr Lys Pro Thr Pro Ala Ser Thr Pro Glu Val Lys Ala Trp				
344	349	354	359	
ctg cag agg agg agg aaa gta aga aaa gca tcc cga agc ttc cag tgt				1338
Leu Gln Arg Arg Arg Lys Val Arg Lys Ala Ser Arg Ser Phe Gln Cys				
360	365	370	375	
gct agg tct acc tct aaa agg cct aag gct gat gag gaa gag gaa gtg				1386
Ala Arg Ser Thr Ser Lys Arg Pro Lys Ala Asp Glu Glu Glu Glu Val				
376	381	386	391	
tca gat gaa gtc gat ggg gca gag gtc cct aac ccc gac tca gtc aca				1434
Ser Asp Glu Val Asp Gly Ala Glu Val Pro Asn Pro Asp Ser Val Thr				
392	397	402	407	
gat gac ctc aag gtc agt gaa aag tca gaa gca gca gtg aag ctg agg				1482
Asp Asp Leu Lys Val Ser Glu Lys Ser Glu Ala Ala Val Lys Leu Arg				
408	413	418	423	
aac aca gaa gca tct tca gaa gaa gag tca tct gct agc agg atg cag				1530
Asn Thr Glu Ala Ser Ser Glu Glu Glu Ser Ser Ala Ser Arg Met Gln				
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Val Glu Gln Asn Leu Ser Asp His Ile Lys Leu Ser Gly Asn Ser Cys				
440	445	450	455	

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Tyr Ala Tyr Arg Ser Val Pro Ser Ile Ser Ser Glu Ala Asp Asp Ser	
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Ile Pro Leu Ser Thr Gly Tyr Glu Lys Pro Glu Lys Ser Asp Pro Ser	
488 493 498 503	
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Glu Leu Ser Trp Pro Lys Ser Pro Glu Ser Cys Ser Ser Val Ala Glu	
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Ser Asn Gly Val Leu Thr Glu Gly Glu Glu Ser Asp Val Glu Ser His	
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Gly Asn Gly Leu Glu Pro Gly Glu Ile Pro Ala Val Pro Ser Gly Glu	
536 541 546 551	
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Arg Asn Ser Phe Lys Val Pro Ser Ile Ala Glu Gly Glu Asn Lys Thr	
552 557 562 567	
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Ser Lys Ser Trp Arg His Pro Leu Ser Arg Pro Pro Ala Arg Ser Pro	
568 573 578 583	
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Met Thr Leu Val Lys Gln Gln Ala Pro Ser Asp Glu Glu Leu Pro Glu	
584 589 594 599	
gtt ctg tcc att gag gag gaa gtg gaa gaa aca gag tct tgg gcg aaa	2058
Val Leu Ser Ile Glu Glu Glu Val Glu Glu Thr Glu Ser Trp Ala Lys	
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Pro Leu Ile His Leu Trp Gln Thr Lys Ser Pro Asn Phe Ala Ala Glu	
616 621 626 631	
caa gag tat aat gca aca gtg gcc agg atg aag cca cac tgt gcc atc	2154
Gln Glu Tyr Asn Ala Thr Val Ala Arg Met Lys Pro His Cys Ala Ile	
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664 669 674 679	

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Thr Ser Leu Leu Ile Ser Cys Ala Lys Cys Cys Val Arg Val His Ala	
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728 733 738 743	
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cca cct gct gag gga gaa gtc gtc caa gtc aag tgg ccc gat ggc aaa	3066
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ctc tat gga gca aaa tat ttt gga tca aat att gcc cac atg tac cag	3114
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gtc act gtc aag ccc gcc aac cag cgc aat aac gtg gtg cga ggg gca      894
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tct ggg cgt ttg aca ggt cct ccc tct gca ggg cct ggg cct gct gag      942
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Pro Asp Ser Asp Asp Asp Ser Ser Asp Leu Val Ile Glu Asn Arg Gln				
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Pro Pro Ser Ser Asn Gly Leu Ser Gln Gly Pro Pro Cys Trp Asp Leu				
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cac cct ggc tgc cga cat cct ggt acc cgc agc tct ctg ccc tcc ctg				1086
His Pro Gly Cys Arg His Pro Gly Thr Arg Ser Ser Leu Pro Ser Leu				
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Asp Asp Gln Glu Gln Ala Ser Ser Gly Trp Gly Ser Arg Ile Arg Gly				
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Asp Gly Ser Gly Phe Ser Leu *				
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Met Ala Ala Gln Pro Pro Arg Gly Ile Arg Leu Ser Ala Leu Cys Pro				
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Lys Phe Leu His Thr Asn Ser Thr Ser His Thr Trp Pro Phe Ser Ala				
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Val Ala Glu Leu Ile Asp Asn Ala Tyr Asp Pro Asp Val Asn Ala Lys				
33 38 43 48				

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Gln Ile Trp Ile Asp Lys Thr Val Ile Asn Asp His Ile Cys Leu Thr	
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Phe Thr Asp Asn Gly Asn Gly Met Thr Ser Asp Lys Leu His Lys Met	
65 70 75 80	
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Leu Ser Phe Gly Phe Ser Asp Lys Val Thr Met Asn Gly His Val Pro	
81 86 91 96	
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Val Gly Leu Tyr Gly Asn Gly Phe Lys Ser Gly Ser Met Arg Leu Gly	
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Lys Asp Ala Ile Val Phe Thr Lys Asn Gly Glu Ser Met Ser Val Gly	
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Leu Leu Ser Gln Thr Tyr Leu Glu Val Ile Lys Ala Glu His Val Val	
129 134 139 144	
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Val Pro Ile Val Ala Phe Asn Lys His Arg Gln Met Ile Asn Leu Ala	
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Gly Thr Arg Ile Ile Ile Trp Asn Leu Arg Ser Tyr Lys Asn Ala Thr	
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Glu Phe Asp Phe Glu Lys Asp Lys Tyr Asp Ile Arg Ile Pro Glu Asp	
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Leu Asp Glu Ile Thr Gly Lys Lys Gly Tyr Lys Lys Gln Glu Arg Met	
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Asp Gln Ile Ala Pro Glu Ser Asp Tyr Ser Leu Arg Ala Tyr Cys Ser	
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Leu Lys Trp Arg Lys Leu Pro Asp Gly Met Asp Gln Leu Pro Glu Lys	
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Trp Tyr Cys Ser Asn Asn Pro Asp Pro Gln Phe Arg Asn Cys Glu Val	
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Thr Tyr Lys Lys Thr Asn Lys Glu Lys Phe Arg Ile Arg Gln Pro Glu	
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Met Ile Pro Arg Ile Asn Ala Glu Leu Leu Phe Arg Pro Thr Ala Leu	
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Ser Thr Pro Ser Phe	Ser Ser Pro Lys Glu	Ser Val Pro Arg Arg His	
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Leu Ser Glu Gly Thr	Asn Ser Tyr Ala Thr	Arg Leu Leu Asn Asn His	
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Ser Gln Phe Glu Asn	Ser Val Tyr Lys Gly	Asp Asp Asp Asp Glu Asp	
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Leu Val Thr Glu Glu	Lys Glu Asn Tyr Lys	Arg Gln Cys His Met Phe	
705	710	715	720
act gat caa atc aaa	gtg tta caa cag agg	ata cta gaa atg aat gac	2445
Thr Asp Gln Ile Lys	Val Leu Gln Gln Arg	Ile Leu Glu Met Asn Asp	

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Val Phe Leu Leu Glu Ser Ile Asn Gly Lys Ser Glu Ser Pro Asp His				
753	758	763	768	
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Met Val Ser Gln Tyr Gln Gln Ala Leu Glu Glu Ile Glu Arg Leu Lys				
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Tyr Lys Ser Glu Val Glu Leu Leu Glu Met Glu Lys Ser Gln Ile Arg				
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112 117 122 127

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128 133 138 143

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144 149 154 159

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160 165 170 175

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176 181 186 191

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192 197 202 207

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Asn	Cys	Glu	Gln	Gln	Arg	Phe	Lys	Glu	Asp	Val	Tyr	Thr	Lys	Thr	Ile	
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tct	tta	tgg	tcg	tat	atc	aat	agc	cag	cta	gac	gag	ttt	tct	aat	ccc	1846
Ser	Leu	Trp	Ser	Tyr	Ile	Asn	Ser	Gln	Leu	Asp	Glu	Phe	Ser	Asn	Pro	
560					565					570					575	
ttc	ttt	gtg	aat	tat	gaa	aac	cac	gtg	tta	tat	cct	gtt	gct	agt	ctg	1894
Phe	Phe	Val	Asn	Tyr	Glu	Asn	His	Val	Leu	Tyr	Pro	Val	Ala	Ser	Leu	
576					581					586					591	
agt	cat	ttg	gaa	ttg	tgg	gta	aat	tat	tat	gta	cga	tgg	aat	cca	cgg	1942
Ser	His	Leu	Glu	Leu	Trp	Val	Asn	Tyr	Tyr	Val	Arg	Trp	Asn	Pro	Arg	
592					597					602					607	
atg	aga	cct	cag	atg	ccc	att	cac	cag	aat	ctc	aag	gag	ctg	ctg	gcc	1990
Met	Arg	Pro	Gln	Met	Pro	Ile	His	Gln	Asn	Leu	Lys	Glu	Leu	Leu	Ala	
608					613					618					623	
gtc	agg	gag	gag	ctg	cag	aag	cgt	gtg	gag	ggc	cta	cag	cgg	gag	gtg	2038
Val	Arg	Ala	Glu	Leu	Gln	Lys	Arg	Val	Glu	Gly	Leu	Gln	Arg	Glu	Val	
624					629					634					639	
gcc	acg	cgc	gcc	gtc	tca	tcc	tca	tct	gag	cgg	ggc	tcc	tcg	ccc	tcc	2086
Ala	Thr	Arg	Ala	Val	Ser	Ser	Ser	Ser	Glu	Arg	Gly	Ser	Ser	Pro	Ser	
640					645					650					655	
cac	tcc	gcc	acc	tcc	gtc	cac	acc	tcg	gtc	tga	tgggcgag	aaatatgtaa				2137
His	Ser	Ala	Thr	Ser	Val	His	Thr	Ser	Val	*						
656					661					666						

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gaggctgggg gggctctgtc agcaggaccc tagaggagac tctcattcga ttttaaagaa	2317
gcacaacggg tcattttcct ttgtatgttc ctagegcaga actgtttcta aaacaacttg	2377
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aagccgttat gggttcagggt tttaaaaact ggtacagtat tgtatttgtc tcattctgtt	2497
cactgtatTT caatcatctg taattaaaat gatcatatgt ttgctccctg gtctttttta	2557
agtaagtaag taagtatctt agtagatTTT tcctttgagg aaaatcggta ataaaataac	2617
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accggatgta agaaccaaaac actttcctgc ctcttaatgc aaccaaagaa agcttaggag	180
gcacggtttt ttgttttgat cgtgaatac tgaattcctg ccttctctcc tagttcacgt	240
tccttggggt aagttttgaa ttgtttgttt acagaccagc gtttggatct atgcaaacta	300
aaccctcag atactgatgc agttcgtggc cagatagtgg tcagtttaca gacacgagac	360
agaataggaa ccggcggctc ggtggtggac tgcagaggac tgtagaaaa tgaaggaacg	420
gtgtatgaag actccgggcc tgggaggccg ctcagctgct tc	474
	atg gag gaa cca
	Met Glu Glu Pro
	1
gcc cct tac aca gat agc acc ggt gct gct gct gga gga ggg aat tgc	522

Ala	Pro	Tyr	Thr	Asp	Ser	Thr	Gly	Ala	Ala	Ala	Gly	Gly	Gly	Asn	Cys	
5					10					15					20	
agg	ttc	gtg	gag	tcc	cca	agt	caa	gat	caa	aga	ctt	cag	gca	cag	cgg	570
Arg	Phe	Val	Glu	Ser	Pro	Ser	Gln	Asp	Gln	Arg	Leu	Gln	Ala	Gln	Arg	
21					26					31					36	
ctt	cga	aac	cct	gat	gtg	cga	ggt	tca	cta	cag	acg	ccc	cag	aac	cga	618
Leu	Arg	Asn	Pro	Asp	Val	Arg	Gly	Ser	Leu	Gln	Thr	Pro	Gln	Asn	Arg	
37					42					47					52	
cca	cac	ggc	cac	cag	tcc	ccg	gaa	ctg	ccc	gaa	ggc	tac	gaa	caa	aga	666
Pro	His	Gly	His	Gln	Ser	Pro	Glu	Leu	Pro	Glu	Gly	Tyr	Glu	Gln	Arg	
53					58					63					68	
aca	aca	gtc	cag	ggc	caa	gtt	tac	ttt	ttg	cat	aca	cag	act	gga	gtt	714
Thr	Thr	Val	Gln	Gly	Gln	Val	Tyr	Phe	Leu	His	Thr	Gln	Thr	Gly	Val	
69					74					79					84	
agc	acg	tgg	cac	gac	ccc	agg	ata	cca	aga	gac	ctt	aac	agt	gtg	aac	762
Ser	Thr	Trp	His	Asp	Pro	Arg	Ile	Pro	Arg	Asp	Leu	Asn	Ser	Val	Asn	
85					90					95					100	
tgt	gat	gaa	ctt	gga	cca	ctg	ccg	cca	ggc	tgg	gaa	gtc	aga	agt	aca	810
Cys	Asp	Glu	Leu	Gly	Pro	Leu	Pro	Pro	Gly	Trp	Glu	Val	Arg	Ser	Thr	
101					106					111					116	
gtt	tct	ggg	agg	ata	tat	ttt	gta	gat	cat	aat	aac	cga	aca	acc	cag	858
Val	Ser	Gly	Arg	Ile	Tyr	Phe	Val	Asp	His	Asn	Asn	Arg	Thr	Thr	Gln	
117					122					127					132	
ttt	aca	gac	cca	agg	tta	cac	cac	atc	atg	aat	cac	cag	tgc	caa	ctc	906
Phe	Thr	Asp	Pro	Arg	Leu	His	His	Ile	Met	Asn	His	Gln	Cys	Gln	Leu	
133					138					143					148	
aag	gag	ccc	agc	cag	ccg	ctg	cca	ctg	ccc	agt	gag	ggc	tct	ctg	gag	954
Lys	Glu	Pro	Ser	Gln	Pro	Leu	Pro	Leu	Pro	Ser	Glu	Gly	Ser	Leu	Glu	
149					154					159					164	
gac	gag	gag	ctt	cct	gcc	cag	aga	tac	gaa	aga	gat	cta	gtc	cag	aag	1002
Asp	Glu	Glu	Leu	Pro	Ala	Gln	Arg	Tyr	Glu	Arg	Asp	Leu	Val	Gln	Lys	
165					170					175					180	
ctg	aaa	gtc	ctc	aga	cac	gaa	ctg	tcg	ctt	cag	cag	ccc	caa	gct	ggt	1050
Leu	Lys	Val	Leu	Arg	His	Glu	Leu	Ser	Leu	Gln	Gln	Pro	Gln	Ala	Gly	
181					186					191					196	
cat	tgc	cgc	atc	gaa	gtg	tcc	aga	gaa	gaa	atc	ttt	gag	gag	tct	tac	1098
His	Cys	Arg	Ile	Glu	Val	Ser	Arg	Glu	Glu	Ile	Phe	Glu	Glu	Ser	Tyr	
197					202					207					212	
cgc	cag	ata	atg	aag	atg	cga	ccg	aaa	gac	ttg	aaa	aaa	cgg	ctg	atg	1146
Arg	Gln	Ile	Met	Lys	Met	Arg	Pro	Lys	Asp	Leu	Lys	Lys	Arg	Leu	Met	
213					218					223					228	
gtg	aaa	ttc	cgt	ggg	gaa	gaa	ggt	ttg	gat	tac	ggt	ggt	gtg	gcc	agg	1194
Val	Lys	Phe	Arg	Gly	Glu	Glu	Gly	Leu	Asp	Tyr	Gly	Gly	Val	Ala	Arg	

229	234	239	244	
gag tgg ctt tac ttg ctg tgc cat gaa atg ctg aat cct tat tac ggg				1242
Glu Trp Leu Tyr Leu Leu Cys His Glu Met Leu Asn Pro Tyr Tyr Gly				
245	250	255	260	
ctc ttc cag tat tct acg gac aat att tac atg ttg caa ata aat ccg				1290
Leu Phe Gln Tyr Ser Thr Asp Asn Ile Tyr Met Leu Gln Ile Asn Pro				
261	266	271	276	
gat tct tca atc aac ccc gac cac ttg tct tat ttc cac ttt gtg ggg				1338
Asp Ser Ser Ile Asn Pro Asp His Leu Ser Tyr Phe His Phe Val Gly				
277	282	287	292	
cgg atc atg ggg ctg ggc tgt gtt cca tgg aca cta cat caa cgg ggg				1386
Arg Ile Met Gly Leu Gly Cys Val Pro Trp Thr Leu His Gln Arg Gly				
293	298	303	308	
ctt cac agt gcc ctt cta caa gca gct gct ggg gaa gcc cat cca gct				1434
Leu His Ser Ala Leu Leu Gln Ala Ala Ala Gly Glu Ala His Pro Ala				
309	314	319	324	
ctc aga tct gga atc tgt gga ccc aga gct gca taa gagg ttggtgtgga				1484
Leu Arg Ser Gly Ile Cys Gly Pro Arg Ala Ala *				
325	330	335		
tcctagagaa cgacatcacg cctgtactgg accacacctt ctgcgtggaa cacaacgcct				1544
tcggggcggat cctgcagcat gaactgaaac ccaatgggca gaaatgtgcc agtcacagag				1604
gagaataaga aagaatacgt ccggttgtat gtaaactgga ggtttatgag aggaatcgaa				1664
gcccagttct tagctctgca gaaggggttc aatgagctca tccctcaaca tctgctgaag				1724
ccttttgacc agaaggaact ggagctgac ataggcggcc tggataaaat agacttgaac				1784
gactggaagt cgaacacgcg gctgaagcac tgtgtggccg acagcaacat cgtgcggtgg				1844
ttctggcaag cgggtggagac gtctgatgaa gaaaggaggg ccaggctcct gcagtttgtg				1904
actgggtcca cgcgagtccc gctccaaggc ttcaaggctt tgcaagggtc tacaggcgcg				1964
gcagggcccc ggctgttcac catccacctg atagacgcga acacagacaa ccttccgaag				2024
gcccatacct gctttaaccg gatcgacatt ccaccatatg agtcctatga gaagctctac				2084
gagaagctgc tgacagccgt ggaggagacc tgcgggtttg ctgtggagtg aaaagcaacc				2144
aaaggcaaca gagtctagct catggccacc agaccaaag catccagctt ctgtgcacct				2204
cctgcaaagc tggcagaggc cctggaattc cagatcacct gaggggaaag ggttgtctct				2264
ctcctttctg ttgggggagg gggatggggg acttttggtg gtggctcca cccatatatc				2324
cctcctttac catagtactc ccaccactt ccatcaccca tccaataaaa tgcagccagg				2384
tttagccttt ggctttggtc acacagg				2411

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 <213> Homo sapiens

<220>
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<400> 205

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caacctgcct agacacactc agaaccaggt ttaagaagat cattcccatc ccagagcaga      180
gc  atg gtt cag atg gtg tgt cac ctt ctg gaa tgt ctc ctg acc acg      227
    Met Val Gln Met Val Cys His Leu Leu Glu Cys Leu Leu Thr Thr
      1             5             10

gag gac atc cct gca gac tgc cct aag gaa att tat gag cat tat ttt      275
Glu Asp Ile Pro Ala Asp Cys Pro Lys Glu Ile Tyr Glu His Tyr Phe
  16             21             26             31

gtg ttt gct gcc atc tgg gct ttc ggc gga gca atg gtc caa gat cag      323
Val Phe Ala Ala Ile Trp Ala Phe Gly Gly Ala Met Val Gln Asp Gln
  32             37             42             47

ctt gtg gac tac cgg gca gag ttc agc aaa tgg tgg ctg act gag ttc      371
Leu Val Asp Tyr Arg Ala Glu Phe Ser Lys Trp Trp Leu Thr Glu Phe
  48             53             58             63

aaa aca gtc aag ttt cct tcc caa gga acc atc ttt gac tat tac atc      419
Lys Thr Val Lys Phe Pro Ser Gln Gly Thr Ile Phe Asp Tyr Tyr Ile
  64             69             74             79

gac cca gag acc aag aaa ttc gag cct tgg tcc aag ctc gtc ccc cag      467
Asp Pro Glu Thr Lys Lys Phe Glu Pro Trp Ser Lys Leu Val Pro Gln
  80             85             90             95

ttc gaa ttt gac ccc gag atg ccc ttg cag gcg tgt ttg gtg cac acg      515
Phe Glu Phe Asp Pro Glu Met Pro Leu Gln Ala Cys Leu Val His Thr
  96             101            106            111

agt gag acc atc cgt gtg tgc tac ttc atg gag cgg ttg atg gcg cgg      563
Ser Glu Thr Ile Arg Val Cys Tyr Phe Met Glu Arg Leu Met Ala Arg
  112            117            122            127

cag cgg cct gtc atg ctg gtg ggc acg gct ggc act ggc aag tcg gtg      611
Gln Arg Pro Val Met Leu Val Gly Thr Ala Gly Thr Gly Lys Ser Val
  128            133            138            143

ctg gtg gga gct aag ctg gcc agc ctt gac ccc gag gca tac ctg gtg      659

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Leu Val Gly Ala Lys	Leu Ala Ser Leu Asp	Pro Glu Ala Tyr Leu Val	
144	149	154	159
aaa aac gtg cca ttc	aac tac tac acc acg	tca gca atg ctg cag gct	707
Lys Asn Val Pro Phe	Asn Tyr Tyr Thr Thr	Ser Ala Met Leu Gln Ala	
160	165	170	175
gtc ctg gag aag cct	ctg gaa aag aag gct	ggc aga aac tat ggc cct	755
Val Leu Glu Lys Pro	Leu Glu Lys Lys Ala	Gly Arg Asn Tyr Gly Pro	
176	181	186	191
cca ggg aac aag aaa	ctc atc tat ttc att	gat gac atg aac atg cct	803
Pro Gly Asn Lys Lys	Leu Ile Tyr Phe Ile	Asp Asp Met Asn Met Pro	
192	197	202	207
gag gtg gat gcc tac	ggg acg gtg cag ccc	cac acc atc atc cgg cag	851
Glu Val Asp Ala Tyr	Gly Thr Val Gln Pro	His Thr Ile Ile Arg Gln	
208	213	218	223
cat ctg gac tat ggc	cac tgg tat gat cgg	agc aag ctg tcc cta aag	899
His Leu Asp Tyr Gly	His Trp Tyr Asp Arg	Ser Lys Leu Ser Leu Lys	
224	229	234	239
gag atc aca aat gta	cag tat gtt tcc tgt	atg aac ccc acg gca ggc	947
Glu Ile Thr Asn Val	Gln Tyr Val Ser Cys	Met Asn Pro Thr Ala Gly	
240	245	250	255
agc ttc acc atc aac	ccc cgg ctt cag cgt	cac ttc agc gtg ttt gtc	995
Ser Phe Thr Ile Asn	Pro Arg Leu Gln Arg	His Phe Ser Val Phe Val	
256	261	266	271
ctc tcc ttc ccg ggg	gca gat gcc ctg tcc	tct atc tac agc atc atc	1043
Leu Ser Phe Pro Gly	Ala Asp Ala Leu Ser	Ser Ile Tyr Ser Ile Ile	
272	277	282	287
ctc act cag cat ctg	aag ctc gga aac ttc	ccg gcg tcc ctg cag aaa	1091
Leu Thr Gln His Leu	Lys Leu Gly Asn Phe	Pro Ala Ser Leu Gln Lys	
288	293	298	303
tcc atc ccc cca ctg	atc gat ctg gcc ctc	gcc ttc cac cag aaa att	1139
Ser Ile Pro Pro Leu	Ile Asp Leu Ala Leu	Ala Phe His Gln Lys Ile	
304	309	314	319
gct acc acc ttc cta	ccc aca gga atc aaa	ttc cac tac atc ttc aac	1187
Ala Thr Thr Phe Leu	Pro Thr Gly Ile Lys	Phe His Tyr Ile Phe Asn	
320	325	330	335
ctc aga gat ttt gcc	aac att ttc cag ggc	att ctc ttc tcc tca gtg	1235
Leu Arg Asp Phe Ala	Asn Ile Phe Gln Gly	Ile Leu Phe Ser Ser Val	
336	341	346	351
gaa tgt gtg aaa tcc	aca tgg gat ctt ata	agg ctc tat ctg cat gaa	1283
Glu Cys Val Lys Ser	Thr Trp Asp Leu Ile	Arg Leu Tyr Leu His Glu	
352	357	362	367
tca aat cga gtt tat	cgg gat aag atg gta	gaa gaa aag gac ttt gat	1331
Ser Asn Arg Val Tyr	Arg Asp Lys Met Val	Glu Glu Lys Asp Phe Asp	

368	373	378	383	
ctt ttt gat aaa atc cag aca gaa gtg ctc aag aaa act ttt gat gat				1379
Leu Phe Asp Lys Ile Gln Thr Glu Val Leu Lys Lys Thr Phe Asp Asp				
384	389	394	399	
att gaa gac cct gtg gag cag acc caa agc ccg aac ctg tat tgt cac				1427
Ile Glu Asp Pro Val Glu Gln Thr Gln Ser Pro Asn Leu Tyr Cys His				
400	405	410	415	
ttt gca aat ggt att ggg gag ccc aaa tac atg cct gta cag tct tgg				1475
Phe Ala Asn Gly Ile Gly Glu Pro Lys Tyr Met Pro Val Gln Ser Trp				
416	421	426	431	
gaa ctt ttg acc cag act ctg gtg gag gcc ttg gag aac cac aat gaa				1523
Glu Leu Leu Thr Gln Thr Leu Val Glu Ala Leu Glu Asn His Asn Glu				
432	437	442	447	
gtc aac aca gtg atg gac cta gtt ctc ttt gag gat gcc atg cgc cat				1571
Val Asn Thr Val Met Asp Leu Val Leu Phe Glu Asp Ala Met Arg His				
448	453	458	463	
gtc tgc cat atc aat cgc atc ttg gag tcc ccg cgg gga aat gct ctg				1619
Val Cys His Ile Asn Arg Ile Leu Glu Ser Pro Arg Gly Asn Ala Leu				
464	469	474	479	
ctg gtt ggt gta ggt ggg agc ggc aag cag agc ctg aca agg ctg gca				1667
Leu Val Gly Val Gly Gly Ser Gly Lys Gln Ser Leu Thr Arg Leu Ala				
480	485	490	495	
gct ttc atc agc tcc atg gat gtc ttc cag atc aca ctg cgc aaa ggc				1715
Ala Phe Ile Ser Ser Met Asp Val Phe Gln Ile Thr Leu Arg Lys Gly				
496	501	506	511	
tac cag atc cag gac ttc aag atg gac ctg gcc agc ctg tgt ctg aaa				1763
Tyr Gln Ile Gln Asp Phe Lys Met Asp Leu Ala Ser Leu Cys Leu Lys				
512	517	522	527	
gct gga gtg aag aat ctc aac aca gtg ttt ctc atg act gat gcc caa				1811
Ala Gly Val Lys Asn Leu Asn Thr Val Phe Leu Met Thr Asp Ala Gln				
528	533	538	543	
gtg gct gat gag agg ttc ctt gtg ctc atc aat gat ctt ttg gca tct				1859
Val Ala Asp Glu Arg Phe Leu Val Leu Ile Asn Asp Leu Leu Ala Ser				
544	549	554	559	
ggg gag atc cca gat ctc tac tct gat gat gaa gtt gaa aac atc ata				1907
Gly Glu Ile Pro Asp Leu Tyr Ser Asp Asp Glu Val Glu Asn Ile Ile				
560	565	570	575	
agc aat gtg agg aat gaa gtc aag agc cag ggt ctg gtt gac aac aga				1955
Ser Asn Val Arg Asn Glu Val Lys Ser Gln Gly Leu Val Asp Asn Arg				
576	581	586	591	
gag aac tgt tgg aag ttc ttt ata gat cgg atc cgg cga cag ctg aag				2003
Glu Asn Cys Trp Lys Phe Phe Ile Asp Arg Ile Arg Arg Gln Leu Lys				
592	597	602	607	

gtg act ctc tgt ttc tcc cct gtg gga aac aag cta aga gtc cgc agc	2051
Val Thr Leu Cys Phe Ser Pro Val Gly Asn Lys Leu Arg Val Arg Ser	
608 613 618 623	
agg aag ttc cca gcc att gtg aac tgc aca gcc atc cac tgg ttc cac	2099
Arg Lys Phe Pro Ala Ile Val Asn Cys Thr Ala Ile His Trp Phe His	
624 629 634 639	
gag tgg cct cag caa gca ttg gag tct gtc agc ctc cgc ttc ttg cag	2147
Glu Trp Pro Gln Gln Ala Leu Glu Ser Val Ser Leu Arg Phe Leu Gln	
640 645 650 655	
aac aca gag ggc att gag ccc aca gta aag cag tgc att agc aaa ttc	2195
Asn Thr Glu Gly Ile Glu Pro Thr Val Lys Gln Ser Ile Ser Lys Phe	
656 661 666 671	
atg gcc ttt gtc cac aca agt gtc aac caa aca tcc cag tct tat ctg	2243
Met Ala Phe Val His Thr Ser Val Asn Gln Thr Ser Gln Ser Tyr Leu	
672 677 682 687	
agc aat gaa cag cgc tac aac tat aca act ccc aag tcc ttt ctg gag	2291
Ser Asn Glu Gln Arg Tyr Asn Tyr Thr Thr Pro Lys Ser Phe Leu Glu	
688 693 698 703	
ttc atc aga ctc tac cag agc ttg ttg cac agg cac aga aaa gag ctc	2339
Phe Ile Arg Leu Tyr Gln Ser Leu Leu His Arg His Arg Lys Glu Leu	
704 709 714 719	
aag tgc aag aca gag cgg ttg gag aac ggg ctg ctg aag ctg cat agc	2387
Lys Cys Lys Thr Glu Arg Leu Glu Asn Gly Leu Leu Lys Leu His Ser	
720 725 730 735	
acc tct gcc cag gtg gat gat ctg aaa gca aag ctg gct gcc cag gaa	2435
Thr Ser Ala Gln Val Asp Asp Leu Lys Ala Lys Leu Ala Ala Gln Glu	
736 741 746 751	
gta gag ctg aag cag aaa aat gaa gat gca gac aaa ctg att cag gtc	2483
Val Glu Leu Lys Gln Lys Asn Glu Asp Ala Asp Lys Leu Ile Gln Val	
752 757 762 767	
gtg ggt gtg gag act gac aaa gtg agc aga gag aaa gcc atg gca gat	2531
Val Gly Val Glu Thr Asp Lys Val Ser Arg Glu Lys Ala Met Ala Asp	
768 773 778 783	
gaa gag gag cag aag gtg gcc gtc atc atg cta gag gtg aaa cag aag	2579
Glu Glu Glu Gln Lys Val Ala Val Ile Met Leu Glu Val Lys Gln Lys	
784 789 794 799	
cag aag gac tgt gag gag gac ctg gca aag gct gag cca gca ctc aca	2627
Gln Lys Asp Cys Glu Glu Asp Leu Ala Lys Ala Glu Pro Ala Leu Thr	
800 805 810 815	
gca gcg cag gca gct ctc aac acc ctg aac aag acc aac ctg aca gag	2675
Ala Ala Gln Ala Ala Leu Asn Thr Leu Asn Lys Thr Asn Leu Thr Glu	
816 821 826 831	

ctg aag tca ttt ggc tct ccg cct ctg gcc gtc agc aat gtc agc gct	2723
Leu Lys Ser Phe Gly Ser Pro Pro Leu Ala Val Ser Asn Val Ser Ala	
832 837 842 847	
gcg gtg atg gta ctg atg gct ccc agg ggt agg gtg ccc aag gac cgg	2771
Ala Val Met Val Leu Met Ala Pro Arg Gly Arg Val Pro Lys Asp Arg	
848 853 858 863	
agc tgg aag gct gct aag gtc acc atg gcc aaa gtg gat ggc ttc ctg	2819
Ser Trp Lys Ala Ala Lys Val Thr Met Ala Lys Val Asp Gly Phe Leu	
864 869 874 879	
gac tcg cta ata aac ttc aac aaa gag aac att cac gag aac tgc ctc	2867
Asp Ser Leu Ile Asn Phe Asn Lys Glu Asn Ile His Glu Asn Cys Leu	
880 885 890 895	
aaa gcc atc agg ccg tat ctg caa gac ccg gag ttc aat cct gag ttt	2915
Lys Ala Ile Arg Pro Tyr Leu Gln Asp Pro Glu Phe Asn Pro Glu Phe	
896 901 906 911	
gtg gcc acc aaa tcc tat gcg gct gca ggc ctc tgc tcc tgg gtc atc	2963
Val Ala Thr Lys Ser Tyr Ala Ala Ala Gly Leu Cys Ser Trp Val Ile	
912 917 922 927	
aat att gtg aga ttt tat gag gtg ttc tgt gat gtg gaa ccc aag cgc	3011
Asn Ile Val Arg Phe Tyr Glu Val Phe Cys Asp Val Glu Pro Lys Arg	
928 933 938 943	
cag gca ctg aac aaa gcc acc gcg gac ctc aca gct gcc cag gag aag	3059
Gln Ala Leu Asn Lys Ala Thr Ala Asp Leu Thr Ala Ala Gln Glu Lys	
944 949 954 959	
ctg gct gcc atc aaa gcc aag atc gct cac ctt aat gaa aac ctg gca	3107
Leu Ala Ala Ile Lys Ala Lys Ile Ala His Leu Asn Glu Asn Leu Ala	
960 965 970 975	
aag ctc aca gcc agg ttt gag aaa gca aca gca gac aaa ctc aaa tgt	3155
Lys Leu Thr Ala Arg Phe Glu Lys Ala Thr Ala Asp Lys Leu Lys Cys	
976 981 986 991	
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Gln Gln Glu Ala Glu Val Thr Ala Val Thr Ile Ser Leu Ala Asn Arg	
992 997 1002 1007	
ctg gtt gga gga ctc gct tct gaa aac gtg agg tgg gca gat gcc gtg	3251
Leu Val Gly Gly Leu Ala Ser Glu Asn Val Arg Trp Ala Asp Ala Val	
1008 1013 1018 1023	
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Gln Asn Phe Lys Gln Gln Glu Arg Thr Leu Cys Gly Asp Ile Leu Leu	
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Ile Thr Ala Phe Ile Ser Tyr Leu Gly Phe Phe Thr Lys Lys Tyr Arg	
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cag agc ctc ctg gac aga act tgg agg ccc tac ctg agc cag ctg aaa	3395

Gln Ser Leu Leu Asp Arg Thr Trp Arg Pro Tyr Leu Ser Gln Leu Lys	
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act ccc att cca gtc acc cca gcc ctg gat ccc ctg agg atg ctg atg	3443
Thr Pro Ile Pro Val Thr Pro Ala Leu Asp Pro Leu Arg Met Leu Met	
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gat gat gct gac gtg gct gcc tgg cag aac gag ggc ctc cca gcc gac	3491
Asp Asp Ala Asp Val Ala Ala Trp Gln Asn Glu Gly Leu Pro Ala Asp	
1088	1093 1098 1103
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Arg Met Ser Val Glu Asn Ala Thr Ile Leu Ile Asn Cys Glu Arg Trp	
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1168	1173 1178 1183
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Arg Glu Val Ile Lys Lys Gly Arg Phe Ile Lys Ile Gly Asp Lys Glu	
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Cys Glu Tyr Asn Pro Lys Phe Arg Leu Ile Leu His Thr Lys Leu Ala	
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Asn Pro His Tyr Gln Pro Glu Leu Gln Ala Gln Ala Thr Leu Ile Asn	
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1232	1237 1242 1247
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Phe Ile Met Asn Asp Leu Ser Lys Ile His Pro Met Tyr Gln Phe Ser			
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Pro Asp Glu Ser Leu Arg Glu Arg Val Ala Asn Leu Ile Asp Ser Ile			
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Thr Phe Ser Val Tyr Gln Tyr Thr Ile Arg Gly Leu Phe Glu Cys Asp			
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Lys Leu Thr Tyr Leu Ala Gln Leu Thr Phe Gln Ile Leu Leu Met Asn			
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1984	1989 1994 1999
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Ser Asn Glu Gln Arg	Tyr Asn Tyr Thr Thr	Pro Lys Ser Phe Leu	Glu	
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Lys Cys Lys Thr Glu	Arg Leu Glu Asn Gly	Leu Leu Lys Leu His	Ser	
720	725	730	735	
acc tct gcc cag gtg	gat gat ctg aaa gca	aag ctg gct gcc cag	gaa	2435
Thr Ser Ala Gln Val	Asp Asp Leu Lys Ala	Lys Leu Ala Ala Gln	Glu	
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gta gag ctg aag cag	aaa aat gaa gat gca	gac aaa ctg att cag	gtc	2483
Val Glu Leu Lys Gln	Lys Asn Glu Asp Ala	Asp Lys Leu Ile Gln	Val	
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gtg ggt gtg gag act	gac aaa gtg agc aga	gag aaa gcc atg gca	gat	2531
Val Gly Val Glu Thr	Asp Lys Val Ser Arg	Glu Lys Ala Met Ala	Asp	
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Glu Glu Glu Gln Lys	Val Ala Val Ile Met	Leu Glu Val Lys Gln	Lys	
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Gln Lys Asp Cys Glu	Glu Asp Leu Ala Lys	Ala Glu Pro Ala Leu	Thr	
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Ala Ala Gln Ala Ala	Leu Asn Thr Leu Asn	Lys Thr Asn Leu Thr	Glu	
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Leu Lys Ser Phe Gly	Ser Pro Pro Leu Ala	Val Ser Asn Val Ser	Ala	
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Ser Trp Lys Ala Ala	Lys Val Thr Met Ala	Lys Val Asp Gly Phe	Leu	
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Asp Ser Leu Ile Asn	Phe Asn Lys Glu Asn	Ile His Glu Asn Cys	Leu	
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Asn Ile Val Arg Phe Tyr Glu Val Phe Cys Asp Val Glu Pro Lys Arg	
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Lys Leu Thr Ala Arg Phe Glu Lys Ala Thr Ala Asp Lys Leu Lys Cys	
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Met Thr Asn His Gln Lys Lys Arg Ala Ala Glu Met Met Ala Ser Leu	
543 548 553 558	
cta aaa gac ctt gca gaa ata gga att gct gtg gga aat aat gat gta	2149
Leu Lys Asp Leu Ala Glu Ile Gly Ile Ala Val Gly Asn Asn Asp Val	
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Lys Gln Pro Glu Gly Thr Gly Met Ile Asp Glu Glu Phe Thr Val Ala	
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aga ctc tac att agc aaa atg aag tca gaa gta aaa acc atg gtg aaa	2245
Arg Leu Tyr Ile Ser Lys Met Lys Ser Glu Val Lys Thr Met Val Lys	
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Arg Cys Lys Gln Leu Glu Ser Thr Gln Thr Glu Ser Asn Lys Lys Met	
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Glu Glu Asn Glu Lys Glu Leu Ala Ala Cys Gln Leu Arg Ile Ser Gln	
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cat gaa gcc aaa atc aag tca ttg act gaa tac ctt caa aat gtg gaa	2389
His Glu Ala Lys Ile Lys Ser Leu Thr Glu Tyr Leu Gln Asn Val Glu	
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Gln Lys Lys Arg Gln Leu Glu Glu Ser Val Asp Ala Leu Ser Glu Glu	
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cta gtc cag ctt cga gca caa gag aaa gtc cat gaa atg gaa aag gag	2485
Leu Val Gln Leu Arg Ala Gln Glu Lys Val His Glu Met Glu Lys Glu	
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Leu Arg Asp Glu Val Glu Ala Lys Ala Lys Leu Ile Thr Asp Leu Gln	
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Asp Gln Asn Gln Lys Met Met Leu Glu Gln Glu Arg Leu Arg Val Glu	
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Cys Arg Gly Cys Val Asn Phe Glu Gly Ala Asp Arg Ile Glu Leu Leu				
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Ile Asp Ala Ala Arg Gln Leu Lys Arg Ser His Val Leu Pro Glu Gly				
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Arg Ser Pro Gly Pro Pro Ala Leu Lys His Pro Ala Thr Lys Asp Leu				
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Pro Gln Pro Ser Gly Thr Gly Gly Gly Val Ser Gly Gln Asp Arg Tyr				
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Asp Arg Ala Thr Ser Ser Gly Arg Leu Pro Leu Pro Ser Pro Ala Leu				
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ttg atg ccc cct ggg ctg ctg gca gct gca gtg tct ggc ctg gga agc				528
Leu Met Pro Pro Gly Leu Leu Ala Ala Ala Val Ser Gly Leu Gly Ser				
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Arg Gly Leu Thr Leu Ala Pro Gly Leu Ser Pro Ala Arg Pro Leu Phe				
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Gly Ser Asp Phe Glu Lys Glu Lys Gln Gln Arg Asn Ala Asp Cys Leu				
193	198	203	208	
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Ala Glu Leu Asn Glu Ala Met Arg Gly Arg Ala Glu Glu Trp His Gly				
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Pro Phe Asn Val Arg Phe Lys Lys Asp His Gly Leu Val Gly Arg Val				
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Phe Ala Phe Asp Ala Thr Ala Arg Pro Pro Gly Tyr Glu Phe Glu Leu	
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Lys Leu Phe Thr Glu Tyr Pro Cys Gly Ser Gly Asn Val Tyr Ala Gly	
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Val Leu Ala Val Ala Arg Gln Met Phe His Asp Ala Leu Arg Glu Pro	
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Gly Val Arg Ser Phe Arg Glu Pro Ala Pro Ala Glu Ala Leu Pro Gln	
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Tyr Cys Pro Ser Gly Asp Lys Cys Pro Leu Val Gly Ser Ser Val Pro	
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Trp Ala Phe Met Gln Gly Glu Ile Ala Thr Ile Leu Ala Gly Asp Ile	
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Asn Leu Arg Arg His Tyr Gln Thr Asn His Ser Lys His Tyr Asp Gln	
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Tyr Met Glu Arg Met Arg Asp Glu Lys Leu His Glu Leu Lys Lys Gly	
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Leu Arg Lys Tyr Leu Leu Gly Ser Ser Asp Thr Glu Cys Pro Glu Gln	
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Lys Gln Val Phe Ala Asn Pro Ser Pro Thr Gln Lys Ser Pro Val Gln	
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Pro Val Glu Asp Leu Ala Gly Asn Leu Trp Glu Lys Leu Arg Glu Lys	
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Ile Arg Ser Phe Val Ala Tyr Ser Ile Ala Ile Asp Glu Ile Thr Asp	
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Leu Lys Thr Glu Phe Gln Lys Arg Leu Ser Asp Phe Lys Leu Tyr Glu				
462	467	472	477	
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Val His Glu Glu Leu Gln Met Glu Val Ile Asp Leu Gln Cys Asn Thr				
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Thr Leu Asn Pro Thr Ala Lys Arg His Leu Val Leu Ala Cys His Tyr	
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Lys Met Ala Ser Thr Pro His Pro Pro Gly Ala Arg Gly Thr Ser Gln	
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Asn Pro Thr Phe Pro Asn Phe Phe Pro Asn Ser Ala Arg Trp Phe Glu	
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aga ctt caa gca att gaa cat gaa ctt cat gaa ttg ggt ttg ctc aag	866
Arg Leu Gln Ala Ile Glu His Glu Leu His Glu Leu Gly Leu Leu Lys	
270 275 280 285	
gat cac tct ttg gag ggg cgg tat ttc cag aat tac agt tat gga ggt	914
Asp His Ser Leu Glu Gly Arg Tyr Phe Gln Asn Tyr Ser Tyr Gly Gly	
286 291 296 301	
gtg att cag gat gac cat att cca ttt tta aga aga ggt gtt cca gtt	962
Val Ile Gln Asp Asp His Ile Pro Phe Leu Arg Arg Gly Val Pro Val	
302 307 312 317	
ctg cat ctg ata ccg tct cct ttc cct gaa gtc tgg cac acc atg gat	1010
Leu His Leu Ile Pro Ser Pro Phe Pro Glu Val Trp His Thr Met Asp	
318 323 328 333	
gac aat gaa gaa aat ttg gat gaa tca acc att gac aat cta aac aaa	1058
Asp Asn Glu Glu Asn Leu Asp Glu Ser Thr Ile Asp Asn Leu Asn Lys	
334 339 344 349	
atc cta caa gtc ttt gtg ttg gaa tat ctt cat ttg taa tactctgatt	1107
Ile Leu Gln Val Phe Val Leu Glu Tyr Leu His Leu *	
350 355 360	
tagtttagga taattggttc tagaattgaa ttcaaaagtc aaggcatcat ttaaaataat	1167
ctgatttcag acaaatgctg tgtggaaaca tctatcctat agatcatcct attcctatgt	1227
gtcttttggtt atcagatcaa ttacagaata attgtgttgt gatattgtgt cctaaattgc	1287

tcattaatTTT ttatttacag attgaaaaag aggcaccgtg taaagaaaat ggcaaaataa 1347
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 aggtagcctt tcgaatttta tgattttttc atatgtggaa atctattaca tgtaatacaa 1467
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cac ctg ctg ctg ctg gtg gcc gcc ctg ccc tgg gca tcc agg ggg gtc 98
 His Leu Leu Leu Leu Val Ala Ala Leu Pro Trp Ala Ser Arg Gly Val
 14 19 24 29

agt ccg agt gcc tca gcc tgg cca gag gag aag cac atc atg cag cga 146
 Ser Pro Ser Ala Ser Ala Trp Pro Glu Glu Lys His Ile Met Gln Arg
 30 35 40 45

att cag agg ctt cag gct gac tgg gtc ttg gaa ata gac acc ttc ttg 194
 Ile Gln Arg Leu Gln Ala Asp Trp Val Leu Glu Ile Asp Thr Phe Leu
 46 51 56 61

agt cag aca ccc tat ggg tac cgg tct ttc tca aat atc atc agc acc 242
 Ser Gln Thr Pro Tyr Gly Tyr Arg Ser Phe Ser Asn Ile Ile Ser Thr
 62 67 72 77

ctc aat ccc act gct aaa cga cat ttg gtc ctc gcc tgc cac tat gac 290
 Leu Asn Pro Thr Ala Lys Arg His Leu Val Leu Ala Cys His Tyr Asp
 78 83 88 93

tcc aag tat ttt tcc cac tgg aac aac aga gtg ttt gta gga gcc act 338
 Ser Lys Tyr Phe Ser His Trp Asn Asn Arg Val Phe Val Gly Ala Thr
 94 99 104 109

gat tca gcc gtg cca tgt gca atg atg ttg gaa ctt gct cgt gcc tta 386
 Asp Ser Ala Val Pro Cys Ala Met Met Leu Glu Leu Ala Arg Ala Leu
 110 115 120 125

gac aag aaa ctc ctt tcc tta aag act gtt tca gac tcc aag cca gat 434
 Asp Lys Lys Leu Leu Ser Leu Lys Thr Val Ser Asp Ser Lys Pro Asp

126	131	136	141	
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Leu Ser Leu Gln Leu Ile Phe Phe Asp Gly Glu Glu Ala Phe Leu His				
142	147	152	157	
tggt tct cct caa gat tct ctc tat ggg tct cga cac tta gct gca aag				530
Trp Ser Pro Gln Asp Ser Leu Tyr Gly Ser Arg His Leu Ala Ala Lys				
158	163	168	173	
atg gca tgc acc ccg cac cca cct gga gcg aga ggc acc agc caa ctg				578
Met Ala Ser Thr Pro His Pro Pro Gly Ala Arg Gly Thr Ser Gln Leu				
174	179	184	189	
cat ggc atg gat tta ttg gtc tta ttg gat ttg att gga gct cca aac				626
His Gly Met Asp Leu Leu Val Leu Leu Asp Leu Ile Gly Ala Pro Asn				
190	195	200	205	
cca acg ttt ccc aat ttt ttt cca aac tca gcc agg tgg ttc gaa aga				674
Pro Thr Phe Pro Asn Phe Phe Pro Asn Ser Ala Arg Trp Phe Glu Arg				
206	211	216	221	
ctt caa gca att gaa cat gaa ctt cat gaa ttg ggt ttg ctc aag gat				722
Leu Gln Ala Ile Glu His Glu Leu His Glu Leu Gly Leu Leu Lys Asp				
222	227	232	237	
cac tct ttg gag ggg cgg tat ttc cag aat tac agt tat gga ggt gtg				770
His Ser Leu Glu Gly Arg Tyr Phe Gln Asn Tyr Ser Tyr Gly Gly Val				
238	243	248	253	
att cag gat gac cat att cca ttt tta aga aga ggt gtt cca gtt ctg				818
Ile Gln Asp Asp His Ile Pro Phe Leu Arg Arg Gly Val Pro Val Leu				
254	259	264	269	
cat ctg ata ccg tct cct ttc cct gaa gtc tgg cac acc atg gat gac				866
His Leu Ile Pro Ser Pro Phe Pro Glu Val Trp His Thr Met Asp Asp				
270	275	280	285	
aat gaa gaa aat ttg gat gaa tca acc att gac aat cta aac aaa atc				914
Asn Glu Glu Asn Leu Asp Glu Ser Thr Ile Asp Asn Leu Asn Lys Ile				
286	291	296	301	
cta caa gtc ttt gtg ttg gaa tat ctt cat ttg taa tact ctgatttagt				964
Leu Gln Val Phe Val Leu Glu Tyr Leu His Leu *				
302	307	312		
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tttcagacaa atgctgtgtg gaaacatcta tcctatagat catcctattc ttatgtgtct				1084
ttggttatca gatcaattac agaataattg tggtgtgata ttgtgtccta aattgctcat				1144
taatttttat ttacagattg aaaaagaggc accgtgtaaa gaaaatggca aaataaatat				1204
ctttccaagg atcatcatca cgatagctaa acagtactta aatagcggtt ggaactaggt				1264
agccttttoga attttatgat tttttcatat gtggaaatct attacatgta atacaaaaca				1324

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acc atg tcg agc aaa aga aca aag acc aag acc aag aag cgc cct cag 168
Met Ser Ser Lys Arg Thr Lys Thr Lys Thr Lys Lys Arg Pro Gln
1 5 10
cgt gca aca tcc aat gtg ttt gct atg ttt gac cag tca cag att cag 216
Arg Ala Thr Ser Asn Val Phe Ala Met Phe Asp Gln Ser Gln Ile Gln
16 21 26 31
gag ttc aaa gag gcc ttc aac atg att gat cag aac aga gat ggt ttc 264
Glu Phe Lys Glu Ala Phe Asn Met Ile Asp Gln Asn Arg Asp Gly Phe
32 37 42 47
atc gac aag gaa gat ttg cat gat atg ctt gct tca ttg ggg aag aat 312
Ile Asp Lys Glu Asp Leu His Asp Met Leu Ala Ser Leu Gly Lys Asn
48 53 58 63
cca act gat gag tat cta gat gcc atg atg aat gag gct cca ggc ccc 360
Pro Thr Asp Glu Tyr Leu Asp Ala Met Met Asn Glu Ala Pro Gly Pro
64 69 74 79
atc aat ttc acc atg ttc ctc acc atg ttt ggt gag aag tta aat ggc 408
Ile Asn Phe Thr Met Phe Leu Thr Met Phe Gly Glu Lys Leu Asn Gly
80 85 90 95
aca gat cct gaa gat gtc atc aga aat gcc ttt gct tgc ttt gat gaa 456
Thr Asp Pro Glu Asp Val Ile Arg Asn Ala Phe Ala Cys Phe Asp Glu
96 101 106 111
gaa gca act ggc acc ata cag gaa gat tac ttg aga gag ctg ctg aca 504
Glu Ala Thr Gly Thr Ile Gln Glu Asp Tyr Leu Arg Glu Leu Leu Thr
112 117 122 127
acc atg ggg gat cgg ttt aca gat gag gaa gtg gat gag ctg tac aga 552
Thr Met Gly Asp Arg Phe Thr Asp Glu Glu Val Asp Glu Leu Tyr Arg
128 133 138 143

gaa gca cct att gat aaa aag ggg aat ttc aat tac atc gag ttc aca	600
Glu Ala Pro Ile Asp Lys Lys Gly Asn Phe Asn Tyr Ile Glu Phe Thr	
144 149 154 159	
cgc atc ctg aaa cat gga gcc aaa gac aaa gat gac tga aataacttca	649
Arg Ile Leu Lys His Gly Ala Lys Asp Lys Asp Asp *	
160 165 170	
aattccagcc aaacgttcct tgttgccact ttgggtattc tgagattttc tcttgcacgc	709
ccttagcttt acagcttttg catttcctgt tgtattttatt ctcagccatt ttgggcatat	769
gtatctttat aatcagactg gaaacgggac tttctattaa tatcattttc agaataaaaa	829
atagggtaat ttaacctacc agcccttctc cccaataac tgtgggtctat acagagtcaa	889
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ctc tct acc tat cgg ctc cag agc cgc agt cgt cct tcc gcc cca gag	96
Leu Ser Thr Tyr Arg Leu Gln Ser Arg Ser Arg Pro Ser Ala Pro Glu	
17 22 27 32	
acc gat gat agt cga gtt ggg ggc att atg aga gga gag aaa aac tac	144
Thr Asp Asp Ser Arg Val Gly Gly Ile Met Arg Gly Glu Lys Asn Tyr	
33 38 43 48	
tac ttc cgt gga gct gcg ggg gac cac ggt tcc tgc ccc act aca act	192
Tyr Phe Arg Gly Ala Ala Gly Asp His Gly Ser Cys Pro Thr Thr Thr	
49 54 59 64	
tcg cct ctg gcc tcg gcc ctc ttg atg ccc tcg gag gca gtc tca agc	240
Ser Pro Leu Ala Ser Ala Leu Leu Met Pro Ser Glu Ala Val Ser Ser	
65 70 75 80	
agc tgg tct gag tct gga ggc ggt ttg tca ggg gga gat gaa gag gac	288
Ser Trp Ser Glu Ser Gly Gly Gly Leu Ser Gly Gly Asp Glu Glu Asp	
81 86 91 96	

act cgg ctc ctt caa ctc ctc cgc act gcc cgg gat cct tct gag gcc	336
Thr Arg Leu Leu Gln Leu Leu Arg Thr Ala Arg Asp Pro Ser Glu Ala	
97 102 107 112	
ttc cag gct ttg caa gct gct ttg ccg cgg cgg ggc ggt cga ctt ggc	384
Phe Gln Ala Leu Gln Ala Ala Leu Pro Arg Arg Gly Gly Arg Leu Gly	
113 118 123 128	
ttc ccc cga cgc aag gaa gct ttg tat cgg gca ctg ggc cga gtg ctt	432
Phe Pro Arg Arg Lys Glu Ala Leu Tyr Arg Ala Leu Gly Arg Val Leu	
129 134 139 144	
gtg gaa gga ggt agt gat gag aag cgg ctc tgc ttg caa ctt ctc tcg	480
Val Glu Gly Gly Ser Asp Glu Lys Arg Leu Cys Leu Gln Leu Leu Ser	
145 150 155 160	
gac gtt ctc cgg ggt cag ggg gag gca ggc cag ctt gaa gag gcc ttt	528
Asp Val Leu Arg Gly Gln Gly Glu Ala Gly Gln Leu Glu Glu Ala Phe	
161 166 171 176	
agc tta gca ctt ttg cct caa cta gtt gtc tcg tta cgg gaa gag aat	576
Ser Leu Ala Leu Leu Pro Gln Leu Val Val Ser Leu Arg Glu Glu Asn	
177 182 187 192	
cca gcc ctg cgg aaa gat gcg ctg cag atc ctt cat ata tgt ctg aaa	624
Pro Ala Leu Arg Lys Asp Ala Leu Gln Ile Leu His Ile Cys Leu Lys	
193 198 203 208	
cgt agt cct gga gag gtg ctg aga acg ctt ata caa caa gga ctg gaa	672
Arg Ser Pro Gly Glu Val Leu Arg Thr Leu Ile Gln Gln Gly Leu Glu	
209 214 219 224	
agt acc gat gcc cga ctt aga gct tcc aca gca cta ctg ctt ccc atc	720
Ser Thr Asp Ala Arg Leu Arg Ala Ser Thr Ala Leu Leu Leu Pro Ile	
225 230 235 240	
ttg ctt act act gag gac ttg ttg ctt ggt ctg gat ctc acc gag gtg	768
Leu Leu Thr Thr Glu Asp Leu Leu Leu Gly Leu Asp Leu Thr Glu Val	
241 246 251 256	
ata ata tcc cta gcc cga aag ctt ggt gat cag gag aca gaa gaa gaa	816
Ile Ile Ser Leu Ala Arg Lys Leu Gly Asp Gln Glu Thr Glu Glu Glu	
257 262 267 272	
tct gag aca gct ttc tcc gca ctt caa caa att ggg gag cga ctt ggc	864
Ser Glu Thr Ala Phe Ser Ala Leu Gln Gln Ile Gly Glu Arg Leu Gly	
273 278 283 288	
caa gac agg ttt caa tct tac att tct cgt ctg ccc tct gcc ctg agg	912
Gln Asp Arg Phe Gln Ser Tyr Ile Ser Arg Leu Pro Ser Ala Leu Arg	
289 294 299 304	
aga cac tac aat cgc cgc ctg gag tcc cag ttt gga agt cag gtt cct	960
Arg His Tyr Asn Arg Arg Leu Glu Ser Gln Phe Gly Ser Gln Val Pro	
305 310 315 320	

tat tat ttg gaa ctt gaa gcc tct gga ttt cct gaa gat ccc ctt ccc	1008
Tyr Tyr Leu Glu Leu Glu Ala Ser Gly Phe Pro Glu Asp Pro Leu Pro	
321 326 331 336	
tggt gca gtg act ctt tcc aac agc aat ctt aaa ttt ggg att att cct	1056
Cys Ala Val Thr Leu Ser Asn Ser Asn Leu Lys Phe Gly Ile Ile Pro	
337 342 347 352	
cag gag ctg cat tca cga tta ttg gat cag gaa gac tat aag aac cgg	1104
Gln Glu Leu His Ser Arg Leu Leu Asp Gln Glu Asp Tyr Lys Asn Arg	
353 358 363 368	
acc cag gcc gtc gaa gaa cta aag cag gtg ctg gga aaa ttt aac cct	1152
Thr Gln Ala Val Glu Glu Leu Lys Gln Val Leu Gly Lys Phe Asn Pro	
369 374 379 384	
agt tct act cct cat tct agt ctt gtt ggc ttc att agt ttg cta tat	1200
Ser Ser Thr Pro His Ser Ser Leu Val Gly Phe Ile Ser Leu Leu Tyr	
385 390 395 400	
aat ttg tta gac gat tct aac ttc aaa gtg gtg cat ggc aca ctt gaa	1248
Asn Leu Leu Asp Asp Ser Asn Phe Lys Val Val His Gly Thr Leu Glu	
401 406 411 416	
gtc ctg cat tta ctg gtt att cgc ctt gga gag cag gta cag cag ttc	1296
Val Leu His Leu Leu Val Ile Arg Leu Gly Glu Gln Val Gln Gln Phe	
417 422 427 432	
ttg gga cca gtt ata gca gct tct gtc aaa gtg ctg gcg gac aac aag	1344
Leu Gly Pro Val Ile Ala Ala Ser Val Lys Val Leu Ala Asp Asn Lys	
433 438 443 448	
ttg gtg atc aaa caa gaa tac atg aaa atc ttc ctc aag cta atg aag	1392
Leu Val Ile Lys Gln Glu Tyr Met Lys Ile Phe Leu Lys Leu Met Lys	
449 454 459 464	
gaa gta gga cct cag cag gtg ctt tgt tta ctc ctg gaa cat ctc aaa	1440
Glu Val Gly Pro Gln Gln Val Leu Cys Leu Leu Leu Glu His Leu Lys	
465 470 475 480	
cat aag cat tcc aga gtg aga gag gag gtg gtg aac att tgc atc tgc	1488
His Lys His Ser Arg Val Arg Glu Glu Val Val Asn Ile Cys Ile Cys	
481 486 491 496	
tcc ctg ctg acc tat cct agt gag gat ttt gac ttg ccc aaa ctg tcc	1536
Ser Leu Leu Thr Tyr Pro Ser Glu Asp Phe Asp Leu Pro Lys Leu Ser	
497 502 507 512	
ttt gat ctt gcc cca gct ctt gta gat agc aaa cgc agg gta cgc caa	1584
Phe Asp Leu Ala Pro Ala Leu Val Asp Ser Lys Arg Arg Val Arg Gln	
513 518 523 528	
gca gct tta gaa gct ttt gcc gta ttg gca tca tca atg ggc tca ggt	1632
Ala Ala Leu Glu Ala Phe Ala Val Leu Ala Ser Ser Met Gly Ser Gly	
529 534 539 544	
aaa acc agc atc ctt ttt aaa gct gtg gat aca gtt gaa ctg caa gat	1680

Lys	Thr	Ser	Ile	Leu	Phe	Lys	Ala	Val	Asp	Thr	Val	Glu	Leu	Gln	Asp	
545					550					555					560	
aat	gga	gat	gga	gtg	atg	aat	gct	gtg	cag	gcc	aga	ttg	gct	agg	aaa	1728
Asn	Gly	Asp	Gly	Val	Met	Asn	Ala	Val	Gln	Ala	Arg	Leu	Ala	Arg	Lys	
561					566					571					576	
acc	tta	cca	agg	ctc	aca	gag	cag	gga	ttt	gtg	gaa	tat	gca	gta	ctg	1776
Thr	Leu	Pro	Arg	Leu	Thr	Glu	Gln	Gly	Phe	Val	Glu	Tyr	Ala	Val	Leu	
577					582					587					592	
atg	cca	tct	tct	gcc	ggg	ggt	agg	tca	aac	cat	ttg	gca	cat	gga	gca	1824
Met	Pro	Ser	Ser	Ala	Gly	Gly	Arg	Ser	Asn	His	Leu	Ala	His	Gly	Ala	
593					598					603					608	
gat	acg	gac	tgg	ctt	ttg	gct	ggt	aac	aga	act	cag	agt	gca	cac	tgt	1872
Asp	Thr	Asp	Trp	Leu	Leu	Ala	Gly	Asn	Arg	Thr	Gln	Ser	Ala	His	Cys	
609					614					619					624	
cac	tgt	ggt	gac	cac	gtg	agg	gat	agc	atg	cac	att	tat	gga	tct	tac	1920
His	Cys	Gly	Asp	His	Val	Arg	Asp	Ser	Met	His	Ile	Tyr	Gly	Ser	Tyr	
625					630					635					640	
agc	cca	act	atc	tgt	acc	cga	agg	gta	tta	agt	gca	gga	aaa	gga	aaa	1968
Ser	Pro	Thr	Ile	Cys	Thr	Arg	Arg	Val	Leu	Ser	Ala	Gly	Lys	Gly	Lys	
641					646					651					656	
aat	aaa	tta	cca	tgg	gaa	aat	gag	caa	cct	gga	atc	atg	gga	gaa	aac	2016
Asn	Lys	Leu	Pro	Trp	Glu	Asn	Glu	Gln	Pro	Gly	Ile	Met	Gly	Glu	Asn	
657					662					667					672	
cag	acc	tcc	act	tcc	aag	gat	ata	gag	cag	ttt	tca	aca	tat	gat	ttc	2064
Gln	Thr	Ser	Thr	Ser	Lys	Asp	Ile	Glu	Gln	Phe	Ser	Thr	Tyr	Asp	Phe	
673					678					683					688	
atc	cca	tct	gca	aaa	tta	aag	ctt	tct	caa	gga	atg	cca	gtc	aat	gat	2112
Ile	Pro	Ser	Ala	Lys	Leu	Lys	Leu	Ser	Gln	Gly	Met	Pro	Val	Asn	Asp	
689					694					699					704	
gat	tta	tgt	ttt	agc	aga	aaa	aga	gta	tca	aga	aac	tta	ttt	cag	aat	2160
Asp	Leu	Cys	Phe	Ser	Arg	Lys	Arg	Val	Ser	Arg	Asn	Leu	Phe	Gln	Asn	
705					710					715					720	
agt	cgg	gat	ttt	aac	cca	gat	tgt	ctt	cct	tta	tgt	gct	gct	ggt	act	2208
Ser	Arg	Asp	Phe	Asn	Pro	Asp	Cys	Leu	Pro	Leu	Cys	Ala	Ala	Gly	Thr	
721					726					731					736	
act	ggg	act	cat	caa	aca	aat	ctt	tct	ggg	aaa	tgt	gca	caa	ctt	gga	2256
Thr	Gly	Thr	His	Gln	Thr	Asn	Leu	Ser	Gly	Lys	Cys	Ala	Gln	Leu	Gly	
737					742					747					752	
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Phe	Ser	Gln	Ile	Cys	Gly	Lys	Thr	Gly	Ser	Val	Gly	Ser	Asp	Leu	Gln	
753					758					763					768	
ttc	cta	ggg	aca	act	agc	agt	cat	caa	gaa	aaa	gtg	tat	gct	agc	ctc	2352
Phe	Leu	Gly	Thr	Thr	Ser	Ser	His	Gln	Glu	Lys	Val	Tyr	Ala	Ser	Leu	

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Asn Phe Gly Ser Lys	Thr Gln Gln Thr Phe	Gly Ser Gln Thr Glu Cys		
785	790	795	800	
act tcc tca aat ggt	caa aat cca agt cca	gga gct tac atc ctt cca		2448
Thr Ser Ser Asn Gly	Gln Asn Pro Ser Pro	Gly Ala Tyr Ile Leu Pro		
801	806	811	816	
tcc tat cct gtc tca	tca cct cga act agt	cca aag cat aca tct cct		2496
Ser Tyr Pro Val Ser	Ser Pro Arg Thr Ser	Pro Lys His Thr Ser Pro		
817	822	827	832	
ctt att ata tct cca	aag aag tct caa gat	aat tct gtt aat ttc tca		2544
Leu Ile Ile Ser Pro	Lys Lys Ser Gln Asp	Asn Ser Val Asn Phe Ser		
833	838	843	848	
aat tcc tgg cct ctt	aaa agc ttc gaa gga	cta tca aag cca agt cca		2592
Asn Ser Trp Pro Leu	Lys Ser Phe Glu Gly	Leu Ser Lys Pro Ser Pro		
849	854	859	864	
cag aag aag ctt gtc	agc caa aaa tcg tct	gat cct acg ggt aga aat		2640
Gln Lys Lys Leu Val	Ser Gln Lys Ser Ser	Asp Pro Thr Gly Arg Asn		
865	870	875	880	
cat gga gaa aat tct	caa gaa aaa cct cca	gtt cag ctt aca cct gcc		2688
His Gly Glu Asn Ser	Gln Glu Lys Pro Pro	Val Gln Leu Thr Pro Ala		
881	886	891	896	
ttg gtg aga tcg cca	tct tcc cga cga ggt	cta aat ggg aca aag cct		2736
Leu Val Arg Ser Pro	Ser Ser Arg Arg Gly	Leu Asn Gly Thr Lys Pro		
897	902	907	912	
gtt cct ccc ata cca	agg gga ata agc ctt	ttg cct gat aaa gct gat		2784
Val Pro Pro Ile Pro	Arg Gly Ile Ser Leu	Leu Pro Asp Lys Ala Asp		
913	918	923	928	
tta agc aca gtg gga	cac aaa aag aaa gag	cct gat gat att tgg aag		2832
Leu Ser Thr Val Gly	His Lys Lys Lys Glu	Pro Asp Asp Ile Trp Lys		
929	934	939	944	
tgt gaa aaa gat agt	ctt cca att gat ctt	tca gaa tta aat ttc aag		2880
Cys Glu Lys Asp Ser	Leu Pro Ile Asp Leu	Ser Glu Leu Asn Phe Lys		
945	950	955	960	
gat aaa gat ttg gat	caa gaa gag atg cat	agc tct ctt agg tcc ctt		2928
Asp Lys Asp Leu Asp	Gln Glu Glu Met His	Ser Ser Leu Arg Ser Leu		
961	966	971	976	
cgt aat agt gca gct	aag aaa aga gca aaa	ctg agt ggc agt act tca		2976
Arg Asn Ser Ala Ala	Lys Lys Arg Ala Lys	Leu Ser Gly Ser Thr Ser		
977	982	987	992	
gat ctt gaa agc cct	gat tct gca atg aag	ctc gac ttg acg atg gac		3024
Asp Leu Glu Ser Pro	Asp Ser Ala Met Lys	Leu Asp Leu Thr Met Asp		
993	998	1003	1008	

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Ala Ala Ser Gln Pro Pro His Ile Lys Lys Ser Leu Glu Glu Leu Leu				
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Asp Met Thr Ile Leu Asn Glu Leu *				
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 aatatttagc catttaccta aaa atg gta ttt ttt aca tgc aat gca tgt 530
 Met Val Phe Phe Thr Cys Asn Ala Cys
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 Gly Glu Ser Val Lys Lys Ile Gln Val Glu Lys His Val Ser Val Cys
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 Arg Asn Cys Glu Cys Leu Ser Cys Ile Asp Cys Gly Lys Asp Phe Trp
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 Gly Asp Asp Tyr Lys Asn His Val Lys Cys Ile Ser Glu Asp Gln Lys
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 tat ggt ggc aaa ggc tat gaa ggt aaa acc cac aaa ggc gac atc aaa 722
 Tyr Gly Gly Lys Gly Tyr Glu Gly Lys Thr His Lys Gly Asp Ile Lys
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 Val Ser Pro Lys Val Arg Glu Leu Leu Glu Gln Ile Ser Ala Phe Asp
 90 95 100 105
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 Pro Leu His Pro Val Ala Asn Pro His Ala Glu Ile Ser Thr Lys Val
 154 159 164 169
 cca gcc tcc aaa gtg aaa gac gcc gtg gaa cag caa ggg gag gtg aag 1058

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Lys	Lys	Lys	Lys	Gln	Arg	Lys	Asp	Ser	Ala	Ser	Glu	Glu	Glu	Ala	Arg	
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Ser	Lys	Lys	Lys	Lys	Met	Lys	Leu	Pro	Glu	His	Pro	Glu	Gly	Gly	Glu	
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Pro	Glu	Asp	Asp	Glu	Ala	Pro	Ala	Lys	Asp	Pro	Trp	Gln	Met	Leu	Leu	
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Ile	Lys	Cys	Ser	Ile	Tyr	Phe	Pro	Leu	Thr	Ala	Arg	Trp	Lys	Pro	Gln	
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aat	cct	gaa	gag	cac	cgg	aaa	atc	act	gcc	agt	tga					1526
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Met Ser Asp Ser Gly Ala Ser Arg Leu Arg Arg Gln Leu Glu Ser Gly
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Gly Phe Glu Ala Arg Leu Tyr Val Lys Gln Leu Ser Gln Gln Ser Asp
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Gly Asp Arg Asp Leu Gln Glu His Arg Gln Arg Ile Gln Ala Leu Ala
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gag gag acg gcg cag aac ctg aag cgc aac gtc tac cag aac tac cgg      305
Glu Glu Thr Ala Gln Asn Leu Lys Arg Asn Val Tyr Gln Asn Tyr Arg
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cag ttc ata gag acg gcc cgc gag atc tcc tac ctg gag agc gag atg      353
Gln Phe Ile Glu Thr Ala Arg Glu Ile Ser Tyr Leu Glu Ser Glu Met
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tac cag ctc agc cat ttg ctg acc gag cag aaa agc agc ctg gag agc      401
Tyr Gln Leu Ser His Leu Leu Thr Glu Gln Lys Ser Ser Leu Glu Ser
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atc ccg ctt acg ttg ctg cct gcc gct gct gcc gcc gga gcc gcc gcc      449
Ile Pro Leu Thr Leu Leu Pro Ala Ala Ala Ala Ala Gly Ala Ala Ala
 101                106                111                116

gcc tct gga ggg gag gag gga gtc ggt ggg gcg ggg ggc cga gac cac      497
Ala Ser Gly Gly Glu Glu Gly Val Gly Gly Ala Gly Gly Arg Asp His
 117                122                127                132

ctc cga ggc cag gcc ggc ttt ttc tcc acc ccc ggg ggt gcc tcc cgc      545
Leu Arg Gly Gln Ala Gly Phe Phe Ser Thr Pro Gly Gly Ala Ser Arg
 133                138                143                148

gac ggc tcc ggt cca ggc gag gaa gga aag cag cgc act ctc acc acc      593
Asp Gly Ser Gly Pro Gly Glu Glu Gly Lys Gln Arg Thr Leu Thr Thr
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ctg ctt gag aag gtg gaa ggc tgc agg cat ctg ctg gag acg ccg gga      641
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Met Ala Gln Leu Gln Arg Val His Gly Phe Leu Met Asn Asp Cys Leu				
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Leu Val Ala Thr Trp Leu Pro Gln Arg Arg Gly Met Tyr Arg Tyr Asn				
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Ala Leu Tyr Ser Leu Asp Gly Leu Ala Val Val Asn Val Lys Asp Asn				
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357	362	367	372	
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373	378	383	388	
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Gln Leu Thr Glu Val Leu Val Phe Glu Leu Ser Pro Asp Arg Ser Leu				
389	394	399	404	

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Thr Ala Ala Glu Cys Val Lys Val Ala Lys Glu His Cys Gln Gln Leu	
517 522 527 532	
ggt gat atc gga ctg gat ctc acc ttc atc atc cat gcc ctt ctg gtg	1745
Gly Asp Ile Gly Leu Asp Leu Thr Phe Ile Ile His Ala Leu Leu Val	
533 538 543 548	
aaa gac atc caa ggg gcc ttg cac agt tac aaa gaa atc atc att gaa	1793
Lys Asp Ile Gln Gly Ala Leu His Ser Tyr Lys Glu Ile Ile Ile Glu	
549 554 559 564	
gcc act aaa cat cgc aac tct gaa gag atg tgg agg agg atg aac ttg	1841
Ala Thr Lys His Arg Asn Ser Glu Glu Met Trp Arg Arg Met Asn Leu	
565 570 575 580	
atg acg cca gaa gcc ctg ggt aag ctc aaa gaa gag atg aaa agt tgt	1889
Met Thr Pro Glu Ala Leu Gly Lys Leu Lys Glu Glu Met Lys Ser Cys	
581 586 591 596	
ggg gta agt aac ttt gag cag tac aca ggg gat gac tgc tgg gtg aac	1937
Gly Val Ser Asn Phe Glu Gln Tyr Thr Gly Asp Asp Cys Trp Val Asn	
597 602 607 612	
cta agt tac aca gtg gtt gct ttc acc aaa cag acc atg ggc ttc ttg	1985
Leu Ser Tyr Thr Val Val Ala Phe Thr Lys Gln Thr Met Gly Phe Leu	
613 618 623 628	

gaa gag gcc ctg aag ctg tat ttc cca gag ctg cac atg gta ctt ttg	2033
Glu Glu Ala Leu Lys Leu Tyr Phe Pro Glu Leu His Met Val Leu Leu	
629 634 639 644	
 gag agc ctg gtg gaa atc att ttg gtt gct gtt cag cat gtg gat tat	2081
Glu Ser Leu Val Glu Ile Ile Leu Val Ala Val Gln His Val Asp Tyr	
645 650 655 660	
 agt ctt cga tgt gag cag gat cca gag aag aaa gct ttt atc aga cag	2129
Ser Leu Arg Cys Glu Gln Asp Pro Glu Lys Lys Ala Phe Ile Arg Gln	
661 666 671 676	
 aat gca tcc ttt tta tat gaa aca gtc ctc cct gtg gtg gag aaa agg	2177
Asn Ala Ser Phe Leu Tyr Glu Thr Val Leu Pro Val Val Glu Lys Arg	
677 682 687 692	
 ttt gaa gaa ggt gtg ggg aaa cct gcc aag caa ctc caa gat ctg agg	2225
Phe Glu Glu Gly Val Gly Lys Pro Ala Lys Gln Leu Gln Asp Leu Arg	
693 698 703 708	
 aat gca tct aga ctt att cgt gtg aat cct gaa agt aca aca tca gtg	2273
Asn Ala Ser Arg Leu Ile Arg Val Asn Pro Glu Ser Thr Thr Ser Val	
709 714 719 724	
 gtc taa tgcttgggtc tgttttatatg tgtatatatg cagagagctt tatattattt	2329
Val *	
725	
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agtgcctct taaaaataca aaaaaaaaaa a	2420

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Met Glu Asp Gly Val Leu Lys Glu Gly Phe Leu Val Lys Arg	
1 5 10	
 ggc cac att gtc cac aac tgg aag gcg cga tgg ttc atc ctt cgg cag	157
Gly His Ile Val His Asn Trp Lys Ala Arg Trp Phe Ile Leu Arg Gln	
15 20 25 30	
 aac acg ctg gtg tac tac aag ctt gag ggg ggt cgg aga gtg acc cct	205
Asn Thr Leu Val Tyr Tyr Lys Leu Glu Gly Gly Arg Arg Val Thr Pro	

31	36	41	46	
ccc aag ggc cgg atc ctc ctg gat ggc tgc acc atc acc tgc ccc tgc				253
Pro Lys Gly Arg Ile Leu Leu Asp Gly Cys Thr Ile Thr Cys Pro Cys				
47	52	57	62	
ctg gag tat gaa aac cga ccg ctc ctc att aag ctg aag act caa aca				301
Leu Glu Tyr Glu Asn Arg Pro Leu Leu Ile Lys Leu Lys Thr Gln Thr				
63	68	73	78	
tcc acg gag tac ttc ctg gag gcc tgt tct cga gag gag cgg gat gcc				349
Ser Thr Glu Tyr Phe Leu Glu Ala Cys Ser Arg Glu Glu Arg Asp Ala				
79	84	89	94	
tgg gcc ttt gag atc acc ggg gct att cat gca ggg cag ccg ggg aag				397
Trp Ala Phe Glu Ile Thr Gly Ala Ile His Ala Gly Gln Pro Gly Lys				
95	100	105	110	
gtc cag cag ctg cac agc ctg aga aac tcc ttc aag ctg ccc ccg cac				445
Val Gln Gln Leu His Ser Leu Arg Asn Ser Phe Lys Leu Pro Pro His				
111	116	121	126	
atc agc ctg cat cgc att gtg gac aag atg cac gat agc aac acc gga				493
Ile Ser Leu His Arg Ile Val Asp Lys Met His Asp Ser Asn Thr Gly				
127	132	137	142	
atc cgt tca agc ccc aac atg gag cag gga agc acc tat aaa aag acc				541
Ile Arg Ser Ser Pro Asn Met Glu Gln Gly Ser Thr Tyr Lys Lys Thr				
143	148	153	158	
ttc ctc ggc tcc tcc ctg gtg gac tgg ctc atc tcc aac agc ttc acg				589
Phe Leu Gly Ser Ser Leu Val Asp Trp Leu Ile Ser Asn Ser Phe Thr				
159	164	169	174	
gcc agc cgt ctg gag gcg gtg acc ctg gcc tcc atg ctc atg gag gag				637
Ala Ser Arg Leu Glu Ala Val Thr Leu Ala Ser Met Leu Met Glu Glu				
175	180	185	190	
aac ttc ctc agg cct gtg ggt gtc cga agc atg gga gcc att cgc tct				685
Asn Phe Leu Arg Pro Val Gly Val Arg Ser Met Gly Ala Ile Arg Ser				
191	196	201	206	
ggg gat ctg gcc gag cag ttc ctg gat gac tcc aca gcc ctg tac act				733
Gly Asp Leu Ala Glu Gln Phe Leu Asp Asp Ser Thr Ala Leu Tyr Thr				
207	212	217	222	
ttt gct gag agc tac aaa aag aag ata agc ccc aag gaa gaa att agc				781
Phe Ala Glu Ser Tyr Lys Lys Lys Ile Ser Pro Lys Glu Glu Ile Ser				
223	228	233	238	
ctg agc act gtg gag tta agt ggc acg gtg gtg aaa caa ggc tac ctg				829
Leu Ser Thr Val Glu Leu Ser Gly Thr Val Val Lys Gln Gly Tyr Leu				
239	244	249	254	
gcc aag cag gga cac aag agg aaa aac tgg aag gtg cgt cgc ttt gtt				877
Ala Lys Gln Gly His Lys Arg Lys Asn Trp Lys Val Arg Arg Phe Val				
255	260	265	270	

cta agg aag gat cca gct ttc ctg cat tac tat gac cct tcc aaa gaa	925
Leu Arg Lys Asp Pro Ala Phe Leu His Tyr Tyr Asp Pro Ser Lys Glu	
271 276 281 286	
gag aac agg cca gtg ggt ggg ttt tct ctt cgt ggt tca ctc gtg tct	973
Glu Asn Arg Pro Val Gly Gly Phe Ser Leu Arg Gly Ser Leu Val Ser	
287 292 297 302	
gct ctg gaa gat aat ggc gtt ccc act ggg gtt aaa ggg aat gtc cag	1021
Ala Leu Glu Asp Asn Gly Val Pro Thr Gly Val Lys Gly Asn Val Gln	
303 308 313 318	
gga aac ctc ttc aaa gtg att act aag gat gac aca cac tat tac att	1069
Gly Asn Leu Phe Lys Val Ile Thr Lys Asp Asp Thr His Tyr Tyr Ile	
319 324 329 334	
cag gcc agc agc aag gct gag cga gcc gag tgg att gaa gct atc aaa	1117
Gln Ala Ser Ser Lys Ala Glu Arg Ala Glu Trp Ile Glu Ala Ile Lys	
335 340 345 350	
aag cta aca tga caa ggacctgagg gaaccaggat tcctccctcc taccagatga	1172
Lys Leu Thr *	
351	
cacagacaag agttcctgga gaatgggagt gttaagactt ttgacttctt tgtaagtttt	1232
gtactgcttt ggagagtga tgctgccaag agttcctcag attacaaaca gcagtgggtgc	1292
catttccttc cccatcttca tgttacaaac ctggaaaggc tagaacagcc attaggcgtc	1352
agcatcttga cttttcccca gcatcacaaa cagccatttc ctggggcacc aaagtaggtt	1412
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aaaaaaaaa	1482

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	Met Gly Arg
	1
aat tcc aag cac act tct cag agc aga gca gaa gag gtt gac tat gga	162

Asn	Ser	Lys	His	Thr	Ser	Gln	Ser	Arg	Ala	Glu	Glu	Val	Asp	Tyr	Gly	
4					9					14					19	
gag gag aat gaa gat ggg acc cag gtg agc ccg ggt gcc cac tac tgc																210
Glu	Glu	Asn	Glu	Asp	Gly	Thr	Gln	Val	Ser	Pro	Gly	Ala	His	Tyr	Cys	
20					25					30					35	
agc ccc act ggc gca ggc tgc ccc agg ccc tgt gca gac aca cca ggc																258
Ser	Pro	Thr	Gly	Ala	Gly	Cys	Pro	Arg	Pro	Cys	Ala	Asp	Thr	Pro	Gly	
36					41					46					51	
cct cag ccg cag ccc atg gac ctg cgg gtg ggc cag cgg ccc cca gtg																306
Pro	Gln	Pro	Gln	Pro	Met	Asp	Leu	Arg	Val	Gly	Gln	Arg	Pro	Pro	Val	
52					57					62					67	
gag ccc cca cca gag ccc aca ttg ctg gcc ctg cag cgt ccc cag cgc																354
Glu	Pro	Pro	Pro	Glu	Pro	Thr	Leu	Leu	Ala	Leu	Gln	Arg	Pro	Gln	Arg	
68					73					78					83	
ctg cac cac cac ctc ttc cta gca ggc ctg cag cag cag cgc tcg gtg																402
Leu	His	His	His	Leu	Phe	Leu	Ala	Gly	Leu	Gln	Gln	Gln	Arg	Ser	Val	
84					89					94					99	
gag ccc atg agg ctc tcc atg gac acg ccg atg ccc gag ttg cag gtg																450
Glu	Pro	Met	Arg	Leu	Ser	Met	Asp	Thr	Pro	Met	Pro	Glu	Leu	Gln	Val	
100					105					110					115	
gga ccc cag gaa caa gag ctg cgg cag ctt ctc cac aag gac aag agc																498
Gly	Pro	Gln	Glu	Gln	Glu	Leu	Arg	Gln	Leu	Leu	His	Lys	Asp	Lys	Ser	
116					121					126					131	
aag cga agt gct gta gcc agc agc gtg gtc aag cag aag cta gcg gag																546
Lys	Arg	Ser	Ala	Val	Ala	Ser	Ser	Val	Val	Lys	Gln	Lys	Leu	Ala	Glu	
132					137					142					147	
gtg att ctg aaa aaa cag cag gcg gcc cta gaa aga aca gtc cat ccc																594
Val	Ile	Leu	Lys	Lys	Gln	Gln	Ala	Ala	Leu	Glu	Arg	Thr	Val	His	Pro	
148					153					158					163	
aac agc ccc ggc att ccc tac aga acc ctg gag ccc ctg gag acg gaa																642
Asn	Ser	Pro	Gly	Ile	Pro	Tyr	Arg	Thr	Leu	Glu	Pro	Leu	Glu	Thr	Glu	
164					169					174					179	
gga gcc acc cgc tcc atg ctc agc agc ttt ttg cct cct gtt ccc agc																690
Gly	Ala	Thr	Arg	Ser	Met	Leu	Ser	Ser	Phe	Leu	Pro	Pro	Val	Pro	Ser	
180					185					190					195	
ctg ccc agt gac ccc cca gag cac ttc cct ctg cgc aag aca gtc tct																738
Leu	Pro	Ser	Asp	Pro	Pro	Glu	His	Phe	Pro	Leu	Arg	Lys	Thr	Val	Ser	
196					201					206					211	
gag ccc aac ctg aag ctg cgc tat aag ccc aag aag tcc ctg gag cgg																786
Glu	Pro	Asn	Leu	Lys	Leu	Arg	Tyr	Lys	Pro	Lys	Lys	Ser	Leu	Glu	Arg	
212					217					222					227	
agg aag aat cca ctg ctc cga aag gag agt gcg ccc ccc agc ctc cgg																834
Arg	Lys	Asn	Pro	Leu	Leu	Arg	Lys	Glu	Ser	Ala	Pro	Pro	Ser	Leu	Arg	

228	233	238	243	
cgg cgg ccc gca gag acc ctc gga gac tcc tcc cca agt agt agc agc				882
Arg Arg Pro Ala Glu Thr Leu Gly Asp Ser Ser Pro Ser Ser Ser Ser				
244	249	254	259	
acg ccc gca tca gga tgc agc tcc ccc aat gac agc gag cac ggc ccc				930
Thr Pro Ala Ser Gly Cys Ser Ser Pro Asn Asp Ser Glu His Gly Pro				
260	265	270	275	
aat ccc atc ctg ggc tgc gag gcg ctc ttg ggc cag cgg ctg cgg ctg				978
Asn Pro Ile Leu Gly Ser Glu Ala Leu Leu Gly Gln Arg Leu Arg Leu				
276	281	286	291	
cag gag act tct gtg gcc ccg ttc gcc ttg ccg aca gtg tcc ttg ctg				1026
Gln Glu Thr Ser Val Ala Pro Phe Ala Leu Pro Thr Val Ser Leu Leu				
292	297	302	307	
ccc gca atc act ctg ggg ctg ccc gcc cct gcc agg gct gac agt gac				1074
Pro Ala Ile Thr Leu Gly Leu Pro Ala Pro Ala Arg Ala Asp Ser Asp				
308	313	318	323	
cgc agg acc cat ccg act ctg ggc cct cgg ggg cca atc ctg ggg agc				1122
Arg Arg Thr His Pro Thr Leu Gly Pro Arg Gly Pro Ile Leu Gly Ser				
324	329	334	339	
ccc cac act ccc ctc ttc ctg ccc cat ggc ttg gag ccc gag gct ggg				1170
Pro His Thr Pro Leu Phe Leu Pro His Gly Leu Glu Pro Glu Ala Gly				
340	345	350	355	
ggc acc ttg ccc tct cgc ctg cag ccc att ctc ctc ctg gac ccc tca				1218
Gly Thr Leu Pro Ser Arg Leu Gln Pro Ile Leu Leu Leu Asp Pro Ser				
356	361	366	371	
ggc tct cat gcc ccg ctg ctg act gtg ccc ggg ctt ggg ccc ttg ccc				1266
Gly Ser His Ala Pro Leu Leu Thr Val Pro Gly Leu Gly Pro Leu Pro				
372	377	382	387	
ttc cac ttt gcc cag tcc tta atg acc acc gag cgg ctc tct ggg tca				1314
Phe His Phe Ala Gln Ser Leu Met Thr Thr Glu Arg Leu Ser Gly Ser				
388	393	398	403	
ggc ctc cac tgg cca ctg agc cgg act cgc tca gag ccc ctg ccc ccc				1362
Gly Leu His Trp Pro Leu Ser Arg Thr Arg Ser Glu Pro Leu Pro Pro				
404	409	414	419	
agt gcc acc gct ccc cca ccg ccg ggc ccc atg cag ccc cgc ctg gag				1410
Ser Ala Thr Ala Pro Pro Pro Pro Gly Pro Met Gln Pro Arg Leu Glu				
420	425	430	435	
cag ctc aaa act cac gtc cag gtg atc aag agg tca gcc aag ccg agt				1458
Gln Leu Lys Thr His Val Gln Val Ile Lys Arg Ser Ala Lys Pro Ser				
436	441	446	451	
gag aag ccc cgg ctg cgg cag ata ccc tcg gct gaa gac ctg gag aca				1506
Glu Lys Pro Arg Leu Arg Gln Ile Pro Ser Ala Glu Asp Leu Glu Thr				
452	457	462	467	

gat ggc ggg gga ccg ggc cag gtg gtg gac gat ggc ctg gag cac agg Asp Gly Gly Gly Pro Gly Gln Val Val Asp Asp Gly Leu Glu His Arg 468 473 478 483	1554
gag ctg ggc cat ggg cag cct gag gcc aga ggc ccc gct cct ctc cag Glu Leu Gly His Gly Gln Pro Glu Ala Arg Gly Pro Ala Pro Leu Gln 484 489 494 499	1602
cag cac cct cag gtg ttg ctc tgg gaa cag cag cga ctg gct ggg cgg Gln His Pro Gln Val Leu Leu Trp Glu Gln Gln Arg Leu Ala Gly Arg 500 505 510 515	1650
ctc ccc cgg ggc agc acc ggg gac act gtg ctg ctt cct ctg gcc cag Leu Pro Arg Gly Ser Thr Gly Asp Thr Val Leu Leu Pro Leu Ala Gln 516 521 526 531	1698
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gcc tca ctg tca gcc cca gag cct gcc agc cag gcc cga gtc ctc tcc Ala Ser Leu Ser Ala Pro Glu Pro Ala Ser Gln Ala Arg Val Leu Ser 548 553 558 563	1794
agc tca gag acc cct gcc agg acc ctg ccc ttc acc aca ggg ctg atc Ser Ser Glu Thr Pro Ala Arg Thr Leu Pro Phe Thr Thr Gly Leu Ile 564 569 574 579	1842
tat gac tcg gtc atg ctg aag cac cag tgc tcc tgc ggt gac aac agc Tyr Asp Ser Val Met Leu Lys His Gln Cys Ser Cys Gly Asp Asn Ser 580 585 590 595	1890
agg cac ccg gag cac gcc ggc cgc atc cag agc atc tgg tcc cgg ctg Arg His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser Arg Leu 596 601 606 611	1938
cag gag cgg ggg ctc cgg agc cag tgt gag tgt ctc cga ggc cgg aag Gln Glu Arg Gly Leu Arg Ser Gln Cys Glu Cys Leu Arg Gly Arg Lys 612 617 622 627	1986
gcc tcc ctg gaa gag ctg cag tca gtc cac tct gag cgg cac gtg ctc Ala Ser Leu Glu Glu Leu Gln Ser Val His Ser Glu Arg His Val Leu 628 633 638 643	2034
ctc tac ggc acc aac ccg ctc agc cgc ctc aaa ctg gac aac ggg aag Leu Tyr Gly Thr Asn Pro Leu Ser Arg Leu Lys Leu Asp Asn Gly Lys 644 649 654 659	2082
ctg gca ggg ctc ctg gca cag cgg atg ttt gtg atg ctg ccc tgt ggt Leu Ala Gly Leu Leu Ala Gln Arg Met Phe Val Met Leu Pro Cys Gly 660 665 670 675	2130
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Asn Ala Ala Arg Trp Ala Ala Gly Ser Val Thr Asp Leu Ala Phe Lys	
692 697 702 707	
gtg gct tct cgt gag cta aag aat ggt ttc gct gtg gtg cgg ccc cca	2274
Val Ala Ser Arg Glu Leu Lys Asn Gly Phe Ala Val Val Arg Pro Pro	
708 713 718 723	
gga cac cat gca gat cat tca aca gcc atg ggc ttc tgc ttc ttc aac	2322
Gly His His Ala Asp His Ser Thr Ala Met Gly Phe Cys Phe Phe Asn	
724 729 734 739	
tca gtg gcc atc gcc tgc cgg cag ctg caa cag cag agc aag gcc agc	2370
Ser Val Ala Ile Ala Cys Arg Gln Leu Gln Gln Gln Ser Lys Ala Ser	
740 745 750 755	
aag atc ctc att gta gac tgg gac gtg cac cat ggc aac ggc acc cag	2418
Lys Ile Leu Ile Val Asp Trp Asp Val His His Gly Asn Gly Thr Gln	
756 761 766 771	
caa acc ttc tac caa gac ccc agt gtg ctc tac atc tcc ctg cat cgc	2466
Gln Thr Phe Tyr Gln Asp Pro Ser Val Leu Tyr Ile Ser Leu His Arg	
772 777 782 787	
cat gac gac ggc aac ttc ttc ccg ggg agt ggg gct gtg gat gag gta	2514
His Asp Asp Gly Asn Phe Phe Pro Gly Ser Gly Ala Val Asp Glu Val	
788 793 798 803	
ggg gct ggc agc ggt gag ggc ttc aat gtc aat gtg gcc tgg gct gga	2562
Gly Ala Gly Ser Gly Glu Gly Phe Asn Val Asn Val Ala Trp Ala Gly	
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ggg ctg gac ccc ccc atg ggg gat cct gag tac ctg gct gct ttc agg	2610
Gly Leu Asp Pro Pro Met Gly Asp Pro Glu Tyr Leu Ala Ala Phe Arg	
820 825 830 835	
ata gtc gtg atg ccc atc gcc cga gag ttc tct cca gac cta gtc ctg	2658
Ile Val Val Met Pro Ile Ala Arg Glu Phe Ser Pro Asp Leu Val Leu	
836 841 846 851	
gtg tct gct gga ttt gat gct gct gag ggt cac ccg gcc cca ctg ggt	2706
Val Ser Ala Gly Phe Asp Ala Ala Glu Gly His Pro Ala Pro Leu Gly	
852 857 862 867	
ggc tac cat gtt tct gcc aaa tgt ttt gga tac atg acg cag caa ctg	2754
Gly Tyr His Val Ser Ala Lys Cys Phe Gly Tyr Met Thr Gln Gln Leu	
868 873 878 883	
atg aac ctg gca gga ggc gca gtg gtg ctg gcc ttg gag ggt ggc cat	2802
Met Asn Leu Ala Gly Gly Ala Val Val Leu Ala Leu Glu Gly Gly His	
884 889 894 899	
gac ctc aca gcc atc tgt gac gcc tct gag gcc tgt gtg gct gct ctt	2850
Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ala Ala Leu	
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Glu Pro Val Arg Leu Glu Arg Asp Ile Cys Arg Ala Ile Glu Leu Leu
6 11 16 21

gaa aaa cta caa agg agt gga gaa gta cca cca cag aaa ctt cag gct 149
Glu Lys Leu Gln Arg Ser Gly Glu Val Pro Pro Gln Lys Leu Gln Ala
22 27 32 37

ttg caa aga gtc ctt caa agt gaa ttc tgc aat gct gtg aga gag gta 197
Leu Gln Arg Val Leu Gln Ser Glu Phe Cys Asn Ala Val Arg Glu Val
38 43 48 53

tat gaa cat gtc tat gag act gtg gac atc agt agc agt cct gaa gtg 245
Tyr Glu His Val Tyr Glu Thr Val Asp Ile Ser Ser Ser Pro Glu Val
54 59 64 69

aga gcg aac gct act gca aag gct act gtt gct gca ttt gct gcc agt 293
Arg Ala Asn Ala Thr Ala Lys Ala Thr Val Ala Ala Phe Ala Ala Ser
70 75 80 85

gaa gga cat tct cat cct cga gtt gtt gag cta cca aaa aca gag gag 341
Glu Gly His Ser His Pro Arg Val Val Glu Leu Pro Lys Thr Glu Glu
86 91 96 101

ggc ctt gga ttc aat att atg gga ggc aaa gaa caa aac tct cca atc 389
Gly Leu Gly Phe Asn Ile Met Gly Gly Lys Glu Gln Asn Ser Pro Ile
102 107 112 117

tat ata tcc cga ata att cca ggt gga att gct gat aga cat ggg ggc 437
Tyr Ile Ser Arg Ile Ile Pro Gly Gly Ile Ala Asp Arg His Gly Gly
118 123 128 133

ctc aaa cgt gga gat caa ctc ctc tct gtt aat gga gtg agt gtt gaa	485
Leu Lys Arg Gly Asp Gln Leu Leu Ser Val Asn Gly Val Ser Val Glu	
134 139 144 149	
gga gaa cat cat gaa aaa gct gta gaa ctg ctg aaa gcc gca caa gga	533
Gly Glu His His Glu Lys Ala Val Glu Leu Leu Lys Ala Ala Gln Gly	
150 155 160 165	
aag gtt aaa tta gtg gta cga tac aca ccc aaa gtc tta gaa gaa atg	581
Lys Val Lys Leu Val Val Arg Tyr Thr Pro Lys Val Leu Glu Glu Met	
166 171 176 181	
gag tcg cgc ttt gaa aaa atg aga tca gca aaa cgc agg caa cag acc	629
Glu Ser Arg Phe Glu Lys Met Arg Ser Ala Lys Arg Arg Gln Gln Thr	
182 187 192 197	
taa taca tttcaaaact tgatatttca ttttgcgttt tagctagaga agttttcctt	686
*	
198	
gtgacttact aatggctgca atgccaatga ttgtaagaaa acaaacaaat ttatcatgaa	746
attctccttg tcattttata aatgcctatt ttaacatcat ttatgggtcc agagatgcat	806
acactttttt ctgacaagaa aaagtaaaag gtgatgaggg caattctgtc ctactgtttt	866
tacaggcctt tttcaaatgc agattttgtc ataaagttgt tatagatttt ttaaaatgct	926
tttttaatat taaaatgtac ttttacattc ttaatctttt tttagaaagg aaaagttttc	986
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cgccccgcac tcccggaccc gaagccggga agattccttt cttgtctgtt agaaacgtat 180

gtcaaacgag gatacagtgt ctggaactat tggttctaag atataagtgg aatgagcctg 240

gatcaggaga agtatgctga gctagagttg aaggaagctt ctcttttctaa caagagaaaag 300

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Met Ala Glu Thr Ser Leu Leu Glu Ala Gly Ala Ser
1 5 10

gca gcc tct aca gct gcg gct ttg gag aac tta cag gtg gag gcg agc 396
Ala Ala Ser Thr Ala Ala Ala Leu Glu Asn Leu Gln Val Glu Ala Ser
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Cys Ser Val Cys Leu Glu Tyr Leu Lys Glu Pro Val Ile Ile Glu Cys
29 34 39 44

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Gly His Asn Phe Cys Lys Ala Cys Ile Thr Arg Trp Trp Glu Asp Leu
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gag agg gac ttc cct tgt cct gtc tgt cga aag aca tcc cgc tac cgc 540
Glu Arg Asp Phe Pro Cys Pro Val Cys Arg Lys Thr Ser Arg Tyr Arg
61 66 71 76

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Ser Leu Arg Pro Asn Arg Gln Leu Gly Ser Met Val Glu Ile Ala Lys
77 82 87 92

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Gln Leu Gln Ala Val Lys Arg Lys Ile Arg Asp Glu Ser Leu Cys Pro
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Gln His His Glu Ala Leu Ser Leu Phe Cys Tyr Glu Asp Gln Glu Ala
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Val Cys Leu Ile Cys Ala Ile Ser His Thr His Arg Ala His Thr Val
125 130 135 140

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Val Pro Leu Asp Asp Ala Thr Gln Glu Tyr Lys Glu Lys Leu Gln Lys
141 146 151 156

tgt ctg gag ccc ctg gaa cag aag ctg cag gag atc act cgc tgc aag 828
Cys Leu Glu Pro Leu Glu Gln Lys Leu Gln Glu Ile Thr Arg Cys Lys
157 162 167 172

tcc tct gag gag aag aag cct ggt gag ctc aag aga cta gtg gaa agt 876
Ser Ser Glu Glu Lys Lys Pro Gly Glu Leu Lys Arg Leu Val Glu Ser

173	178	183	188	
cgc cga cag cag atc ttg agg gag ttt gaa gag ctt cat agg cgg ctg				924
Arg Arg Gln Gln Ile Leu Arg Glu Phe Glu Glu Leu His Arg Arg Leu				
189	194	199	204	
gat gaa gag cag cag gtg ttg ctt tca cga ctg gaa gaa gag gaa cag				972
Asp Glu Glu Gln Gln Val Leu Leu Ser Arg Leu Glu Glu Glu Glu Gln				
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Asp Ile Leu Gln Arg Leu Arg Glu Asn Ala Ala His Leu Gly Asp Lys				
221	226	231	236	
cgc cgg gac ctg gcc cac ttg gct gcc gag gtg gag ggc aag tgc tta				1068
Arg Arg Asp Leu Ala His Leu Ala Ala Glu Val Glu Gly Lys Cys Leu				
237	242	247	252	
cag tca ggc ttc gag atg ctt aag gtt cga cct ttg ccc ctg cat agc				1116
Gln Ser Gly Phe Glu Met Leu Lys Val Arg Pro Leu Pro Leu His Ser				
253	258	263	268	
ccc tca ggc tga gtg cagcgtagct ttgcgtagcc tgggatttgt cagcctggga				1171
Pro Ser Gly *				
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Gln His Glu Ala Ala Val Pro Gln Leu Ala Ala Ala Leu Ala Arg Cys	
190 195 200 205	
acc gag aac ccc atg gtg cgg cac gag tgc gcg gag gcc ctg ggc gcc	793
Thr Glu Asn Pro Met Val Arg His Glu Cys Ala Glu Ala Leu Gly Ala	
206 211 216 221	
att gcc cgg ccc gcc tgc ctg gcc gcg ctg cag gct cac gcg gac gac	841
Ile Ala Arg Pro Ala Cys Leu Ala Ala Leu Gln Ala His Ala Asp Asp	
222 227 232 237	
cca gag cgc gtg gtg cgt gag agc tgc gag gtg gct ctg gac atg tat	889
Pro Glu Arg Val Val Arg Glu Ser Cys Glu Val Ala Leu Asp Met Tyr	
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gag cac gag acc ggg cgg gcc ttc cag tac gcg gac ggc ctg gag cag	937
Glu His Glu Thr Gly Arg Ala Phe Gln Tyr Ala Asp Gly Leu Glu Gln	
254 259 264 269	
ctg cgc ggg gcc ccc tcc tag gg cccaccctc acccgagct cccggaggac	990
Leu Arg Gly Ala Pro Ser *	
270 275	
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ctcaagatgt cacggaagac tgtggtatgg ctgaacatct tgaaaagtcc tccctttcga     900
ataatgagtg tggttctctt gacaaaacca gtccagaa      atg tca aac agt aat     953
                                   Met Ser Asn Ser Asn
                                   1

aat gat gaa aga aaa aaa gct tta att tca tca agg aaa aca tca act     1001
Asn Asp Glu Arg Lys Lys Ala Leu Ile Ser Ser Arg Lys Thr Ser Thr
   6              11              16              21

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Glu Cys Ala Ser Ser Thr Glu Asn Ser Phe Val Val Ser Ser Ser Ser
  22              27              32              37

gtt tct aat acc act gtt gct gga act ccc cca tac cct aca agt cgg     1097
Val Ser Asn Thr Thr Val Ala Gly Thr Pro Pro Tyr Pro Thr Ser Arg
  38              43              48              53

agg caa acc ttt att act ttg gag aag ttt gat ggt tca gaa aat aga     1145
Arg Gln Thr Phe Ile Thr Leu Glu Lys Phe Asp Gly Ser Glu Asn Arg
  54              59              64              69

cct ttt agt cca tcc ccc ttg aat aat att tca tca act gtt aca gtg     1193
Pro Phe Ser Pro Ser Pro Leu Asn Asn Ile Ser Ser Thr Val Thr Val
  70              75              80              85
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Lys Gln Arg Glu Gly Thr Phe Ser Lys Ser Asp Ser Glu Lys Ile Val	
102 107 112 117	
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Asn Gly Thr Lys Arg Ser Ser Arg Arg Ala Gly Lys Ala Glu Gln Thr	
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Gly Asn Lys Arg Ser Lys Pro Leu Met Arg Ser Glu Pro Glu Lys Asn	
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Thr Glu Glu Ser Val Glu Gly Ile Val Val Leu Glu Asn Asn Pro Pro	
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Gly Leu Leu Asn Gln Thr Glu Cys Val Ser Asp Asn Gln Val His Leu	
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Ser Glu Ser Thr Met Glu His Asp Asn Thr Lys Leu Lys Ala Ala Thr	
182 187 192 197	
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Asn Gln Lys Thr Leu Arg Arg Ser Ser Arg Arg Arg Ser Glu Val Val	
246 251 256 261	
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Glu Ser Thr Thr Glu Ser Gln Asp Lys Glu Asn Ser His Gln Lys Lys	
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Ile Lys Asp Asp Val Leu Pro Lys Gln Lys Leu Ile Ala Glu Gln Thr	
294 299 304 309	
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Leu Gln Glu Asn Leu Ile Glu Lys Gly Ser Asn Leu His Glu Lys Thr	
310 315 320 325	
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Leu Gly Glu Thr Ser Ala Asn Ala Glu Thr Glu Gln Asn Lys Lys Lys	
326 331 336 341	
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Ala Asp Pro Glu Asn Ile Lys Ser Glu Gly Asp Gly Thr Gln Asp Ile	
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Val Asp Lys Ser Ser Glu Lys Leu Val Arg Gly Arg Thr Arg Tyr Gln	
358 363 368 373	
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Thr Arg Arg Ala Ser Gln Gly Leu Leu Ser Ser Ile Glu Asn Ser Glu	
374 379 384 389	
tct gat agt tcg gag gca aaa gaa gaa ggt tct agg aag aag aga tct	2153
Ser Asp Ser Ser Glu Ala Lys Glu Glu Gly Ser Arg Lys Lys Arg Ser	
390 395 400 405	
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Gly Lys Trp Lys Asn Lys Ser Asn Glu Ser Val Asp Ile Gln Asp Gln	
406 411 416 421	
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Glu Glu Lys Val Val Lys Gln Glu Cys Ile Lys Ala Glu Asn Gln Ser	
422 427 432 437	
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His Asp Tyr Lys Ala Thr Ser Glu Glu Asp Val Ser Ile Lys Ser Pro	
438 443 448 453	
att tgc gaa aaa caa gat gaa agt aat act gta ata tgt cag gat tct	2345
Ile Cys Glu Lys Gln Asp Glu Ser Asn Thr Val Ile Cys Gln Asp Ser	
454 459 464 469	
aca gta act tca gat ttg ttg caa gtt cct gat gat tta cca aat gtg	2393
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Cys Glu Glu Lys Asn Glu Thr Ser Lys Tyr Ala Glu Tyr Ser Phe Thr	
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518 523 528 533	
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Ser Lys Ile Gly Ile Ser Asp Ile Ser Ser Leu Ser Glu Lys Thr Phe	

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gta aca gaa tcc aat Val Thr Glu Ser Asn 742	cta gag aaa gca aaa Leu Glu Lys Ala Lys 747	act atg gaa ttg aat gta Thr Met Glu Leu Asn Val 752		3209
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Asn Ser Asp Ile Ser Leu Ser Asp Asn Thr Thr Pro Val Lys Leu Asn	
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Lys Pro Asp Glu Ala Glu Thr Asn Met Leu Thr Ala Glu Met Asp Asn	
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Phe Val Cys Asp Thr Val Glu Met Ser Thr Glu Glu Gly Ile Ile Asp	
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Leu Asp Asn Asn Gln Met Val Met Glu Ser Asp Ile Leu Gln Glu Asp	
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His His Thr Ser Gln Lys Val Glu Glu Pro Ser Gln Cys Leu Ala Ser	
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Phe Leu Ser Pro Gly Ser Arg Ser Pro Lys Phe Lys Ser Ser Lys Lys	
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<213> Homo sapiens

<220>

<221> CDS

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Ser	Ser	Asn	Asn	Ser	Ala	Pro	Pro	Lys	Pro	Met	Ser	Leu	Lys	Ile	Glu	
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aga	att	agc	tcg	tgg	aaa	aca	cca	cca	cag	gaa	aat	aga	gat	aaa	aat	963
Arg	Ile	Ser	Ser	Trp	Lys	Thr	Pro	Pro	Gln	Glu	Asn	Arg	Asp	Lys	Asn	
218					223					228					233	
ctt	tcc	agg	aga	cgt	caa	gac	aga	aga	gca	aca	cct	act	gga	agg	cca	1011
Leu	Ser	Arg	Arg	Arg	Gln	Asp	Arg	Arg	Ala	Thr	Pro	Thr	Gly	Arg	Pro	
234					239					244					249	
act	ccc	tgt	gca	gag	aga	cgg	ggg	ggt	gtc	tga	agatggaa	aggtggcctc				1062
Thr	Pro	Cys	Ala	Glu	Arg	Arg	Gly	Gly	Val	*						
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Met Asn Pro Thr Leu Gly Leu Ala Ile Phe Leu Ala Val Leu Leu Thr							
1 5 10 15							
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Val Lys Gly Leu Leu Lys Pro Ser Phe Ser Pro Arg Asn Tyr Lys Ala							
17 22 27 32							
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Leu Ser Glu Val Gln Gly Trp Lys Gln Arg Met Ala Ala Lys Glu Leu							
33 38 43 48							
gca agg cag aac atg gac tta ggc ttt aag ctg ctc aag aag ctg gcc							552

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Phe	Tyr	Asn	Pro	Gly	Arg	Asn	Ile	Phe	Leu	Ser	Pro	Leu	Ser	Ile	Ser		
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aca	gct	ttc	tcc	atg	ctg	tgc	ctg	ggt	gcc	cag	gac	agc	acc	ctg	gac	648	
Thr	Ala	Phe	Ser	Met	Leu	Cys	Leu	Gly	Ala	Gln	Asp	Ser	Thr	Leu	Asp		
81					86					91					96		
gag	atc	aag	cag	ggg	ttc	aac	ttc	aga	aag	atg	cca	gaa	aaa	gat	ctt	696	
Glu	Ile	Lys	Gln	Gly	Phe	Asn	Phe	Arg	Lys	Met	Pro	Glu	Lys	Asp	Leu		
97					102					107					112		
cat	gag	ggc	ttc	cat	tac	atc	atc	cac	gag	ctg	acc	cag	aag	acc	cag	744	
His	Glu	Gly	Phe	His	Tyr	Ile	Ile	His	Glu	Leu	Thr	Gln	Lys	Thr	Gln		
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Asp	Leu	Lys	Leu	Ser	Ile	Gly	Asn	Thr	Leu	Phe	Ile	Asp	Gln	Arg	Leu		
129					134					139					144		
cag	cca	cag	cgt	aag	ttt	ttg	gaa	gat	gcc	aag	aac	ttt	tac	agt	gcc	840	
Gln	Pro	Gln	Arg	Lys	Phe	Leu	Glu	Asp	Ala	Lys	Asn	Phe	Tyr	Ser	Ala		
145					150					155					160		
gaa	acc	atc	ctt	acc	aac	ttt	cag	aat	ttg	gaa	atg	gct	cag	aag	cag	888	
Glu	Thr	Ile	Leu	Thr	Asn	Phe	Gln	Asn	Leu	Glu	Met	Ala	Gln	Lys	Gln		
161					166					171					176		
atc	aat	gac	ttt	atc	agt	caa	aaa	acc	cat	ggg	aaa	att	aac	aac	ctg	936	
Ile	Asn	Asp	Phe	Ile	Ser	Gln	Lys	Thr	His	Gly	Lys	Ile	Asn	Asn	Leu		
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Ile	Glu	Asn	Ile	Asp	Pro	Gly	Thr	Val	Met	Leu	Leu	Ala	Asn	Tyr	Ile		
193					198					203					208		
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Glu	Glu	Asp	Phe	Phe	Leu	Glu	Lys	Asn	Ser	Ser	Val	Lys	Val	Pro	Met		
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Met	Phe	Arg	Ser	Gly	Ile	Tyr	Gln	Val	Gly	Tyr	Asp	Asp	Lys	Leu	Ser		
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Cys	Thr	Ile	Leu	Glu	Ile	Pro	Tyr	Gln	Lys	Asn	Ile	Thr	Ala	Ile	Phe		
257					262					267					272		
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Val Asp Thr Phe Ser Arg Trp Lys Thr Leu Leu Ser Arg Arg Val Val				
289	294	299	304	
gac gtg tct gta ccc aga ctc cac atg acg ggc acc ttc gac ctg aag				1320
Asp Val Ser Val Pro Arg Leu His Met Thr Gly Thr Phe Asp Leu Lys				
305	310	315	320	
aag act ctc tcc tac ata ggt gtc tcc aaa atc ttt gag gaa cat ggt				1368
Lys Thr Leu Ser Tyr Ile Gly Val Ser Lys Ile Phe Glu Glu His Gly				
321	326	331	336	
gat ctc acc aag atc gcc cct cat cgc agc ctg aaa gtg ggc gag gct				1416
Asp Leu Thr Lys Ile Ala Pro His Arg Ser Leu Lys Val Gly Glu Ala				
337	342	347	352	
gtg aac aag gct gag ctg aag atg gat gag agg ggt acg gaa ggg gcc				1464
Val Asn Lys Ala Glu Leu Lys Met Asp Glu Arg Gly Thr Glu Gly Ala				
353	358	363	368	
gct ggc acc gga gca cag act ctg ccc atg gag aca cca ctc gtc gtc				1512
Ala Gly Thr Gly Ala Gln Thr Leu Pro Met Glu Thr Pro Leu Val Val				
369	374	379	384	
aag ata gac aaa ccc tat ctg ctg ctg att tac agc gag aaa ata cct				1560
Lys Ile Asp Lys Pro Tyr Leu Leu Leu Ile Tyr Ser Glu Lys Ile Pro				
385	390	395	400	
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gatgatattg acagagaact gagtgagggc cagggggcag ctgccatccc aattggtagc	180
acatcctctg agacagaaac agcatccact gtgggatctg aagaaacct catccagacc	240

ccttcgtag tcactcaggg gacagcaacc cgaagtagga agacagccca aaagactgca 300

atg cag tgc tgc ttg gag tat gtc caa cag ttt ctt acc aga ctt atc 348
Met Gln Cys Cys Leu Glu Tyr Val Gln Gln Phe Leu Thr Arg Leu Ile
1 5 10 15

aac ctc tac atc att cag aat aac tct ttt tct cag tct ttg gct aca 396
Asn Leu Tyr Ile Ile Gln Asn Asn Ser Phe Ser Gln Ser Leu Ala Thr
17 22 27 32

gaa cat caa ggg gat ctt ggt cga gaa caa gga gag act tca aaa tgg 444
Glu His Gln Gly Asp Leu Gly Arg Glu Gln Gly Glu Thr Ser Lys Trp
33 38 43 48

gac aga aat tca caa gga gat gta aaa gag aaa aac ata agt aaa caa 492
Asp Arg Asn Ser Gln Gly Asp Val Lys Glu Lys Asn Ile Ser Lys Gln
49 54 59 64

aaa act tct aaa gaa tac ctg tct gcc ttc ctt gct gcc tgt cag ctc 540
Lys Thr Ser Lys Glu Tyr Leu Ser Ala Phe Leu Ala Ala Cys Gln Leu
65 70 75 80

ttc cta gag tgc tca agt ttc cca gtt tac att gct gag ggg aac cat 588
Phe Leu Glu Cys Ser Ser Phe Pro Val Tyr Ile Ala Glu Gly Asn His
81 86 91 96

aca tca gag tta cgt tct gaa aaa ttg gag act gac tgt gag cat gtg 636
Thr Ser Glu Leu Arg Ser Glu Lys Leu Glu Thr Asp Cys Glu His Val
97 102 107 112

cag cct cca cag tgg ctc cag act ctg atg aat gct tgc agc caa gca 684
Gln Pro Pro Gln Trp Leu Gln Thr Leu Met Asn Ala Cys Ser Gln Ala
113 118 123 128

agt gat ttc agt gtt cag agt gtt gct att tca cta gtt atg gac ctg 732
Ser Asp Phe Ser Val Gln Ser Val Ala Ile Ser Leu Val Met Asp Leu
129 134 139 144

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Val Gly Leu Thr Gln Ser Val Ala Met Val Thr Gly Glu Asn Ile Asn
145 150 155 160

agt gta gag cct gca caa ccc tta agt cca aac cag gga aga gta gct 828
Ser Val Glu Pro Ala Gln Pro Leu Ser Pro Asn Gln Gly Arg Val Ala
161 166 171 176

gtg gtt att aga cct ccc ctc act cag ggc aat ctg agg tac ata gct 876
Val Val Ile Arg Pro Pro Leu Thr Gln Gly Asn Leu Arg Tyr Ile Ala
177 182 187 192

gag aag act gaa ttt ttc aag cat gta gct tta aca ttg tgg gac cag 924
Glu Lys Thr Glu Phe Phe Lys His Val Ala Leu Thr Leu Trp Asp Gln
193 198 203 208

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Leu Gly Asp Gly Thr Pro Gln His His Gln Lys Ser Val Glu Leu Phe
209 214 219 224

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Gln	Ala	Trp	Leu	Asn	Gln	Val	Leu	Gln	Arg	His	Asp	Ile	Ala	Arg	Val	
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369					374					379					384	
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Lys	Pro	Leu	Thr	Met	Asp	Glu	Ile	Glu	Asn	Phe	Ser	Leu	Thr	Val	Asn	
385					390					395					400	
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Pro	Leu	Ser	Asp	Arg	Leu	Ser	Leu	Leu	Ser	Thr	Ser	Ser	Glu	Thr	Ile	
401					406					411					416	
cca	atg	gtt	gtg	tct	gat	ttt	gat	ctt	cca	gac	caa	cag	ata	gaa	ata	1596
Pro	Met	Val	Val	Ser	Asp	Phe	Asp	Leu	Pro	Asp	Gln	Gln	Ile	Glu	Ile	
417					422					427					432	
ctt	cag	agt	tct	gac	tcg	gga	tgt	tca	cag	tcc	tct	gct	ggg	gac	aac	1644
Leu	Gln	Ser	Ser	Asp	Ser	Gly	Cys	Ser	Gln	Ser	Ser	Ala	Gly	Asp	Asn	
433					438					443					448	

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Leu Ser Tyr Glu Val Asp Pro Glu Thr Val Asn Ala Gln Glu Asp Ser	
449 454 459 464	
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Gln Met Pro Lys Glu Ser Ser Pro Asp Asp Asp Val Gln Gln Val Val	
465 470 475 480	
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Phe Asp Leu Ile Cys Lys Val Val Ser Gly Leu Glu Val Glu Ser Ala	
481 486 491 496	
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Ser Val Thr Ser Gln Leu Glu Ile Glu Ala Met Pro Pro Lys Cys Ser	
497 502 507 512	
gat ata gat cca gat gaa gag acg att aaa att gaa gat gac tcc att	1884
Asp Ile Asp Pro Asp Glu Glu Thr Ile Lys Ile Glu Asp Asp Ser Ile	
513 518 523 528	
cga cag agt cag aat gct ttg ctg agt aat gaa agt tct cag ttt ctg	1932
Arg Gln Ser Gln Asn Ala Leu Leu Ser Asn Glu Ser Ser Gln Phe Leu	
529 534 539 544	
tct gtg tct gca gag gga ggc cat gag tgt gtg gca aat gga atc tcc	1980
Ser Val Ser Ala Glu Gly Gly His Glu Cys Val Ala Asn Gly Ile Ser	
545 550 555 560	
agg aat agc tcc tca cct tgt att tca gga acc aca cac act ctt cat	2028
Arg Asn Ser Ser Ser Pro Cys Ile Ser Gly Thr Thr His Thr Leu His	
561 566 571 576	
gac tct tct gtt gct tcc ata gaa acc aaa tct aga caa agg agt cac	2076
Asp Ser Ser Val Ala Ser Ile Glu Thr Lys Ser Arg Gln Arg Ser His	
577 582 587 592	
agt agt att caa ttc agc ttc aaa gaa aaa tta tca gaa aaa gtt tcg	2124
Ser Ser Ile Gln Phe Ser Phe Lys Glu Lys Leu Ser Glu Lys Val Ser	
593 598 603 608	
gag aag gaa aca ata gtt aag gag tca ggt aaa caa cca gga gca aaa	2172
Glu Lys Glu Thr Ile Val Lys Glu Ser Gly Lys Gln Pro Gly Ala Lys	
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Cys	Lys	Val	Gln	Lys	Val	Ile	Leu	His	Cys	Leu	Leu	Ser	Ser	Ile	Phe	
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Ser	Ala	Gln	Lys	Trp	His	Ser	Glu	Lys	Met	Ala	Gly	Lys	Asn	Leu	Val	
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gct	gtg	gaa	gaa	ggt	ttc	tca	gag	gac	agc	ctt	att	aat	ttc	tca	gag	2988
Ala	Val	Glu	Glu	Gly	Phe	Ser	Glu	Asp	Ser	Leu	Ile	Asn	Phe	Ser	Glu	
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Asp	Glu	Phe	Asp	Asn	Gly	Ser	Thr	Leu	Gln	Ser	Gln	Leu	Leu	Lys	Val	
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Leu	Gln	Arg	Leu	Ile	Val	Leu	Glu	His	Arg	Val	Met	Thr	Ile	Pro	Glu	
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Ser	Pro	His	Gln	Pro	Met	Thr	Ser	Leu	Gln	Tyr	Leu	His	Ala	Gln	Pro	
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Ile	Thr	Cys	Gln	Gly	Met	Phe	Leu	Cys	Ala	Val	Ile	Arg	Ala	Leu	His	
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Gln	His	Cys	Ala	Cys	Lys	Met	His	Pro	Gln	Trp	Ile	Gly	Leu	Ile	Thr	
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Ser	Thr	Leu	Pro	Tyr	Met	Gly	Lys	Val	Leu	Gln	Arg	Val	Val	Val	Ser	
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Val	Thr	Leu	Gln	Leu	Cys	Arg	Asn	Leu	Asp	Asn	Leu	Ile	Gln	Gln	Tyr	

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Ile Ile Pro Pro Asp Met Ile Leu Thr Leu Leu Glu Gly Ile Thr Ala				
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Ile Ile His Tyr Cys Leu Leu Asp Pro Thr Thr Gln Tyr His Gln Leu				
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Leu Val Ser Val Asp Gln Lys His Leu Phe Glu Ala Arg Ser Gly Ile				
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Leu Ser Ile Leu His Met Ile Met Ser Ser Val Thr Leu Leu Trp Ser				
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Ile Leu His Gln Ala Asp Ser Ser Glu Lys Met Thr Ile Ala Ala Ser				
1105	1110	1115	1120	
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Ala Ser Leu Thr Thr Ile Asn Leu Gly Ala Thr Lys Asn Leu Arg Gln				
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Gln Ile Leu Glu Leu Leu Gly Pro Ile Ser Met Asn His Gly Val His				
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Phe Met Ala Ala Ile Ala Phe Val Trp Asn Glu Arg Arg Gln Asn Lys				
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Thr Thr Thr Arg Thr Lys Val Ile Pro Ala Ala Ser Glu Glu Gln Leu				
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Val Ile Gln Thr Val Lys Glu Val Leu Lys Gln Pro Pro Ala Ile Ala				
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Lys Asp Lys Lys His Leu Ser Leu Glu Val Cys Met Leu Gln Phe Phe				
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Tyr Ala Tyr Ile Gln Arg Ile Pro Val Pro Asn Leu Val Asp Ser Trp				
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Lys Asn Pro Ser Leu Glu Asn Lys Lys Asp Gln Arg Asp Leu Gln Asp	
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Val Thr His Lys Ile Val Asp Ala Ile Gly Ala Ile Ala Gly Ser Ser	
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Pro Lys Ile Met Val Asp Gly Thr Asn Leu Glu Ser Asp Val Glu Asp	
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Met Leu Ser Pro Ala Met Glu Thr Ala Asn Ile Thr Pro Ser Val Tyr	
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Asp Met Val Phe Tyr Ser Asp Glu Lys Glu Arg Val Ile Pro Leu Leu	
1377 1382 1387 1392	
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Val Asn Ile Met His Tyr Val Val Pro Tyr Leu Arg Asn His Ser Trp	
1393 1398 1403 1408	
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Arg Ala Ile Met Asp Asn Leu Met Thr His Asp Lys Thr Thr Phe Arg	
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Gln Val Pro Thr Leu His Ser Gln Val Phe Leu Phe Phe Arg Val Leu	
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Ser Leu Thr Leu His Arg Arg Trp His Ser Arg Glu Lys Ala Tyr Lys				
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Cys Asp Glu Cys Gly Lys Ala Phe Thr Trp Ser Thr Asn Leu Leu Glu				
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His Arg Arg Ile His Thr Gly Glu Lys Pro Phe Phe Cys Gly Glu Cys				
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Gly Lys Ala Phe Ser Cys His Ser Ser Leu Asn Val His Gln Arg Ile				
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His Thr Gly Glu Arg Pro Tyr Lys Cys Ser Ala Cys Glu Lys Ala Phe				
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Lys Pro Tyr Arg Cys Gly Glu Cys Gly Lys Ala Phe Asn Gln Arg Thr				
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His Lys Val Gly Ile Thr Pro Pro Cys Phe Asn Leu Phe Ala Leu Phe	
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Asp	Pro	Gly	Pro	Glu	Ser	Ala	Ala	Gly	Pro	Pro	Thr	His	Glu	Val	Leu	
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318					323					328					333	
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Asn	Lys	Glu	Glu	Gly	Ser	Ser	Gly	Ser	Ser	Gly	Arg	Asn	Pro	Gln	Ala	
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Ser	Leu	Phe	Gly	Lys	Lys	Ala	Lys	Ala	His	Lys	Ala	Phe	Gly	Gln	Pro	
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Ala	Asp	Arg	Pro	Arg	Glu	Pro	Leu	Trp	Ala	Tyr	Phe	Cys	Asp	Phe	Arg	
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Asp	Ile	Thr	His	Val	Val	Leu	Lys	Glu	His	Cys	Val	Ser	Ile	His	Arg	
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Gln	Asp	Asn	Lys	Cys	Leu	Glu	Leu	Ser	Leu	Pro	Ser	Arg	Ala	Ala	Ala	
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Leu	Ser	Phe	Val	Ser	Leu	Val	Asp	Gly	Tyr	Phe	Arg	Leu	Thr	Ala	Asp	
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Ser	Ser	His	Tyr	Leu	Cys	His	Glu	Val	Ala	Pro	Pro	Arg	Leu	Val	Met	
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Pro	Asp	Gly	Met	Gln	Ser	Leu	Arg	Leu	Arg	Lys	Phe	Pro	Ile	Glu	Gln	

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Gln His Arg Leu Pro Glu Pro Ser Cys Pro Gln Leu Ala Thr Leu Thr	
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Ser Thr Lys Asp Gln Gln Phe Lys Lys Asp Gln Asn Val Leu Ser Pro	
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Asn Glu Glu Val Lys Lys Thr Met Glu Ala Thr Leu Gln Thr Ile Gln				
384	389	394	399	
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Asp Ile Val Thr Val Glu Asp Phe Asp Val Ser Asp Cys Phe Gln Tyr				
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Ser Asn Ser Met Glu Ser Val Lys Ser Thr Val Ser Glu Thr Phe Met				
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448	453	458	463	
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Arg Lys Gln Asp Ser Ser Gln Ala Ile Pro Leu Val Val Glu Ser Cys				
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Arg Gly Glu Asp Pro Leu Ala Gly Asp Gln Asn Asp His Asp Met Asp				
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Leu Cys Asp Glu Leu Cys Pro Asp Ser Lys Ser Asp Glu Pro Val Cys	
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Ala Ser Asp Asn Ala Thr Tyr Ala Ser Glu Cys Ala Met Lys Glu Ala	
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gcc tgc tcc tca ggt gtg cta ctg gaa gta aag cac tcc gga tct tgc	1260
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Asn Ser Ile Ser Glu Asp Thr Glu Glu Glu Glu Glu Asp Glu Asp Gln	
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cgtcttcctg gggtctgaag taacggaagc taccttgat aaagacctca acactgctga      240
cc  atg atc agc gca gcc tgg agc atc ttc ctc atc ggg act aaa att      287
    Met Ile Ser Ala Ala Trp Ser Ile Phe Leu Ile Gly Thr Lys Ile
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ggg ctg ttc ctt caa gta gca cct cta tca gtt atg gct aaa tcc tgt      335
Gly Leu Phe Leu Gln Val Ala Pro Leu Ser Val Met Ala Lys Ser Cys
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cca tct gtg tgt cgc tgc gat gcg ggt ttc att tac tgt aat gat cgc      383
Pro Ser Val Cys Arg Cys Asp Ala Gly Phe Ile Tyr Cys Asn Asp Arg
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ttt ctg aca tcc att cca aca gga ata cca gag gat gct aca act ctc      431
Phe Leu Thr Ser Ile Pro Thr Gly Ile Pro Glu Asp Ala Thr Thr Leu
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tac ctt cag aac aac caa ata aat aat gct ggg att cct tca gat ttg      479
Tyr Leu Gln Asn Asn Gln Ile Asn Asn Ala Gly Ile Pro Ser Asp Leu
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aaa aac ttg ctg aaa gta gaa aga ata tac cta tac cac aac agt tta      527
Lys Asn Leu Leu Lys Val Glu Arg Ile Tyr Leu Tyr His Asn Ser Leu
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gat gaa ttt cct acc aac ctc cca aag tat gta aaa gag tta cat ttg      575
Asp Glu Phe Pro Thr Asn Leu Pro Lys Tyr Val Lys Glu Leu His Leu
  96             101            106            111

caa gaa aat aac ata agg act atc act tat gat tca ctt tca aaa att      623
Gln Glu Asn Asn Ile Arg Thr Ile Thr Tyr Asp Ser Leu Ser Lys Ile
  112            117            122            127

ccc tat ctg gaa gaa tta cat tta gat gac aac tct gtc tct gca gtt      671
Pro Tyr Leu Glu Glu Leu His Leu Asp Asp Asn Ser Val Ser Ala Val
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agc ata gaa gag gga gca ttc cga gac agc aac tat ctc cga ctg ctt      719
Ser Ile Glu Glu Gly Ala Phe Arg Asp Ser Asn Tyr Leu Arg Leu Leu
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176	181	186	191	
tca cca tct ctt caa ggt ctc act agt cta aaa cgc ctg gtt cta gat				863
Ser Pro Ser Leu Gln Gly Leu Thr Ser Leu Lys Arg Leu Val Leu Asp				
192	197	202	207	
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Gly Asn Leu Leu Asn Asn His Gly Leu Gly Asp Lys Val Phe Phe Asn				
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cta gtt aat ttg aca gag ctg tcc ctg gtg cgg aat tcc ctg act gct				959
Leu Val Asn Leu Thr Glu Leu Ser Leu Val Arg Asn Ser Leu Thr Ala				
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Ala Pro Val Asn Leu Pro Gly Thr Asn Leu Arg Lys Leu Tyr Leu Gln				
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Asp Asn His Ile Asn Arg Val Pro Pro Asn Ala Phe Ser Tyr Leu Arg				
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Asn Asn Pro Trp Tyr Cys Gly Cys Lys Met Lys Trp Val Arg Asp Trp				
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ctg ttt gat tgt aag gac agt ggg att gta agc acc att cag ata acc				1343
Leu Phe Asp Cys Lys Asp Ser Gly Ile Val Ser Thr Ile Gln Ile Thr				
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Thr Ala Ile Pro Asn Thr Val Tyr Pro Ala Gln Gly Gln Trp Pro Ala				
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Pro Val Thr Lys Lys Gln Pro Asp Ile Lys Asn Pro Lys Leu Thr Lys Asp				
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Pro Met Thr Ala Leu Arg Leu Ser Trp Leu Lys Leu Gly His Ser Pro	
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Val Pro Met Glu Thr Ser Asn Leu Tyr Leu Phe Asp Glu Thr Pro Val	
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Cys Ile Glu Thr Glu Thr Ala Pro Leu Arg Met Tyr Asn Pro Thr Thr	
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136 141 146 151

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152 157 162 167

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Tyr Val Cys Val Lys Cys Cys Ala Glu Glu Asp Lys Lys Thr Glu Ile							
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Ala	Gln	Ser	Val	Met	Glu	Gln	Asn	Thr	Val	Lys	Glu	Ile	Pro	Phe	Leu	
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Ser	Ser	Ile	Ser	Ala	Gly	Ser	Leu	Thr	Ser	Leu	Ser	Leu	Arg	Gly	Lys	
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Pro	Pro	Asp	Val	Ser	Thr	Glu	Ala	Phe	Leu	Thr	Asn	Leu	Ser	Ile	Gln	
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Asn Ser Ser Pro Cys Arg Ser Asn Val Gly Lys Gly Asn Ile Asp Gly			
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Asn Val Ser Cys Ser Glu Asn Leu Val Ala Asn Thr Ala Arg Ser Pro			
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Gln Phe Ile Asn Leu Lys Arg Asp Pro Arg Gln Ala Ala Gly Arg Ser			
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Gln Pro Val Thr Thr Ser Glu Ser Lys Asp Gly Asp Ser Cys Arg Asn			
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1176	1181	1186	1191
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Thr Glu Gln Ile Asn Val Glu Glu Lys Leu Cys Ser Ala Glu Lys Asn			
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Ser Cys Val Gln Gln Ser Asp Asn Leu Lys Val Ala Gln Asn Ser Pro			
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tca gta gaa aac ata cag act tct caa gca gaa caa gca aaa ccc tta			5308
Ser Val Glu Asn Ile Gln Thr Ser Gln Ala Glu Gln Ala Lys Pro Leu			
1224	1229	1234	1239
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Gln Glu Asp Ile Leu Met Gln Asn Ile Glu Thr Val His Pro Phe Arg			
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cca tca gaa ttt cct tct aaa agc atc acc ttt act tcc aga agc acc			5452
Pro Ser Glu Phe Pro Ser Lys Ser Ile Thr Phe Thr Ser Arg Ser Thr			
1272	1277	1282	1287
agc ccc aga aca agt aca aac ttt tca ccc atg agg cca cag cag ccc			5500
Ser Pro Arg Thr Ser Thr Asn Phe Ser Pro Met Arg Pro Gln Gln Pro			
1288	1293	1298	1303
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Asn Leu Gln His Leu Lys Ser Ser Pro Pro Gly Phe Pro Phe Pro Gly			
1304	1309	1314	1319

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Gly Thr Asp Gly Lys Ala Ser Arg Asp Ser Arg Asn Val Asp Lys Lys	
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cccagcaggc	ccagccaggc	gtggaggaag	aggcattgag	gactttcctt	acctgttttt	180

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Trp Gln Asp Arg Phe Trp Leu Pro Pro Asn Val Thr Trp Thr Glu Leu		
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Thr Glu Gly His Arg Pro Lys Glu Pro Gln Leu Ser Leu Leu Ala Ala		
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Gln Cys Gly Leu Thr Leu Gln Gln Thr Gln Arg Trp Phe Arg Arg Arg		
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Arg Asn Gln Asp Arg Pro Gln Leu Thr Lys Lys Phe Cys Glu Ala Ser		
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Lys Arg Lys Asp Phe Lys Glu Gln Val Ile His His Phe Val Ala Val		
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Leu Val Leu Leu Leu His Asp Ser Ser Asp Tyr Leu Leu Glu Ala Cys	
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Leu Ile Phe Ser Phe Val Phe Phe Tyr Thr Arg Leu Val Leu Phe Pro	
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acc cag atc ctc tac acc aca tac tac gag tcc atc agc aac agg ggc	1096
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282 287 292 297	
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Phe Met Lys Lys Gly Gln Met Glu Lys Asp Ile Arg Ser Asp Val Glu	
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Leu Lys Asn Gly Thr Ala Gly Gly Pro Arg Pro Ala Pro Thr Asp Gly	
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Pro Arg Ser Arg Val Ala Gly Arg Leu Thr Asn Arg His Thr Thr Ala	
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Ser Ala Arg Leu Arg Thr Val Phe Gln Gly Val Gly His Trp Ala Leu
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Ser Thr Trp Ala Gly Leu Lys Pro Ser Arg Leu Leu Pro Gln Arg Ala
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tct ccc agg ctg ctc tcg gtc ggc cgt gcg gac ctc gcc aag cat cag   196
Ser Pro Arg Leu Leu Ser Val Gly Arg Ala Asp Leu Ala Lys His Gln
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Phe Val Asp Tyr Arg Arg Val Leu Val Cys Gly Gly Asn Gly Gly Ala
      72          77          82          87

ggg gca agc tgc ttc cac agt gag ccc cgc aag gag ttt gga ggc cct   340
Gly Ala Ser Cys Phe His Ser Glu Pro Arg Lys Glu Phe Gly Gly Pro
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gat gga ggg gac gga ggc aac ggt gga cac gtc att ctg aga gtt gac   388
Asp Gly Gly Asp Gly Gly Asn Gly Gly His Val Ile Leu Arg Val Asp
      104          109          114          119

cag caa gtc aag tcc ctg tcg tcg gtc ctg tcg cgg tac cag ggt ttc   436
Gln Gln Val Lys Ser Leu Ser Ser Val Leu Ser Arg Tyr Gln Gly Phe
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agt gga gaa gat gga ggg agt aaa aac tgc ttc ggg cgc agt ggc gcc   484
Ser Gly Glu Asp Gly Gly Ser Lys Asn Cys Phe Gly Arg Ser Gly Ala
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Val Leu Tyr Ile Arg Val Pro Val Gly Thr Leu Val Lys Glu Gly Gly
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184 189 194 199	
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264 269 274 279	
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Pro Gly Ile Ile Arg Gly Ala His Gln Asn Arg Gly Leu Gly Ser Ala	
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Ser Leu Leu Arg Ser Pro Glu Asn Val Ile Glu Thr Ile Ser Ser Leu				
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Leu Ala Ser Val Thr Leu Asp Leu Ser Gln Tyr Ala Met Asp Ile Val				
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Lys Gly Leu Ala Gly His Leu Lys Ser Asn Ser Pro Arg Leu Met Asp				
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Glu Ala Val Leu Ala Leu Arg Asn Leu Ala Arg Gln Cys Ser Asp Ser				
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Ser Ala Met Glu Ser Leu Thr Lys His Leu Phe Ala Ile Leu Gly Gly				
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Thr Val Leu His Leu Thr Glu Arg Leu Phe Leu Asp His Pro His Arg	
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Arg Lys Leu Leu Ser Ser Leu Gly Gly Phe Lys Leu Ala His Gly Leu	
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Phe Ile Thr Arg His Leu Asp Gln Ile Ile Pro Arg Met Thr Thr Gln	
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Glu	Glu	Leu	Ser	Val	Ala	Val	Lys	Arg	Ala	Val	Met	Leu	Leu	His	Thr	
743					748					753					758	
cac	acc	atc	acc	agc	agg	gtg	ggc	aag	ggg	gag	cca	ggg	gct	gcg	ccc	2957
His	Thr	Ile	Thr	Ser	Arg	Val	Gly	Lys	Gly	Glu	Pro	Gly	Ala	Ala	Pro	
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887					892					897					902	
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Glu Ala Leu Ser Gln Ala Val Ala Arg Tyr Gln Arg Gln Ala Ala Glu				
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Val Met Gly Arg Leu Met Glu Ile Tyr Gln Glu Lys Leu Tyr Arg Pro				
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ccc cca gtg ctg gat gct ttg gga cga gtt att tca gaa tct cct cca				3725
Pro Pro Val Leu Asp Ala Leu Gly Arg Val Ile Ser Glu Ser Pro Pro				
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Asp Gln Trp Glu Ala Arg Cys Gly Leu Ala Leu Ala Leu Asn Lys Leu				
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Glu Ser Val Ala Ser Cys Leu Pro Pro Leu Val Pro Ala Ile Lys Glu				
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Phe Glu Asp Leu Leu Pro Trp Leu Met Glu Thr Leu Thr Tyr Glu Gln	
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Ala Gly Leu Gly Val Glu Lys Leu Glu Lys Leu Met Pro Glu Ile Val	
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Ala Thr Ala Ser Lys Val Asp Ile Ala Pro His Val Arg Asp Gly Tyr	
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Ile Met Met Phe Asn Tyr Leu Pro Ile Thr Phe Gly Asp Lys Phe Thr	
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Pro Tyr Val Gly Pro Ile Ile Pro Cys Ile Leu Lys Ala Leu Ala Asp	
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Glu Asn Glu Phe Val Arg Asp Thr Ala Leu Arg Ala Gly Gln Arg Val	
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Ile Ser Met Tyr Ala Glu Thr Ala Ile Ala Leu Leu Leu Pro Gln Leu	
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Phe	Glu	Gln	Leu	His	Ser	Thr	Ile	Gly	His	Gln	Ala	Leu	Glu	Asp	Ile		
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Leu	Pro	Phe	Leu	Leu	Lys	Gln	Leu	Asp	Asp	Glu	Glu	Val	Ser	Glu	Phe		
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Leu Pro Tyr Leu Val Pro Lys Leu Thr Thr Pro Pro Val Asn Thr Arg				
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Val Leu Ala Phe Leu Ser Ser Val Ala Gly Asp Ala Leu Thr Arg His				
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Leu Gly Val Ile Leu Pro Ala Val Met Leu Ala Leu Lys Glu Lys Leu				
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Gly Thr Pro Asp Glu Gln Leu Glu Met Ala Asn Cys Gln Ala Val Ile				
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Leu Ser Val Glu Asp Asp Thr Gly His Arg Ile Ile Ile Glu Asp Leu				
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Leu Glu Ala Thr Arg Ser Pro Glu Val Gly Met Arg Gln Ala Ala Ala				
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Ile Ile Leu Asn Ile Tyr Cys Ser Arg Ser Lys Ala Asp Tyr Thr Ser				
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Lys Lys Leu Asp Ala Gly Asn Gln Leu Ala Leu Ile Glu Glu Leu His				
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Lys Glu Ile Arg Leu Ile Gly Asn Glu Ser Lys Gly Glu His Val Pro				
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Gly Phe Cys Leu Pro Lys Lys Gly Val Thr Ser Ile Leu Pro Val Leu				
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Lys Ala Leu Gly Leu Val Ile Arg Leu Thr Ser Ala Asp Ala Leu Arg				
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	Met Leu Arg Ala Gly Trp	
	1	
ctc cgg ggc gcg gcg gcg ctg gcg ctg ctg ctg gcg gcc cga gtg gtg		161
Leu Arg Gly Ala Ala Leu Ala Leu Leu Leu Ala Ala Arg Val Val		
7 12 17 22		
gcg gcg ttc gag ccc atc acc gtg ggc cta gcc atc ggg gcc gcg tcg		209
Ala Ala Phe Glu Pro Ile Thr Val Gly Leu Ala Ile Gly Ala Ala Ser		
23 28 33 38		
gcc atc acc ggc tac ctg tcc tac aat gac atc tac tgc cgc ttc gcc		257
Ala Ile Thr Gly Tyr Leu Ser Tyr Asn Asp Ile Tyr Cys Arg Phe Ala		
39 44 49 54		
gag tgc tgc cgc gag gag cgg ccg ctc aac gct tcg gct ctc aag ctg		305
Glu Cys Cys Arg Glu Glu Arg Pro Leu Asn Ala Ser Ala Leu Lys Leu		
55 60 65 70		
gat ttg gag gag aag ctg ttt gga cag cat cta gcc acg gaa gtg att		353
Asp Leu Glu Glu Lys Leu Phe Gly Gln His Leu Ala Thr Glu Val Ile		
71 76 81 86		
ttc aag gcg ctg act ggc ttc agg aac aac aaa aat ccc aag aaa cca		401
Phe Lys Ala Leu Thr Gly Phe Arg Asn Asn Lys Asn Pro Lys Lys Pro		
87 92 97 102		
ctg acc ctt tcc tta cac ggc tgg gct ggc aca ggc aag aat ttt gtc		449
Leu Thr Leu Ser Leu His Gly Trp Ala Gly Thr Gly Lys Asn Phe Val		
103 108 113 118		
agt caa att gtg gct gaa aat ctt cac cca aaa ggt ctg aag agt aac		497
Ser Gln Ile Val Ala Glu Asn Leu His Pro Lys Gly Leu Lys Ser Asn		
119 124 129 134		
ttt gtc cac ctg ttt gta tcg act ctg cac ttc cct cat gag cag aag		545
Phe Val His Leu Phe Val Ser Thr Leu His Phe Pro His Glu Gln Lys		
135 140 145 150		
ata aaa ctg tac ccg gac cag tta cag aag tgg atc cgc ggt aat gtg		593
Ile Lys Leu Tyr Pro Asp Gln Leu Gln Lys Trp Ile Arg Gly Asn Val		
151 156 161 166		
agt gca tgt gcg aac tct gtt ttc ata ttt gac gag atg gat aaa ttg		641
Ser Ala Cys Ala Asn Ser Val Phe Ile Phe Asp Glu Met Asp Lys Leu		
167 172 177 182		
cac ccc ggg atc att gac gca atc aag ccg ttt cta gac tac tac gag		689
His Pro Gly Ile Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Glu		
183 188 193 198		
cag gtt gac gga gtg tat tac cgc aaa gcc atc ttc atc ttt ctc agc		737
Gln Val Asp Gly Val Tyr Tyr Arg Lys Ala Ile Phe Ile Phe Leu Ser		
199 204 209 214		
aat gca ggc ggg gac ctt ata act aag acg gct ctt gac ttt tgg cgg		785

Asn Ala Gly Gly Asp Leu Ile Thr Lys Thr Ala Leu Asp Phe Trp Arg	
215 220 225 230	
gcc gga aga aag agg gaa gac att cag ctg aag gac ctg gaa cct gta	833
Ala Gly Arg Lys Arg Glu Asp Ile Gln Leu Lys Asp Leu Glu Pro Val	
231 236 241 246	
ctg tct gtc gga gtc ttc aat aat aaa cac agt ggc ctg tgg cac agt	881
Leu Ser Val Gly Val Phe Asn Asn Lys His Ser Gly Leu Trp His Ser	
247 252 257 262	
gga ctg atc gac aaa aac ctc att gat tac ttt atc ccc ttc ctg cct	929
Gly Leu Ile Asp Lys Asn Leu Ile Asp Tyr Phe Ile Pro Phe Leu Pro	
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Leu Glu Tyr Arg His Val Lys Met Cys Val Met Ala Glu Met Arg Ala	
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cgt ggt tct gcc ata gat gaa gac att gtc aca aga gtg gca gag gaa	1025
Arg Gly Ser Ala Ile Asp Glu Asp Ile Val Thr Arg Val Ala Glu Glu	
295 300 305 310	
atg acg ttt ttt ccc cag aga cga gaa aat cta ctc aga caa ggg ctg	1073
Met Thr Phe Phe Pro Gln Arg Arg Glu Asn Leu Leu Arg Gln Gly Leu	
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caa gac tgt gca gtc gcg gct gga ttt cca ctg agc tcc tat cca gat	1121
Gln Asp Cys Ala Val Ala Ala Gly Phe Pro Leu Ser Ser Tyr Pro Asp	
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Gly Val Gly Asp Ser Trp Glu Ala Pro His Ala Arg Gly Leu Ala Phe	
343 348 353 358	
cag aag aac cct gaa gac cgc ttt ggg gtt ttg cct gtt tgc acc tta	1217
Gln Lys Asn Pro Glu Asp Arg Phe Gly Val Leu Pro Val Cys Thr Leu	
359 364 369 374	
gac ttt tgg gta tag aatctttttt ttgagaagag gtctcactcc gtcaccaag	1272
Asp Phe Trp Val *	
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gaaaaaaa	ccaaggtagc	gtttaaaatt	tttagtacat	atcctcaa	atgagctaag	2712
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acgcgtccgg	attgggaaaa	caacgat	atg gca gga gcc agt ctt ggg gcc	111
			Met Ala Gly Ala Ser Leu Gly Ala	
			1 5	

cgc ttc tac cgg cag atc aaa aga cat ccg ggg atc atc ccg atg atc	159
Arg Phe Tyr Arg Gln Ile Lys Arg His Pro Gly Ile Ile Pro Met Ile	
9 14 19 24	
ggc tta atc tgc ctg ggc atg ggc agc gct gcg ctt tac ttg ctg cga	207
Gly Leu Ile Cys Leu Gly Met Gly Ser Ala Ala Leu Tyr Leu Leu Arg	
25 30 35 40	
ctc gcc ctt cgc agc ccc gac gtc tgc tgg gac aga aag aac aac ccg	255
Leu Ala Leu Arg Ser Pro Asp Val Cys Trp Asp Arg Lys Asn Asn Pro	
41 46 51 56	
gag ccc tgg aac cgc ctg agc ccc aat gac caa tac aag ttc ctt gca	303
Glu Pro Trp Asn Arg Leu Ser Pro Asn Asp Gln Tyr Lys Phe Leu Ala	
57 62 67 72	
gtt tcc act gac tat aag aag ctg aag aag gac cgg cca gac ttc taa	351
Val Ser Thr Asp Tyr Lys Lys Leu Lys Lys Asp Arg Pro Asp Phe *	
73 78 83 88	
gccaggctgg gctgccagtg ccatgcaagc cacagccagc cagcccatcc acttcttcca	411
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caccagcagg ggtccaccaa gagcccagac cagccctctt gccctcctac ccgggcctcg	651
aagggtgtgg cacaggctac gtgttgagcg tggcctacgt gagccaacaa gaagcagggg	711
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accccctcca gccccacacc tgggcctccc cctgccactc cctcccttg ctcccctctg	951
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aaaa	1015

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<400> 244

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                                   Met Arg Arg Leu Leu Leu Val Thr
                                   1                               5

agc ctg gtg gtt gtg ctg ctg tgg gag gca ggt gca gtc cca gca ccc      159
Ser Leu Val Val Val Leu Leu Trp Glu Ala Gly Ala Val Pro Ala Pro
9                               14                               19                               24

aag gtc cct atc aag atg caa gtc aaa cac tgg ccc tca gag cag gac      207
Lys Val Pro Ile Lys Met Gln Val Lys His Trp Pro Ser Glu Gln Asp
25                               30                               35                               40

cca gag aag gcc tgg ggc gcc cgt gtg gtg gag cct ccg gag aag gac      255
Pro Glu Lys Ala Trp Gly Ala Arg Val Val Glu Pro Pro Glu Lys Asp
41                               46                               51                               56

gac cag ctg gtg gtg ctg ttc cct gtc cag aag ccg aaa ctc ttg acc      303
Asp Gln Leu Val Val Leu Phe Pro Val Gln Lys Pro Lys Leu Leu Thr
57                               62                               67                               72

acc gag gag aag cca cga ggc acc aag gcc tgg atg gag acc gag gac      351
Thr Glu Glu Lys Pro Arg Gly Thr Lys Ala Trp Met Glu Thr Glu Asp
73                               78                               83                               88

acc ctg ggc cgt gtc ctg agt ccc gag ccc gac cat gac agc ctg tac      399
Thr Leu Gly Arg Val Leu Ser Pro Glu Pro Asp His Asp Ser Leu Tyr
89                               94                               99                               104

cac cct ccg cct gag gag gac cag ggc gag gag agg ccc ccg ttg tgg      447
His Pro Pro Pro Glu Glu Asp Gln Gly Glu Glu Arg Pro Arg Leu Trp
105                               110                               115                               120

gtg atg cca aat cac cag gtg ctc ctg gga ccg gag gaa gac caa gac      495
Val Met Pro Asn His Gln Val Leu Leu Gly Pro Glu Glu Asp Gln Asp
121                               126                               131                               136

cac atc tac cac ccc cag tag gg ctccaggggc catcactgcc cccgcctgt      548
His Ile Tyr His Pro Gln *
137                               142

cccaaggccc aggctgttgg gactgggacc ctccctaccc tgccccagct agacaaataa      608

accccagcag gccgggaaaa aaaaaaaaaa      636

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<400> 246

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tcc gtc gac ggc ctc acg ctc agc ccg gac ccg gag gag ccg cct ggg	96	
Ser Val Asp Gly Leu Thr Leu Ser Pro Asp Pro Glu Glu Arg Pro Gly		
13 18 23 28		
gcg gag ggc gcc ccg ctg ctg ccg cca ccg ctg cca ccg ccc tcg cca	144	
Ala Glu Gly Ala Pro Leu Leu Pro Pro Pro Leu Pro Pro Pro Ser Pro		
29 34 39 44		
cct gga tcc ggt cgc ggc ccg ggc gcc tca ggg gag cag ccc gag ccc	192	
Pro Gly Ser Gly Arg Gly Pro Gly Ala Ser Gly Glu Gln Pro Glu Pro		
45 50 55 60		
ggg gag gcg gcg gct ggg ggc gcg gcg gag gag gcg ccg ccg ctg gag	240	
Gly Glu Ala Ala Ala Gly Gly Ala Ala Glu Glu Ala Arg Arg Leu Glu		
61 66 71 76		
cag cgc tgg ggt ttc ggc ctg gag gag ttg tac ggc ctg gca ctg cgc	288	
Gln Arg Trp Gly Phe Gly Leu Glu Glu Leu Tyr Gly Leu Ala Leu Arg		
77 82 87 92		
ttc ttc aaa gaa aaa gat ggc aaa gca ttt cat cca act tat gaa gaa	336	
Phe Phe Lys Glu Lys Asp Gly Lys Ala Phe His Pro Thr Tyr Glu Glu		
93 98 103 108		
aaa ttg aag ctt gtg gca ctg cat aag caa gtt ctt atg ggc cca tat	384	
Lys Leu Lys Leu Val Ala Leu His Lys Gln Val Leu Met Gly Pro Tyr		
109 114 119 124		
aat cca gac act tgt cct gag gtt gga ttc ttt gat gtg ttg ggg aat	432	
Asn Pro Asp Thr Cys Pro Glu Val Gly Phe Phe Asp Val Leu Gly Asn		
125 130 135 140		
gac agg agg aga gaa tgg gca gcc ctg gga aac atg tct aaa gag gat	480	
Asp Arg Arg Arg Glu Trp Ala Ala Leu Gly Asn Met Ser Lys Glu Asp		
141 146 151 156		
gcc atg gtg gag ttt gtc aag ctc tta aat agg tgt tgc cat ctc ttt	528	
Ala Met Val Glu Phe Val Lys Leu Leu Asn Arg Cys Cys His Leu Phe		
157 162 167 172		
tca aca tat gtt gcg tcc cac aaa ata gag aag gaa gag caa gac aaa	576	
Ser Thr Tyr Val Ala Ser His Lys Ile Glu Lys Glu Glu Gln Asp Lys		
173 178 183 188		
aaa agg aag gag gaa gag gag cga agg cat cgt gaa gag gaa gaa aga	624	
Lys Arg Lys Glu Glu Glu Glu Arg Arg His Arg Glu Glu Glu Glu Arg		
189 194 199 204		
gaa cgt ctg caa aag gag gaa gag aaa cgt agg aga gaa gaa gag gaa	672	

Glu Arg Leu Gln Lys	Glu Glu Glu Lys Arg	Arg Arg Glu Glu Glu Glu	205	210	215	220
agg ctt cga cgg gag	gaa gag gaa agg aga	cgg ata gaa gaa gaa agg	720	221	231	236
Arg Leu Arg Arg Glu	Glu Glu Glu Arg Arg	Arg Ile Glu Glu Glu Arg				
ctt cgg ttg gag cag	caa aag cag cag ata	atg gca gct tta aac tcc	768	237	247	252
Leu Arg Leu Glu Gln	Gln Lys Gln Gln Ile	Met Ala Ala Leu Asn Ser				
cag act gcc gtg cag	ttc cag cag tat gca	gcc caa cag tat cca ggg	816	253	263	268
Gln Thr Ala Val Gln	Phe Gln Gln Tyr Ala	Ala Gln Gln Tyr Pro Gly				
aac tac gaa cag cag	caa att ctc atc cgc	cag ttg cag gag caa cac	864	269	279	284
Asn Tyr Glu Gln Gln	Gln Ile Leu Ile Arg	Gln Leu Gln Glu Gln His				
tat cag cag tac atg	cag cag ttg tat caa	gtc cag ctt gca cag caa	912	285	295	300
Tyr Gln Gln Tyr Met	Gln Gln Leu Tyr Gln	Val Gln Leu Ala Gln Gln				
cag gca gca tta cag	aaa caa cag gaa gta	gta gtg gct ggg tct tcc	960	301	311	316
Gln Ala Ala Leu Gln	Lys Gln Gln Glu Val	Val Val Ala Gly Ser Ser				
ttg cct aca tca tca	aaa gtg aat gca act	gta cca agt aat atg atg	1008	317	327	332
Leu Pro Thr Ser Ser	Lys Val Asn Ala Thr	Val Pro Ser Asn Met Met				
tca gtt aat gga cag	gcc aaa aca cac act	gac agc tcc gaa aaa gaa	1056	333	343	348
Ser Val Asn Gly Gln	Ala Lys Thr His Thr	Asp Ser Ser Glu Lys Glu				
ctg gaa cca gaa gct	gca gaa gaa gcc ctg	gag aat gga cca aaa gaa	1104	349	359	364
Leu Glu Pro Glu Ala	Ala Glu Glu Ala Leu	Glu Asn Gly Pro Lys Glu				
tct ctt cca gta ata	gca gct cca tcc atg	tgg aca cga cct cag atc	1152	365	375	380
Ser Leu Pro Val Ile	Ala Ala Pro Ser Met	Trp Thr Arg Pro Gln Ile				
aaa gac ttc aaa gag	aag att cag cag gat	gca gat tcc gtg att aca	1200	381	391	396
Lys Asp Phe Lys Glu	Lys Ile Gln Gln Asp	Ala Asp Ser Val Ile Thr				
gtg ggc cga gga gaa	gtg gtc act gtt cga	gta ccc acc cat gaa gaa	1248	397	407	412
Val Gly Arg Gly Glu	Val Val Thr Val Arg	Val Pro Thr His Glu Glu				
gga tca tat ctc ttt	tgg gaa ttt gcc aca	gac aat tat gac att ggg	1296	413	423	428
Gly Ser Tyr Leu Phe	Trp Glu Phe Ala Thr	Asp Asn Tyr Asp Ile Gly				
ttt ggg gtg tat ttt	gaa tgg aca gac tct	cca aac act gct gtc agc	1344			
Phe Gly Val Tyr Phe	Glu Trp Thr Asp Ser	Pro Asn Thr Ala Val Ser				

429	434	439	444	
gtg cat gtc agt gag tcc agc gat gac gac	gag gag gaa gaa gaa aac	1392		
Val His Val Ser Glu Ser Ser Asp Asp Asp	Glu Glu Glu Glu Glu Asn			
445	450	455	460	
atc ggt tgt gaa gag aaa gcc aaa aag aat	gcc aac aag cct ttg ctg	1440		
Ile Gly Cys Glu Glu Lys Ala Lys Lys Asn	Ala Asn Lys Pro Leu Leu			
461	466	471	476	
gat gag att gtg cct gtg tac cga cgg gac	tgt cat gag gag gtg tat	1488		
Asp Glu Ile Val Pro Val Tyr Arg Arg Asp	Cys His Glu Glu Val Tyr			
477	482	487	492	
gct ggc agc cat caa tat cca ggg aga gga	gtc tat ctc ctc aag ttt	1536		
Ala Gly Ser His Gln Tyr Pro Gly Arg Gly	Val Tyr Leu Leu Lys Phe			
493	498	503	508	
gac aac tcc tac tct ttg tgg cgg tca aaa	tca gtc tac tac aga gtc	1584		
Asp Asn Ser Tyr Ser Leu Trp Arg Ser Lys	Ser Val Tyr Tyr Arg Val			
509	514	519	524	
tat tat act aga taa aaatgttggt acaaagtctg	gagtctaggg ttgggcagaa	1639		
Tyr Tyr Thr Arg *				
525				
gatgacattt aatttgga aaatcttttta cttttgtgga	gcattagagt cacagtttac	1699		
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 gttctctctt gcacagccta aaatgaccaa tgtgtgattt cagtgaata a atg gcg 177
 Met Ala
 1
 tcc aaa gtc aca gat gct ata gtc tgg tat caa aag aag att gga gca 225
 Ser Lys Val Thr Asp Ala Ile Val Trp Tyr Gln Lys Lys Ile Gly Ala
 3 8 13 18
 tat gaa caa caa ata tgg gaa aaa tct gtt gaa cag aga gaa atc aag 273
 Tyr Glu Gln Gln Ile Trp Glu Lys Ser Val Glu Gln Arg Glu Ile Lys
 19 24 29 34

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Phe Ile Lys Leu Gly Leu Arg Asn Lys Pro Lys Lys Thr Ala His Val	
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Lys Pro Asp Leu Ile Asp Val Asp Leu Val Arg Gly Ser Ala Phe Ala	
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Lys Ala Lys Pro Glu Ser Pro Trp Thr Ser Leu Pro Arg Lys Gly Ile	
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Val Arg Val Val Phe Phe Pro Phe Phe Phe Arg Trp Trp Leu Gln Val	
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Thr Ser Lys Val Ile Phe Phe Trp Leu Leu Val Leu Tyr Leu Leu Gln	
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Val Ala Ala Ile Val Leu Phe Cys Ser Thr Ser Ser Pro His Ser Ile	
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Pro Leu Thr Glu Val Ile Gly Pro Ile Trp Leu Met Leu Leu Leu Gly	
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Thr Val His Cys Gln Ile Val Ser Thr Arg Thr Pro Lys Pro Pro Leu	
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agt aca ggg ggt aaa aga aga agg aaa tta aga aaa gca gcc cat ttg	705
Ser Thr Gly Gly Lys Arg Arg Arg Lys Leu Arg Lys Ala Ala His Leu	
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Tyr Val Ser Leu Asp Gly Lys Lys Thr Val Lys Ser Gly Glu Asp Gly	
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Ala Trp Asn Thr Gly Thr Leu Arg Asn Gly Pro Ser Lys Asp Thr Gln	
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Arg Thr Ile Thr Asn Val Ser Asp Glu Val Ser Ser Glu Glu Gly Pro	
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Met Ile Met Asn Arg Val Asn Ser His Ile Pro Gly Ile Gly Tyr Gln	
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Ile Phe Gly Asn Ala Val Ser Leu Ile Leu Gly Leu Thr Pro Phe Val	
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Val	Leu	Ser	Met	Val	Ile	Ile	Ser	Phe	Val	Val	Arg	Val	Ser	Leu	Val		
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Trp	Ile	Phe	Phe	Phe	Leu	Leu	Cys	Val	Ala	Glu	Arg	Thr	Tyr	Lys	Gln		
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Val	Gly	Ile	Met	*													
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Pro	Arg	Ile	Ala	Gln	Lys	Ile	Lys	Arg	Phe	Arg	Asn	Lys	Gln	Ala	Gln	
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Glu	Gly	Ser	Cys	Lys	Arg	Thr	Val	Met	Val	Gly	Met	Gly	His	Arg	Trp	
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Arg	Ala	Asp	Cys	Thr	Met	Pro	Asp	Glu	Asp	Leu	Phe	Asn	Pro	Asp	Tyr		
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gta	gaa	gtt	gat	cgc	atc	ttg	gag	gtg	gcc	cac	acc	aag	gat	gca	gaa	411	
Val	Glu	Val	Asp	Arg	Ile	Leu	Glu	Val	Ala	His	Thr	Lys	Asp	Ala	Glu		
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Thr	Gly	Glu	Glu	Val	Thr	His	Tyr	Leu	Val	Lys	Trp	Cys	Ser	Leu	Pro		
88					93					98					103		
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Tyr	Glu	Glu	Ser	Thr	Trp	Glu	Leu	Glu	Glu	Asp	Val	Asp	Pro	Ala	Lys		
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Val	Lys	Glu	Phe	Glu	Ser	Leu	Gln	Val	Leu	Pro	Glu	Ile	Lys	His	Val		
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Trp	Leu	Leu	Phe	Asn	Trp	Tyr	Asn	Arg	Lys	Asn	Cys	Ile	Leu	Ala	Asp		
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Ser	Thr	Ile	Thr	Asn	Trp	Glu	Arg	Glu	Phe	Arg	Thr	Trp	Thr	Glu	Met		
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Asn	Ala	Ile	Val	Tyr	His	Gly	Ser	Gln	Ile	Ser	Arg	Gln	Met	Ile	Gln		
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Gln	Tyr	Glu	Met	Val	Tyr	Arg	Asp	Ala	Gln	Gly	Asn	Pro	Leu	Ser	Gly		
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gaa gcc cac aga ctg	aag aat agg aac tgc	aaa ctt ctg gag ggt cta		1083
Glu Ala His Arg Leu	Lys Asn Arg Asn Cys	Lys Leu Leu Glu Gly Leu		
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Lys Leu Met Ala Leu	Glu His Lys Val Leu	Leu Thr Gly Thr Pro Leu		
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Gln Asn Ser Val Glu	Glu Leu Phe Ser Leu	Leu Asn Phe Leu Glu Pro		
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Ser Gln Phe Pro Ser	Glu Thr Ala Phe Leu	Glu Glu Phe Gly Asp Leu		
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Lys Thr Glu Glu Gln	Val Lys Lys Leu Gln	Ser Ile Leu Lys Pro Met		
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atg ctt cgg cgg ctg	aaa gat gat gtg gaa	aag aac ctt gct ccc aaa		1323
Met Leu Arg Arg Leu	Lys Asp Asp Val Glu	Lys Asn Leu Ala Pro Lys		
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caa gag acg atc att	gag gtg gaa ctg acc	aat atc cag aaa aag tac		1371
Gln Glu Thr Ile Ile	Glu Val Glu Leu Thr	Asn Ile Gln Lys Lys Tyr		
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Tyr Arg Ala Ile Leu	Glu Lys Asn Phe Ser	Phe Leu Thr Lys Gly Ala		
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Asn Gln His Asn Met	Pro Asn Leu Ile Asn	Thr Met Met Glu Leu Arg		
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aag tgc tgt aac cat	ccc tac ctg atc aat	gga gca gag gag aaa att		1515
Lys Cys Cys Asn His	Pro Tyr Leu Ile Asn	Gly Ala Glu Glu Lys Ile		
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cta gaa gat ttc cga	aaa acc cac agc cct	gat gcc cct gac ttt cag		1563
Leu Glu Asp Phe Arg	Lys Thr His Ser Pro	Asp Ala Pro Asp Phe Gln		
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Leu Gln Ala Met Ile	Gln Ala Ala Gly Lys	Leu Val Leu Ile Asp Lys		
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Leu Leu Pro Lys Leu	Ile Ala Gly Gly His	Lys Val Leu Ile Phe Ser		
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Gln Met Val Arg Cys	Leu Asp Ile Leu Glu	Asp Tyr Leu Ile Gln Arg		
504	509	514	519	

aga tac acc tat gag cga att gat ggg cga gta cgg gga aac ctg cgc	1755
Arg Tyr Thr Tyr Glu Arg Ile Asp Gly Arg Val Arg Gly Asn Leu Arg	
520 525 530 535	
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Phe Leu Leu Cys Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Thr Ala	
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Ala Asp Thr Cys Ile Ile Phe Asp Ser Asp Trp Asn Pro Gln Asn Asp	
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Trp Pro Arg Ala Gln Pro Gln Asp Asn Ala Ala Ala Cys Leu Gln	
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Asp Phe Gly Ser Gln Leu Gly Val Gln Ser Glu Glu Thr Gly Pro Phe	
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His Asn Arg Gln Lys Gln Asp Ser Gly Asn Ser His Thr Ala Pro Arg	
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Trp Ala Gln Ala Arg Cys His Arg Ile Gly Gln Ser Lys Ala Val Lys	
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Val Tyr Arg Leu Ile Thr Arg Asn Ser Tyr Glu Arg Glu Met Phe Asp	
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Lys Ala Ser Leu Lys Leu Gly Leu Asp Lys Ala Val Leu Gln Asp Ile	
728 733 738 743	

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Arg Thr Ser Glu Met Asp Leu Ile Asn Lys Glu Ala Gln Lys Arg Trp				
1224	1229	1234	1239	
act agg aga gaa caa gca gac ttc tat aga aca gtg tct tcc ttt ggt				3915
Thr Arg Arg Glu Gln Ala Asp Phe Tyr Arg Thr Val Ser Ser Phe Gly				
1240	1245	1250	1255	
gtt gtt tac gat caa gaa aag aaa acc ttt gac tgg aca cag ttc cgc				3963
Val Val Tyr Asp Gln Glu Lys Lys Thr Phe Asp Trp Thr Gln Phe Arg				
1256	1261	1266	1271	
atc att tcc cgt ttg gac aag aag tgc gat gag agc ctg gaa cag tat				4011
Ile Ile Ser Arg Leu Asp Lys Lys Ser Asp Glu Ser Leu Glu Gln Tyr				
1272	1277	1282	1287	
ttt tat agt ttt gtg gcc atg tgc cgg aat gtc tgt cgt cta ccc aca				4059
Phe Tyr Ser Phe Val Ala Met Cys Arg Asn Val Cys Arg Leu Pro Thr				
1288	1293	1298	1303	
tgg aaa gat ggc ggt ccc cca gat acc acc atc tac gtt gaa ccc atc				4107
Trp Lys Asp Gly Gly Pro Pro Asp Thr Thr Ile Tyr Val Glu Pro Ile				
1304	1309	1314	1319	
act gag gaa cgt gct gca aga act ctg tac cgc att gaa ctg tta cgg				4155
Thr Glu Glu Arg Ala Ala Arg Thr Leu Tyr Arg Ile Glu Leu Leu Arg				
1320	1325	1330	1335	
aaa gtc cga gag caa gtg ctc aag tgc cct cag ctg cat gaa cgc ctc				4203
Lys Val Arg Glu Gln Val Leu Lys Cys Pro Gln Leu His Glu Arg Leu				
1336	1341	1346	1351	
cag ctg tgc agg ccc agc ctc tac ctc cca gtc tgg tgg gag tgt ggg				4251
Gln Leu Cys Arg Pro Ser Leu Tyr Leu Pro Val Trp Trp Glu Cys Gly				
1352	1357	1362	1367	
aag cat gat cga gac ctg ctc atc ggc act gcc aaa cat ggg ctg aac				4299
Lys His Asp Arg Asp Leu Leu Ile Gly Thr Ala Lys His Gly Leu Asn				
1368	1373	1378	1383	
cgc act gac tgt tac atc atg aac gac ccc cag ctg tcc ttc ctg gat				4347
Arg Thr Asp Cys Tyr Ile Met Asn Asp Pro Gln Leu Ser Phe Leu Asp				
1384	1389	1394	1399	
gcc tat aga aac tat gcc cag cat aaa aga tct ggc acc cag gca cca				4395
Ala Tyr Arg Asn Tyr Ala Gln His Lys Arg Ser Gly Thr Gln Ala Pro				
1400	1405	1410	1415	
gga aat ctc tgt tgc ctt tac cag acc aac tcc aag tta tat gaa tct				4443
Gly Asn Leu Cys Cys Leu Tyr Gln Thr Asn Ser Lys Leu Tyr Glu Ser				
1416	1421	1426	1431	

ctt aca tat tct caa atg agt agg act tca gag tcc ctt gaa aat gaa	4491
Leu Thr Tyr Ser Gln Met Ser Arg Thr Ser Glu Ser Leu Glu Asn Glu	
1432 1437 1442 1447	
cct gaa aat cta gtg aga gta gaa agc aga gat gat cat ctc agc ctg	4539
Pro Glu Asn Leu Val Arg Val Glu Ser Arg Asp Asp His Leu Ser Leu	
1448 1453 1458 1463	
cct gat gtg aca tgt gaa aac ttt att tct aaa gtt cag gat gtc att	4587
Pro Asp Val Thr Cys Glu Asn Phe Ile Ser Lys Val Gln Asp Val Ile	
1464 1469 1474 1479	
tcc atc aac cat gat gaa agt ctg ctg cct gag tcc tta gag agc atg	4635
Ser Ile Asn His Asp Glu Ser Leu Leu Pro Glu Ser Leu Glu Ser Met	
1480 1485 1490 1495	
atg tat ggt aag aag gtg ctc agc caa gaa cca agc tct ttt cag gag	4683
Met Tyr Gly Lys Lys Val Leu Ser Gln Glu Pro Ser Ser Phe Gln Glu	
1496 1501 1506 1511	
agc cca agt acc aat act gaa tct aga aaa gat gtt att acc atc tca	4731
Ser Pro Ser Thr Asn Thr Glu Ser Arg Lys Asp Val Ile Thr Ile Ser	
1512 1517 1522 1527	
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Ile Ser Lys Asp Gly Asn Cys Gln Ser Gly Gly Pro Glu Ala Glu Ile	
1528 1533 1538 1543	
gct tct ggc cct act ttt atg ggt agc tta gaa gca gga gga gta gct	4827
Ala Ser Gly Pro Thr Phe Met Gly Ser Leu Glu Ala Gly Gly Val Ala	
1544 1549 1554 1559	
caa gca aac atc aaa aat gga aaa cat ttg ttg atg tct att tca aag	4875
Gln Ala Asn Ile Lys Asn Gly Lys His Leu Leu Met Ser Ile Ser Lys	
1560 1565 1570 1575	
gaa ggg gag ctc tgc tgc agt gag gca gga cag aga cct gaa aac att	4923
Glu Gly Glu Leu Cys Cys Ser Glu Ala Gly Gln Arg Pro Glu Asn Ile	
1576 1581 1586 1591	
ggc cag ctg gaa gcc aag tgt tta gct tcc cct tcc ttg aat cca gga	4971
Gly Gln Leu Glu Ala Lys Cys Leu Ala Ser Pro Ser Leu Asn Pro Gly	
1592 1597 1602 1607	
aat gaa agt ggg ttt gta gat atg tgc agt ctt agt gtc tgt gac tcc	5019
Asn Glu Ser Gly Phe Val Asp Met Cys Ser Leu Ser Val Cys Asp Ser	
1608 1613 1618 1623	
aaa aga aac ctg tca tca gat cag caa tta att gat tta ttg gaa aac	5067
Lys Arg Asn Leu Ser Ser Asp Gln Gln Leu Ile Asp Leu Leu Glu Asn	
1624 1629 1634 1639	
aaa agc tta gaa agt aaa ttg att ttg agt cag aac cac agt gat gag	5115
Lys Ser Leu Glu Ser Lys Leu Ile Leu Ser Gln Asn His Ser Asp Glu	
1640 1645 1650 1655	

gag gaa gaa gag gag gaa aac gag gag gaa aac tta gcc atg gca gta	5163
Glu Glu Glu Glu Glu Glu Asn Glu Glu Glu Asn Leu Ala Met Ala Val	
1656 1661 1666 1671	
ggc atg ggg gaa agg cca gag gta ttg cat ctc acg gag ccc act act	5211
Gly Met Gly Glu Arg Pro Glu Val Leu His Leu Thr Glu Pro Thr Thr	
1672 1677 1682 1687	
aac atc tca agg gaa aag aac caa ggc ttc caa gat gaa acc aag aaa	5259
Asn Ile Ser Arg Glu Lys Asn Gln Gly Phe Gln Asp Glu Thr Lys Lys	
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gga agc tta gag gtg gca aac cag act cct ggg cta cag agg gct ttc	5307
Gly Ser Leu Glu Val Ala Asn Gln Thr Pro Gly Leu Gln Arg Ala Phe	
1704 1709 1714 1719	
ccc gct cca gca gcc tgt cag tgc cac tgc aaa cac atg gag agg tgg	5355
Pro Ala Pro Ala Ala Cys Gln Cys His Cys Lys His Met Glu Arg Trp	
1720 1725 1730 1735	
atg cat ggc ctc gag aat gat gaa ttt gaa atc gag aaa ccc aag gct	5403
Met His Gly Leu Glu Asn Asp Glu Phe Glu Ile Glu Lys Pro Lys Ala	
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tat atc cca gat ctg ttc aaa agt aaa acc aat act atc gcc atg gag	5451
Tyr Ile Pro Asp Leu Phe Lys Ser Lys Thr Asn Thr Ile Ala Met Glu	
1752 1757 1762 1767	
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Gly Glu Pro Thr Ala Ile Pro Ser Gln Pro Phe Lys Val Lys His Glu	
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Leu Leu Lys Glu Pro Trp Lys Glu Ser Ala Glu Gly Gln Asn Val Phe	
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ccc aca tat cct ctt gaa gga agt gag ctc aaa tca gaa gac atg gat	5595
Pro Thr Tyr Pro Leu Glu Gly Ser Glu Leu Lys Ser Glu Asp Met Asp	
1800 1805 1810 1815	
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Phe Glu Asn Lys Asp Asp Tyr Asp Arg Asp Gly Asn Cys His Ser Gln	
1816 1821 1826 1831	
gat tat cca ggg aag tac tct gaa gag gag agc aag agc tca aca tcg	5691
Asp Tyr Pro Gly Lys Tyr Ser Glu Glu Glu Ser Lys Ser Ser Thr Ser	
1832 1837 1842 1847	
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Gly Ile Thr Gly Asp Ile Gly Asp Glu Leu Gln Glu Ala Arg Ala Pro	
1848 1853 1858 1863	
act att gct cag ctg cta cag gag aaa act ctc tat tcc ttc tct gag	5787
Thr Ile Ala Gln Leu Leu Gln Glu Lys Thr Leu Tyr Ser Phe Ser Glu	
1864 1869 1874 1879	
tgg cca aag gac cgc gtg ata att aac cgc cta gat aat atc tgc cac	5835

Trp	Pro	Lys	Asp	Arg	Val	Ile	Ile	Asn	Arg	Leu	Asp	Asn	Ile	Cys	His	
1880					1885					1890					1895	
gtg	gtg	tta	aag	ggg	aag	tgg	ccc	tct	agc	cag	cag	tat	gag	ccc	tca	5883
Val	Val	Leu	Lys	Gly	Lys	Trp	Pro	Ser	Ser	Gln	Gln	Tyr	Glu	Pro	Ser	
1896					1901					1906					1911	
ggc	aca	ctg	ccc	acc	ccg	gta	tta	acc	agc	agt	gct	ggg	tct	cga	acc	5931
Gly	Thr	Leu	Pro	Thr	Pro	Val	Leu	Thr	Ser	Ser	Ala	Gly	Ser	Arg	Thr	
1912					1917					1922					1927	
agc	ctc	tca	gag	ccg	gaa	gca	gca	gaa	cac	agc	ttc	agc	aac	ggc	gca	5979
Ser	Leu	Ser	Glu	Pro	Glu	Ala	Ala	Glu	His	Ser	Phe	Ser	Asn	Gly	Ala	
1928					1933					1938					1943	
gca	ttg	gcg	gcc	cag	atc	cac	aag	gag	agc	ttc	tta	gct	cca	gta	ttc	6027
Ala	Leu	Ala	Ala	Gln	Ile	His	Lys	Glu	Ser	Phe	Leu	Ala	Pro	Val	Phe	
1944					1949					1954					1959	
aca	aag	gat	gaa	caa	aag	cac	agg	cgt	ccc	tat	gag	ttt	gag	gtg	gag	6075
Thr	Lys	Asp	Glu	Gln	Lys	His	Arg	Arg	Pro	Tyr	Glu	Phe	Glu	Val	Glu	
1960					1965					1970					1975	
agg	gat	gca	aag	gct	cgg	ggc	ctg	gag	cag	ttc	tct	gcc	acc	cac	ggg	6123
Arg	Asp	Ala	Lys	Ala	Arg	Gly	Leu	Glu	Gln	Phe	Ser	Ala	Thr	His	Gly	
1976					1981					1986					1991	
cac	acc	cct	atc	atc	ctc	aat	ggc	tgg	cat	ggg	gag	tca	gct	atg	gac	6171
His	Thr	Pro	Ile	Ile	Leu	Asn	Gly	Trp	His	Gly	Glu	Ser	Ala	Met	Asp	
1992					1997					2002					2007	
ctc	tcc	tgc	tca	tca	gag	ggg	tcc	cca	gga	gcc	aca	tcc	cct	ttc	cca	6219
Leu	Ser	Cys	Ser	Ser	Glu	Gly	Ser	Pro	Gly	Ala	Thr	Ser	Pro	Phe	Pro	
2008					2013					2018					2023	
gtg	agc	gcc	agc	acc	cct	aag	att	ggg	gct	atc	agt	tca	ctt	cag	gga	6267
Val	Ser	Ala	Ser	Thr	Pro	Lys	Ile	Gly	Ala	Ile	Ser	Ser	Leu	Gln	Gly	
2024					2029					2034					2039	
gcc	ctt	ggc	atg	gac	ttg	tct	ggg	att	ctg	caa	gct	ggc	ctg	atc	cat	6315
Ala	Leu	Gly	Met	Asp	Leu	Ser	Gly	Ile	Leu	Gln	Ala	Gly	Leu	Ile	His	
2040					2045					2050					2055	
cct	gtg	act	gga	cag	att	gtc	aat	gga	agc	ctc	aga	aga	gat	gat	gca	6363
Pro	Val	Thr	Gly	Gln	Ile	Val	Asn	Gly	Ser	Leu	Arg	Arg	Asp	Asp	Ala	
2056					2061					2066					2071	
gcc	acg	agg	agg	cgg	aga	ggg	agg	cgg	aaa	cat	gtt	gaa	gga	ggg	atg	6411
Ala	Thr	Arg	Arg	Arg	Arg	Gly	Arg	Arg	Lys	His	Val	Glu	Gly	Gly	Met	
2072					2077					2082					2087	
gac	ctc	atc	ttt	ttg	aag	gag	cag	aca	ctt	cag	gcg	gga	atc	ttg	gaa	6459
Asp	Leu	Ile	Phe	Leu	Lys	Glu	Gln	Thr	Leu	Gln	Ala	Gly	Ile	Leu	Glu	
2088					2093					2098					2103	
gtc	cat	gaa	gac	cca	ggg	cag	gcc	acc	ttg	agc	acc	aca	cac	cct	gag	6507
Val	His	Glu	Asp	Pro	Gly	Gln	Ala	Thr	Leu	Ser	Thr	Thr	His	Pro	Glu	

2104	2109	2114	2119	
ggg cca ggg cct gcc acc tcg gct cct gag cca gct acg gca gcc agc				6555
Gly Pro Gly Pro Ala Thr Ser Ala Pro Glu Pro Ala Thr Ala Ala Ser				
2120	2125	2130	2135	
agc caa gcc gag aaa tcc att ccc agc aag agt ctg ctt gac tgg cta				6603
Ser Gln Ala Glu Lys Ser Ile Pro Ser Lys Ser Leu Leu Asp Trp Leu				
2136	2141	2146	2151	
agg cag cag gct gac tac tcc tta gaa gtt cct ggc ttt ggg gca ggg				6651
Arg Gln Gln Ala Asp Tyr Ser Leu Glu Val Pro Gly Phe Gly Ala Gly				
2152	2157	2162	2167	
ttt ctt cca gaa aac aag ttc aat cac act ctg gct gag cct att ctt				6699
Phe Leu Pro Glu Asn Lys Phe Asn His Thr Leu Ala Glu Pro Ile Leu				
2168	2173	2178	2183	
cga gat acg ggc ccc cgc agg agg ggg agg cgg cct cgg agc gaa ctc				6747
Arg Asp Thr Gly Pro Arg Arg Arg Gly Arg Arg Pro Arg Ser Glu Leu				
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ctg aag gct cct tcc att gtg gca gac tct ccc tct gga atg ggg cca				6795
Leu Lys Ala Pro Ser Ile Val Ala Asp Ser Pro Ser Gly Met Gly Pro				
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Leu Phe Met Asn Gly Leu Ile Ala Gly Met Asp Leu Val Gly Leu Gln				
2216	2221	2226	2231	
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Asn Met Arg Asn Met Pro Gly Ile Pro Leu Thr Gly Leu Val Gly Phe				
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cca gct ggc ttt gcc acg atg cca aca ggt gaa gag gtc aaa agt acc				6939
Pro Ala Gly Phe Ala Thr Met Pro Thr Gly Glu Glu Val Lys Ser Thr				
2248	2253	2258	2263	
ctg agc atg ctg ccc atg atg ctg cca ggc atg gct gct gtg ccc cag				6987
Leu Ser Met Leu Pro Met Met Leu Pro Gly Met Ala Ala Val Pro Gln				
2264	2269	2274	2279	
atg ttt ggt gtt ggg gga ctc ctc agt cca ccc atg gca acc acc tgc				7035
Met Phe Gly Val Gly Gly Leu Leu Ser Pro Pro Met Ala Thr Thr Cys				
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act tcc act gcc ccg gcg tct cta tca agc aca acg aaa agt ggt acg				7083
Thr Ser Thr Ala Pro Ala Ser Leu Ser Ser Thr Thr Lys Ser Gly Thr				
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gca gtg act gaa aag act gcg gaa gac aag ccg agt agc cat gat gtg				7131
Ala Val Thr Glu Lys Thr Ala Glu Asp Lys Pro Ser Ser His Asp Val				
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aaa aca gac act tta gct gag gac aag cct ggt cca ggt cca ttt tct				7179
Lys Thr Asp Thr Leu Ala Glu Asp Lys Pro Gly Pro Gly Pro Phe Ser				
2328	2333	2338	2343	

gat cag tct gaa cct gca ata act act agt agt cct gtg gct ttt aac	7227
Asp Gln Ser Glu Pro Ala Ile Thr Thr Ser Ser Pro Val Ala Phe Asn	
2344 2349 2354 2359	
cca ttt ctc atc cca gga gta tct cct gga ctc att tac cca tcc atg	7275
Pro Phe Leu Ile Pro Gly Val Ser Pro Gly Leu Ile Tyr Pro Ser Met	
2360 2365 2370 2375	
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Phe Leu Ser Pro Gly Met Gly Met Ala Leu Pro Ala Met Gln Gln Ala	
2376 2381 2386 2391	
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Arg His Ser Glu Ile Val Gly Leu Glu Ser Gln Lys Arg Lys Lys Lys	
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Lys Thr Lys Gly Asp Asn Pro Asn Ser His Pro Glu Pro Ala Pro Ser	
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Cys Glu Arg Glu Pro Ser Gly Asp Glu Asn Cys Ala Glu Pro Ser Ala	
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Pro Leu Pro Ala Glu Arg Glu His Gly Ala Gln Ala Gly Glu Gly Ala	
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Leu Lys Asp Ser Asn Asn Asp Thr Asn *	
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 agattgcaac ctcccaaaag caccgagact ttgtggcaga gtccgtgggg gaaaagccag 240
 tagggagcct ggccgggatt ggtgaagtt atg gac aag aag ctg gag gaa ggg 293
 Met Asp Lys Lys Leu Glu Glu Gly
 1 5
 tgc ttt gac aag gcc tat gtt gtc ctt ggc cag ttt ctg gtg cta aag 341
 Cys Phe Asp Lys Ala Tyr Val Val Leu Gly Gln Phe Leu Val Leu Lys
 9 14 19 24
 aaa gat gaa gac ctc ttc cgg gaa tgg ctg agg gac act ggt ggt gcc 389
 Lys Asp Glu Asp Leu Phe Arg Glu Trp Leu Arg Asp Thr Gly Gly Ala
 25 30 35 40
 aac gcc aag cag tcc cgg gac tgc ttc gga tgc ctt cga gag tgg tgc 437
 Asn Ala Lys Gln Ser Arg Asp Cys Phe Gly Cys Leu Arg Glu Trp Cys
 41 46 51 56
 gac gcc ttc ttg tga tgctctctgg gaagctctca atccccagcc ctcatccaga 492
 Asp Ala Phe Leu *
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 Met Ser Leu Asp Phe Gly Ser Val Ala Leu Pro
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 Val Gln Asn Glu Asp Glu Glu Tyr Asp Glu Glu Asp Tyr Glu Arg Glu
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 aaa gag ttg cag cag tta ctc aca gac ctt ccc cat gac atg ctg gat 325
 Lys Glu Leu Gln Gln Leu Leu Thr Asp Leu Pro His Asp Met Leu Asp
 28 33 38 43
 gac gac ctc tcc tct cca gag ctc cag tat tgc gac tgc agc gag gat 373
 Asp Asp Leu Ser Ser Pro Glu Leu Gln Tyr Ser Asp Cys Ser Glu Asp
 44 49 54 59
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 Gly Thr Asp Gly Gln Pro His His Pro Glu Gln Leu Glu Met Ser Trp
 60 65 70 75
 aat gag caa atg ctg ccc aaa tct caa agt gta aat ggt ccc agt tgt 469
 Asn Glu Gln Met Leu Pro Lys Ser Gln Ser Val Asn Gly Pro Ser Cys
 76 81 86 91
 caa ggt ttg gaa ccg tat aat aaa gtg aca tat aaa cct tat cag tct 517
 Gln Gly Leu Glu Pro Tyr Asn Lys Val Thr Tyr Lys Pro Tyr Gln Ser
 92 97 102 107
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 Ser Ala Gln Asn Asn Gly Ser Pro Ala Gln Glu Ile Thr Gly Ser Asp

108	113	118	123	
aca ttc gaa ggc ctg	caa caa caa ttt tta	gga gct aat gag aac tct		613
Thr Phe Glu Gly Leu	Gln Gln Gln Phe Leu	Gly Ala Asn Glu Asn Ser		
124	129	134	139	
gca gaa aat atg cag att att caa ctt cag gtt ctt aac aaa gca aaa				661
Ala Glu Asn Met Gln Ile Ile Gln Leu Gln Val Leu Asn Lys Ala Lys				
140	145	150	155	
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Glu Arg Gln Leu Glu Asn Leu Ile Glu Lys Leu Asn Glu Ser Glu Arg				
156	161	166	171	
caa att cga tat ctg aat cac cag ctt gta ata ata aaa gat gaa aag				757
Gln Ile Arg Tyr Leu Asn His Gln Leu Val Ile Ile Lys Asp Glu Lys				
172	177	182	187	
gat ggt ttg act ctc agc ctt cga gaa tca cag aaa ctc ttt cag aat				805
Asp Gly Leu Thr Leu Ser Leu Arg Glu Ser Gln Lys Leu Phe Gln Asn				
188	193	198	203	
gga aaa gaa aga gag ata cag ctt gaa gct caa ata aaa gca ctg gag				853
Gly Lys Glu Arg Glu Ile Gln Leu Glu Ala Gln Ile Lys Ala Leu Glu				
204	209	214	219	
act cag ata caa gca tta aaa gtc aat gaa gaa cag atg atc aag aag				901
Thr Gln Ile Gln Ala Leu Lys Val Asn Glu Glu Gln Met Ile Lys Lys				
220	225	230	235	
tcc aga aca act gaa atg gct ctg gaa agc ttg aag cag cag ctg gtg				949
Ser Arg Thr Thr Glu Met Ala Leu Glu Ser Leu Lys Gln Gln Leu Val				
236	241	246	251	
gac ctt cat cat tct gaa tca ctt caa cga gct aga gaa cag cat gag				997
Asp Leu His His Ser Glu Ser Leu Gln Arg Ala Arg Glu Gln His Glu				
252	257	262	267	
agc att gtt atg ggc ctc aca aag aag tac gaa gag caa gta ttg tcc				1045
Ser Ile Val Met Gly Leu Thr Lys Lys Tyr Glu Glu Gln Val Leu Ser				
268	273	278	283	
tta caa aag aat ttg gat gcc aca gtc acc gca ctt aaa gaa cag gaa				1093
Leu Gln Lys Asn Leu Asp Ala Thr Val Thr Ala Leu Lys Glu Gln Glu				
284	289	294	299	
gac att tgc tct cgt ctg aaa gat cac gtg aaa caa ctg gaa agg aat				1141
Asp Ile Cys Ser Arg Leu Lys Asp His Val Lys Gln Leu Glu Arg Asn				
300	305	310	315	
caa gaa gca atc aag tta gaa aag act gag atc att aat aag ttg aca				1189
Gln Glu Ala Ile Lys Leu Glu Lys Thr Glu Ile Ile Asn Lys Leu Thr				
316	321	326	331	
aga agt cta gag gag agt caa aag cag tgt gcc cac ttg ttg cag tcc				1237
Arg Ser Leu Glu Glu Ser Gln Lys Gln Cys Ala His Leu Leu Gln Ser				
332	337	342	347	

ggg tca gta caa gag gtg gct cag cta cag ttc cag ctg cag caa gca	1285
Gly Ser Val Gln Glu Val Ala Gln Leu Gln Phe Gln Leu Gln Gln Ala	
348 353 358 363	
cag aag gca cat gct atg agt gca aac atg aac aag gct ttg caa gaa	1333
Gln Lys Ala His Ala Met Ser Ala Asn Met Asn Lys Ala Leu Gln Glu	
364 369 374 379	
gaa tta aca gaa cta aaa gat gaa att tct ctc tat gaa tct gct gca	1381
Glu Leu Thr Glu Leu Lys Asp Glu Ile Ser Leu Tyr Glu Ser Ala Ala	
380 385 390 395	
aaa cta gga ata cat cca agt gac tca gaa gga gaa tta aat ata gaa	1429
Lys Leu Gly Ile His Pro Ser Asp Ser Glu Gly Glu Leu Asn Ile Glu	
396 401 406 411	
ctc act gaa tcg tat gtg gat ttg ggt att aaa aag gtc aac tgg aaa	1477
Leu Thr Glu Ser Tyr Val Asp Leu Gly Ile Lys Lys Val Asn Trp Lys	
412 417 422 427	
aaa tcc aaa gtt acc agc att gta caa gaa gaa gac cca aat gaa gag	1525
Lys Ser Lys Val Thr Ser Ile Val Gln Glu Glu Asp Pro Asn Glu Glu	
428 433 438 443	
ctt tca aaa gat gag ttc att ctg aag tta aag gca gaa gta cag cgt	1573
Leu Ser Lys Asp Glu Phe Ile Leu Lys Leu Lys Ala Glu Val Gln Arg	
444 449 454 459	
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Leu Leu Gly Ser Asn Ser Met Lys Arg His Leu Val Ser Gln Leu Gln	
460 465 470 475	
aat gac ctc aaa gac tgt cat aag aaa att gaa gat ctc cac caa gtg	1669
Asn Asp Leu Lys Asp Cys His Lys Lys Ile Glu Asp Leu His Gln Val	
476 481 486 491	
aag aag gat gaa aaa agc att gag gtt gag act aaa aca gat acc tca	1717
Lys Lys Asp Glu Lys Ser Ile Glu Val Glu Thr Lys Thr Asp Thr Ser	
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gaa aaa cca aag aat caa tta tgg cct gag tct tct act tct gat gtt	1765
Glu Lys Pro Lys Asn Gln Leu Trp Pro Glu Ser Ser Thr Ser Asp Val	
508 513 518 523	
gtc aga gat gat att ctg ctg ctt aaa aat gaa att caa gtt tta caa	1813
Val Arg Asp Asp Ile Leu Leu Leu Lys Asn Glu Ile Gln Val Leu Gln	
524 529 534 539	
caa caa aat cag gaa ctt aaa gaa act gaa gga aaa ctg aga aat aca	1861
Gln Gln Asn Gln Glu Leu Lys Glu Thr Glu Gly Lys Leu Arg Asn Thr	
540 545 550 555	
aat caa gac tta tgt aat caa atg aga caa atg gta caa gat ttt gac	1909
Asn Gln Asp Leu Cys Asn Gln Met Arg Gln Met Val Gln Asp Phe Asp	
556 561 566 571	

cat gac aaa caa gaa gct gtg gat agg tgt gaa agg act tat cag cag	1957
His Asp Lys Gln Glu Ala Val Asp Arg Cys Glu Arg Thr Tyr Gln Gln	
572 577 582 587	
 cac cat gaa gcc atg aaa act caa ata cgt gaa agc cta tta gca aag	2005
His His Glu Ala Met Lys Thr Gln Ile Arg Glu Ser Leu Leu Ala Lys	
588 593 598 603	
 cat gct ttg gag aag cag cag ctc ttt gag gct tat gag aga act cat	2053
His Ala Leu Glu Lys Gln Gln Leu Phe Glu Ala Tyr Glu Arg Thr His	
604 609 614 619	
 ttg caa ctg agg tct gag ttg gat aag ttg aat aag gag gtg act gct	2101
Leu Gln Leu Arg Ser Glu Leu Asp Lys Leu Asn Lys Glu Val Thr Ala	
620 625 630 635	
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Val Gln Glu Cys Tyr Leu Glu Val Cys Arg Glu Lys Asp Asn Leu Glu	
636 641 646 651	
 ttg act ctc agg aag acc act gaa aag gag caa cag act cag gag aag	2197
Leu Thr Leu Arg Lys Thr Thr Glu Lys Glu Gln Gln Thr Gln Glu Lys	
652 657 662 667	
 atc aaa gaa aaa ctc att caa cag ctt gaa aag gag tgg cag tct aag	2245
Ile Lys Glu Lys Leu Ile Gln Gln Leu Glu Lys Glu Trp Gln Ser Lys	
668 673 678 683	
 ctg gat caa act ata aag gca atg aaa aag aag acc tta gat tgt ggc	2293
Leu Asp Gln Thr Ile Lys Ala Met Lys Lys Lys Thr Leu Asp Cys Gly	
684 689 694 699	
 agc caa act gac caa gta acc acc agt gat gtt att tcc aag aaa gag	2341
Ser Gln Thr Asp Gln Val Thr Thr Ser Asp Val Ile Ser Lys Lys Glu	
700 705 710 715	
 atg gca att atg ata gaa gag cag aag tgc aca atc cag caa aac tta	2389
Met Ala Ile Met Ile Glu Glu Gln Lys Cys Thr Ile Gln Gln Asn Leu	
716 721 726 731	
 gaa caa gag aag gac ata gcc atc aag ggg gct atg aag aaa ctc gaa	2437
Glu Gln Glu Lys Asp Ile Ala Ile Lys Gly Ala Met Lys Lys Leu Glu	
732 737 742 747	
 att gaa ttg gaa ctc aaa cat tgt gaa aat att acc aaa cag gta gaa	2485
Ile Glu Leu Glu Leu Lys His Cys Glu Asn Ile Thr Lys Gln Val Glu	
748 753 758 763	
 ata gct gtg caa aat gct cat cag cga tgg ctg gga gaa cta cca gag	2533
Ile Ala Val Gln Asn Ala His Gln Arg Trp Leu Gly Glu Leu Pro Glu	
764 769 774 779	
 ctg gca gag tat caa gca ctt gtg aag gca gaa cag aaa aag tgg gaa	2581
Leu Ala Glu Tyr Gln Ala Leu Val Lys Ala Glu Gln Lys Lys Trp Glu	
780 785 790 795	
 gaa cag cat gag gtc tct gtg aac aaa agg ata tca ttt gct gtt tct	2629

Glu	Gln	His	Glu	Val	Ser	Val	Asn	Lys	Arg	Ile	Ser	Phe	Ala	Val	Ser		
796					801					806					811		
gaa	gct	aaa	gag	aaa	tgg	aag	agt	gag	ctt	gaa	aat	atg	agg	aaa	aat	2677	
Glu	Ala	Lys	Glu	Lys	Trp	Lys	Ser	Glu	Leu	Glu	Asn	Met	Arg	Lys	Asn		
812					817					822					827		
ata	ctt	cct	gga	aag	gaa	ttg	gaa	gag	aag	att	cat	tct	ctt	cag	aag	2725	
Ile	Leu	Pro	Gly	Lys	Glu	Leu	Glu	Glu	Lys	Ile	His	Ser	Leu	Gln	Lys		
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gaa	ctt	gag	tta	aag	aac	gaa	gaa	gtc	cct	gtg	gtc	atc	agg	gct	gag	2773	
Glu	Leu	Glu	Leu	Lys	Asn	Glu	Glu	Val	Pro	Val	Val	Ile	Arg	Ala	Glu		
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860					865					870					875		
cac	aga	atc	caa	gaa	caa	aat	gag	caa	gat	tac	cgg	caa	ttt	tta	gat	2869	
His	Arg	Ile	Gln	Glu	Gln	Asn	Glu	Gln	Asp	Tyr	Arg	Gln	Phe	Leu	Asp		
876					881					886					891		
gat	cac	cga	aat	aaa	att	aat	gag	gtg	ctt	gcg	gca	gct	aaa	gaa	gac	2917	
Asp	His	Arg	Asn	Lys	Ile	Asn	Glu	Val	Leu	Ala	Ala	Ala	Lys	Glu	Asp		
892					897					902					907		
ttt	atg	aaa	caa	aaa	act	gaa	cta	ctt	ctt	cag	aag	gag	aca	gaa	tta	2965	
Phe	Met	Lys	Gln	Lys	Thr	Glu	Leu	Leu	Leu	Gln	Lys	Glu	Thr	Glu	Leu		
908					913					918					923		
caa	act	tgt	cta	gac	cag	agt	cgt	aga	gaa	tgg	act	atg	cag	gaa	gcc	3013	
Gln	Thr	Cys	Leu	Asp	Gln	Ser	Arg	Arg	Glu	Trp	Thr	Met	Gln	Glu	Ala		
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Lys	Arg	Ile	Gln	Leu	Glu	Ile	Tyr	Gln	Tyr	Glu	Glu	Asp	Ile	Leu	Thr		
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Val	Leu	Gly	Val	Leu	Leu	Ser	Asp	Thr	Gln	Lys	Glu	His	Ile	Ser	Asp		
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Ser	Glu	Asp	Lys	Gln	Leu	Leu	Glu	Ile	Met	Ser	Thr	Cys	Ser	Ser	Lys		
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Ala	Phe	Gln	Asp	Thr	Leu	Pro	Leu	Leu	Val	Glu	Asn	Ala	Asp	Pro	Glu		
1004					1009					1014					1019		
tgg	aaa	aag	aga	aat	atg	gcc	gag	ctc	tct	aag	gat	tct	gcc	agc	cag	3301	
Trp	Lys	Lys	Arg	Asn	Met	Ala	Glu	Leu	Ser	Lys	Asp	Ser	Ala	Ser	Gln		

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ggc act ggc caa gga gac cct gga cct gct gct gga cac cat gct cag				3349
Gly Thr Gly Gln Gly Asp Pro Gly Pro Ala Ala Gly His His Ala Gln				
1036	1041	1046	1051	
ccc ttg gcc tta caa gca aca gaa gca gaa gct gat aag aaa aag gtc				3397
Pro Leu Ala Leu Gln Ala Thr Glu Ala Glu Ala Asp Lys Lys Lys Val				
1052	1057	1062	1067	
ctt gaa att aag gat tta tgc tgt gga cac tgc ttc caa gaa ctt gaa				3445
Leu Glu Ile Lys Asp Leu Cys Cys Gly His Cys Phe Gln Glu Leu Glu				
1068	1073	1078	1083	
aag gca aag cag gaa tgt caa gat ctg aaa gga aaa ctg gag aaa tgc				3493
Lys Ala Lys Gln Glu Cys Gln Asp Leu Lys Gly Lys Leu Glu Lys Cys				
1084	1089	1094	1099	
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Cys Arg His Leu Gln His Leu Glu Arg Lys His Lys Ala Val Val Glu				
1100	1105	1110	1115	
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Lys Ile Gly Glu Glu Asn Asn Lys Val Val Glu Glu Leu Ile Glu Glu				
1116	1121	1126	1131	
aac aac gac atg aag aat aaa ttg gaa gaa ttg caa aca ctt tgt aaa				3637
Asn Asn Asp Met Lys Asn Lys Leu Glu Glu Leu Gln Thr Leu Cys Lys				
1132	1137	1142	1147	
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Thr Pro Pro Arg Ser Leu Ser Ala Gly Ala Ile Glu Asn Ala Cys Leu				
1148	1153	1158	1163	
cca tgc agt ggg gga gcc ttg gaa gaa ctt cgt ggg cag tac att aaa				3733
Pro Cys Ser Gly Gly Ala Leu Glu Glu Leu Arg Gly Gln Tyr Ile Lys				
1164	1169	1174	1179	
gct gta aaa aaa att aaa tgt gac atg ctt cgt tat att cag gag agt				3781
Ala Val Lys Lys Ile Lys Cys Asp Met Leu Arg Tyr Ile Gln Glu Ser				
1180	1185	1190	1195	
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Lys Glu Arg Ala Ala Glu Met Val Lys Ala Glu Val Leu Arg Glu Arg				
1196	1201	1206	1211	
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Gln Glu Thr Ala Arg Lys Met Arg Lys Tyr Tyr Leu Ile Cys Leu Gln				
1212	1217	1222	1227	
cag att ttg cag gat gat gga aaa gaa ggg gct gag aaa aag att atg				3925
Gln Ile Leu Gln Asp Asp Gly Lys Glu Gly Ala Glu Lys Lys Ile Met				
1228	1233	1238	1243	
aat gct gct agc aaa ctt gct aca atg gca aaa tta ctg gaa aca cct				3973
Asn Ala Ala Ser Lys Leu Ala Thr Met Ala Lys Leu Leu Glu Thr Pro				
1244	1249	1254	1259	

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 Ile Ser Ser Lys Ser Gln Ser Lys Thr Thr Gln Ser Gly Met Ser Lys
 1260 1265 1270 1275

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 1276

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 Met
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 Phe Pro Pro Ala Arg Gly Lys Glu Leu Leu Ser Phe Glu Asp Val Ala
 2 7 12 17

atg tac ttc acc aga gag gag tgg ggc cac ctc aac tgg ggt cag aag 332
 Met Tyr Phe Thr Arg Glu Glu Trp Gly His Leu Asn Trp Gly Gln Lys
 18 23 28 33

gac ctc tac cga gat gtg atg ttg gag aac tac agg aac atg gtc ttg 380
 Asp Leu Tyr Arg Asp Val Met Leu Glu Asn Tyr Arg Asn Met Val Leu
 34 39 44 49

ctg gga ttt cag ttt ccc aaa cct gag atg atc tgt cag ctg gag aac 428
 Leu Gly Phe Gln Phe Pro Lys Pro Glu Met Ile Cys Gln Leu Glu Asn
 50 55 60 65

tgg gac gag cag tgg atc ctg gat cta ccg aga gct ggg aat agg aag 476
 Trp Asp Glu Gln Trp Ile Leu Asp Leu Pro Arg Ala Gly Asn Arg Lys
 66 71 76 81

gct tcc ggt agt gct tgc cca ggc gga ctc tcg ctc tgt cgc cag gct 524
 Ala Ser Gly Ser Ala Cys Pro Gly Gly Leu Ser Leu Cys Arg Gln Ala
 82 87 92 97

gtc tta gcc tcc tga gtggcttgga ctacaggcgc gcgccaccat gcccggtac 579
 Val Leu Ala Ser *
 98

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gacctcgtga tccgcctgcc ccggcctccc aaagtgtctgg gattacaggc gtgagccgtg 699

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cacgcgtccg gcacaccctt tactggccgg ccccgcgctg ctctcctaag acccgcgagg 180

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atg cgg agg ggc gag cgc agg gac gcc gga ggt ccg cgg ccc gag tcc 345

Met Arg Arg Gly Glu Arg Arg Asp Ala Gly Gly Pro Arg Pro Glu Ser
 1 5 10 15

ccg gtg ccc gcg ggc agg gcc tcg ctg gag gag ccg cct gac ggg ccg 393

Pro Val Pro Ala Gly Arg Ala Ser Leu Glu Glu Pro Pro Asp Gly Pro
 17 22 27 32

tct gcc ggc caa gcc acc ggg ccg ggc gag ggc cgc cgc agc acc gag 441

Ser Ala Gly Gln Ala Thr Gly Pro Gly Glu Gly Arg Arg Ser Thr Glu

33	38	43	48	
tcc gag gtc tac gac gac ggc acc aac acc ttc ttc tgg cga gcc cac				489
Ser Glu Val Tyr Asp Asp Gly Thr Asn Thr Phe Phe Trp Arg Ala His				
49	54	59	64	
acc tta acc gtg ctc ttc atc ctc acc tgt acg ctt ggc tat gtg acg				537
Thr Leu Thr Val Leu Phe Ile Leu Thr Cys Thr Leu Gly Tyr Val Thr				
65	70	75	80	
ctg ctg gag gaa aca cct cag gac acg gcc tac aac acc aag aga ggt				585
Leu Leu Glu Glu Thr Pro Gln Asp Thr Ala Tyr Asn Thr Lys Arg Gly				
81	86	91	96	
att gtg gcc agt att ttg gtt ttc tta tgt ttt gga gtc aca caa gct				633
Ile Val Ala Ser Ile Leu Val Phe Leu Cys Phe Gly Val Thr Gln Ala				
97	102	107	112	
aaa gac ggg cca ttt tcc aga cct cat cca gct tac tgg agg ttt tgg				681
Lys Asp Gly Pro Phe Ser Arg Pro His Pro Ala Tyr Trp Arg Phe Trp				
113	118	123	128	
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Leu Cys Val Ser Val Val Tyr Glu Leu Phe Leu Ile Phe Ile Leu Phe				
129	134	139	144	
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Gln Thr Val Gln Asp Gly Arg Gln Phe Leu Lys Tyr Val Asp Pro Lys				
145	150	155	160	
ctg gga gtc cca ctg cca gag aga gac tac ggg gga aac tgc ctc atc				825
Leu Gly Val Pro Leu Pro Glu Arg Asp Tyr Gly Gly Asn Cys Leu Ile				
161	166	171	176	
tac gac cca gac aat gag act gac ccc ttt cac aac atc tgg gac aag				873
Tyr Asp Pro Asp Asn Glu Thr Asp Pro Phe His Asn Ile Trp Asp Lys				
177	182	187	192	
ttg gat ggc ttt gtt ccc gcg cac ttt ctt ggc tgg tac ctg aag acc				921
Leu Asp Gly Phe Val Pro Ala His Phe Leu Gly Trp Tyr Leu Lys Thr				
193	198	203	208	
ctg atg atc cga gac tgg tgg atg tgc atg atc atc agc gtg atg ttc				969
Leu Met Ile Arg Asp Trp Trp Met Cys Met Ile Ile Ser Val Met Phe				
209	214	219	224	
gag ttc ctg gag tac agc ctg gag cac cag ctg ccc aac ttc agc gag				1017
Glu Phe Leu Glu Tyr Ser Leu Glu His Gln Leu Pro Asn Phe Ser Glu				
225	230	235	240	
tgc tgg tgg gat cac tgg atc atg gac gtg ctc gtc tgc aac ggg ctg				1065
Cys Trp Trp Asp His Trp Ile Met Asp Val Leu Val Cys Asn Gly Leu				
241	246	251	256	
ggc atc tac tgc ggc atg aag acc ctt gag tgg ctg tcc ctg aag acg				1113
Gly Ile Tyr Cys Gly Met Lys Thr Leu Glu Trp Leu Ser Leu Lys Thr				
257	262	267	272	

tac aag tgg cag ggc ctc tgg aac att ccg acc tac aag ggc aag atg	1161
Tyr Lys Trp Gln Gly Leu Trp Asn Ile Pro Thr Tyr Lys Gly Lys Met	
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Lys Arg Ile Ala Phe Gln Phe Thr Pro Tyr Ser Trp Val Arg Phe Glu	
289 294 299 304	
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Trp Lys Pro Ala Ser Ser Leu Arg Arg Trp Leu Ala Val Cys Gly Ile	
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Ile Leu Val Phe Leu Leu Ala Glu Leu Asn Thr Phe Tyr Leu Lys Phe	
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Val Leu Trp Met Pro Pro Glu His Tyr Leu Val Leu Leu Arg Leu Val	
337 342 347 352	
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Phe Phe Val Asn Val Gly Gly Val Ala Met Arg Glu Ile Tyr Asp Phe	
353 358 363 368	
atg gat gac ccg aag ccc cac aag aag ctg ggc ccg cag gcc tgg ctg	1449
Met Asp Asp Pro Lys Pro His Lys Lys Leu Gly Pro Gln Ala Trp Leu	
369 374 379 384	
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Val Ala Ala Ile Thr Ala Thr Glu Leu Leu Ile Val Val Lys Tyr Asp	
385 390 395 400	
ccc cac acg ctc acc ctg tcc ctg ccc ttc tac atc tcc cag tgc tgg	1545
Pro His Thr Leu Thr Leu Ser Leu Pro Phe Tyr Ile Ser Gln Cys Trp	
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Thr Leu Gly Ser Val Leu Ala Leu Thr Trp Thr Val Trp Arg Phe Phe	
417 422 427 432	
ctg cgg gac atc aca ttg agg tac aag gag acc cgg tgg cag aag tgg	1641
Leu Arg Asp Ile Thr Leu Arg Tyr Lys Glu Thr Arg Trp Gln Lys Trp	
433 438 443 448	
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Gln Asn Lys Asp Asp Gln Gly Ser Thr Val Gly Asn Gly Asp Gln His	
449 454 459 464	
cca ctg ggg ctg gac gaa gac ctg ctg ggg cct ggg gtg gcc gag ggc	1737
Pro Leu Gly Leu Asp Glu Asp Leu Leu Gly Pro Gly Val Ala Glu Gly	
465 470 475 480	
gag gga gca cca act cca aac tga cctggggccgt ggctgcctcg tgagcctccc	1791
Glu Gly Ala Pro Thr Pro Asn *	
481 486	

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Arg Arg Ala Leu Arg Arg Leu Arg Gly Glu Gln Arg Gly Gln Glu Pro
3 8 13 18

ctc ggg ccc ggc gcc ttg cat ttc gat ctc cgt gat gac gat gac gcg 152
Leu Gly Pro Gly Ala Leu His Phe Asp Leu Arg Asp Asp Asp Ala
19 24 29 34

gaa gaa gaa ggg ccc aag cgg gag ctt ggt gtc cgg cgt ccc ggg ggc 200
Glu Glu Glu Gly Pro Lys Arg Glu Leu Gly Val Arg Arg Pro Gly Gly
35 40 45 50

gca ggg aag gag ggc gtc cga gtc aac aac cgc ttc gag ctg ata aac 248
Ala Gly Lys Glu Gly Val Arg Val Asn Asn Arg Phe Glu Leu Ile Asn
51 56 61 66

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Ile Asp Asp Leu Glu Asp Asp Pro Val Val Asn Gly Glu Arg Ser Gly
67 72 77 82

tgt gcg ctc aca gac gct gtg gca cca ggg aac aaa gga agg ggt cag 344
Cys Ala Leu Thr Asp Ala Val Ala Pro Gly Asn Lys Gly Arg Gly Gln
83 88 93 98

cgt gga aac aca gag agc aag acg gat gga gat gac acc gag aca gtg 392
Arg Gly Asn Thr Glu Ser Lys Thr Asp Gly Asp Asp Thr Glu Thr Val

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Pro Ser Glu Gln Ser His Ala Ser Gly Lys		Leu Arg Lys Lys Lys Lys		
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aaa cag aaa aac aag aaa agc agc acg gga gaa gca tcg gaa aac gga				488
Lys Gln Lys Asn Lys Lys Ser Ser Thr Gly		Glu Ala Ser Glu Asn Gly		
131	136	141	146	
cta gaa gat atc gat cgc atc cta gag agg att gag gac agc act ggg				536
Leu Glu Asp Ile Asp Arg Ile Leu Glu Arg		Ile Glu Asp Ser Thr Gly		
147	152	157	162	
ttg aac cgt ccc ggc cca gct ccc ctg agc tcc agg aag cac gtt ctc				584
Leu Asn Arg Pro Gly Pro Ala Pro Leu Ser		Ser Arg Lys His Val Leu		
163	168	173	178	
tac gtg gag cac aga cac ttg aat cca gac aca gaa ctg aaa agg tat				632
Tyr Val Glu His Arg His Leu Asn Pro Asp Thr Glu Leu Lys Arg Tyr				
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ttt ggt gcc cgg gca atc ctg ggg gag caa agg cca cgg cag aga caa				680
Phe Gly Ala Arg Ala Ile Leu Gly Glu Gln Arg		Pro Arg Gln Arg Gln		
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cgt gtg tac ccc aag tgc aca tgg ctg acc acc cct aaa agc acc tgg				728
Arg Val Tyr Pro Lys Cys Thr Trp Leu Thr Thr Pro Lys Ser Thr Trp				
211	216	221	226	
ccc cgc tac agc aaa cca ggt ctg tcc atg cgg ctg ctg gaa tca aaa				776
Pro Arg Tyr Ser Lys Pro Gly Leu Ser Met Arg Leu Leu Glu Ser Lys				
227	232	237	242	
aaa ggc ctc tcc ttc ttt gcg ttt gag cac agt gag gag tac cag cag				824
Lys Gly Leu Ser Phe Phe Ala Phe Glu His Ser Glu Glu Tyr Gln Gln				
243	248	253	258	
gct cag cac aag ttc ctg gtg gcc gtg gag tct atg gag ccg aac aac				872
Ala Gln His Lys Phe Leu Val Ala Val Glu Ser Met Glu Pro Asn Asn				
259	264	269	274	
atc gtg gtt ctg ctc cag acg agc cct tac cac gtt gac tca ctc ctg				920
Ile Val Val Leu Leu Gln Thr Ser Pro Tyr His Val Asp Ser Leu Leu				
275	280	285	290	
cag ctc agc gat gcc tgc cgc ttt caa gag gat cag gag atg gct cga				968
Gln Leu Ser Asp Ala Cys Arg Phe Gln Glu Asp Gln Glu Met Ala Arg				
291	296	301	306	
gac ctc gta gag aga gcg ctg tac agc atg gaa tgt gcg ttc cac ccc				1016
Asp Leu Val Glu Arg Ala Leu Tyr Ser Met Glu Cys Ala Phe His Pro				
307	312	317	322	
ctg ttc agt ctc acc agt ggg gcc tgc cgg ctg gat tac cgc aga ccc				1064
Leu Phe Ser Leu Thr Ser Gly Ala Cys Arg Leu Asp Tyr Arg Arg Pro				
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gag aac agg agc ttc tac ctg gcc ctc tac aag cag atg agc ttc ctg	1112
Glu Asn Arg Ser Phe Tyr Leu Ala Leu Tyr Lys Gln Met Ser Phe Leu	
339 344 349 354	
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Glu Lys Arg Gly Cys Pro Arg Thr Ala Leu Glu Tyr Cys Lys Leu Ile	
355 360 365 370	
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Leu Ser Leu Glu Pro Asp Glu Asp Pro Leu Cys Met Leu Leu Leu Ile	
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Asp His Leu Ala Leu Arg Ala Arg Asn Tyr Glu Tyr Leu Ile Arg Leu	
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Phe Gln Glu Trp Glu Val Gly Ala Ser Leu Ala His Arg Asn Leu Ser	
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Gln Leu Pro Asn Phe Ala Phe Ser Val Pro Leu Ala Tyr Phe Leu Leu	
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Lys Ala Ser Leu Leu Ile Gln Gln Ala Leu Thr Met Phe Pro Gly Val	
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Leu Leu Pro Leu Leu Glu Ser Cys Ser Val Arg Pro Asp Ala Ser Val	
467 472 477 482	
tcc agt cac cgc ttc ttt gga ccc aat gct gaa ata agc cag ccc cct	1544
Ser Ser His Arg Phe Phe Gly Pro Asn Ala Glu Ile Ser Gln Pro Pro	
483 488 493 498	
gcc ctg agc cag ctg gtg aac ctg tac ctt ggg agg tca cac ttt ctc	1592
Ala Leu Ser Gln Leu Val Asn Leu Tyr Leu Gly Arg Ser His Phe Leu	
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Trp Lys Glu Pro Ala Thr Met Ser Trp Leu Glu Glu Asn Val His Glu	
515 520 525 530	
gtt ctg caa gca gtg gac gcc ggg gac cca gcc gtg gaa gcc tgt gag	1688
Val Leu Gln Ala Val Asp Ala Gly Asp Pro Ala Val Glu Ala Cys Glu	
531 536 541 546	
aac cgg cgg aag gtg ctc tac cag cgt gca ccc agg aat atc cac cgc	1736
Asn Arg Arg Lys Val Leu Tyr Gln Arg Ala Pro Arg Asn Ile His Arg	
547 552 557 562	

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His Val Ile Leu Ser Glu Ile Lys Glu Ala Val Ala Ala Leu Pro Pro	
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Asp Val Thr Thr Gln Ser Val Met Gly Phe Asp Pro Leu Pro Pro Ser	
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His Gly Asn Thr Ile Ala Leu Phe Phe Arg Ser Leu Leu Pro Asn Tyr	
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Thr Met Glu Gly Glu Arg Pro Glu Glu Gly Val Ala Gly Gly Leu Asn	
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659 664 669 674	
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Glu Gly Glu Gly Glu Trp Asp *	
675 680	
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35 40 45 50				
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Cys Ala Leu Thr Asp Ala Val Ala Pro Gly Asn Lys Gly Arg Gly Gln				
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Lys Gln Lys Asn Lys Lys Ser Ser Thr Gly Glu Ala Ser Glu Asn Gly				
131 136 141 146				
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Tyr Val Glu His Arg His Leu Asn Pro Asp Thr Glu Leu Lys Arg Tyr				
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Phe Gly Ala Arg Ala Ile Leu Gly Glu Gln Arg Pro Arg Gln Arg Gln				
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Arg Val Tyr Pro Lys Cys Thr Trp Leu Thr Thr Pro Lys Ser Thr Trp				
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ccc cgc tac agc aaa cca ggt ctg tcc atg cgg ctg ctg gaa tca aaa	776			
Pro Arg Tyr Ser Lys Pro Gly Leu Ser Met Arg Leu Leu Glu Ser Lys				
227 232 237 242				

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Lys Gly Leu Ser Phe Phe Ala Phe Glu His Ser Glu Glu Tyr Gln Gln	
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Ala Gln His Lys Phe Leu Val Ala Val Glu Ser Met Glu Pro Asn Asn	
259 264 269 274	
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Ile Val Leu Ser Asp Ala Cys Arg Phe Gln Glu Asp Gln Glu Met Ala	
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Pro Leu Phe Ser Leu Thr Ser Gly Ala Cys Arg Leu Asp Tyr Arg Arg	
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Pro Glu Asn Arg Ser Phe Tyr Leu Ala Leu Tyr Lys Gln Met Ser Phe	
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467 472 477 482	
cct gcc ctg agc cag ctg gtg aac ctg tac ctt ggg agg tca cac ttt	1544
Pro Ala Leu Ser Gln Leu Val Asn Leu Tyr Leu Gly Arg Ser His Phe	
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Leu Trp Lys Glu Pro Ala Thr Met Ser Trp Leu Glu Glu Asn Val His	
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Glu Val Leu Gln Ala Val Asp Ala Gly Asp Pro Ala Val Glu Ala Cys	
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Glu Asn Arg Arg Lys Val Leu Tyr Gln Arg Ala Pro Arg Asn Ile His	
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cgc cat gtg atc ctc tct gag atc aag gaa gcc gtc gct gcc ctg ccc	1736
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Ser Asp Thr Ile Tyr Ser Tyr Val Arg Pro Glu Arg Leu Ser Pro Ile	
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Ser His Gly Asn Thr Ile Ala Leu Phe Phe Arg Ser Leu Leu Pro Asn	
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tat acc atg gag ggg gag agg ccc gag gaa gga gtg gct ggg ggt ctg	1928
Tyr Thr Met Glu Gly Glu Arg Pro Glu Glu Gly Val Ala Gly Gly Leu	
611 616 621 626	
aac cgc aac cag ggc ctg aac agg ctg atg ctg gct gtg cgc gac atg	1976
Asn Arg Asn Gln Gly Leu Asn Arg Leu Met Leu Ala Val Arg Asp Met	
627 632 637 642	
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Ala Glu Gly Glu Gly Glu Trp Asp *	
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Asn Val Leu Gln Arg His Thr Gly Cys Phe Ala Thr Ile Trp Leu Ala
   6                      11                      16                      21

gcg act cgc ggc agc cgg ttg gtg aag cgc gaa tac ctg agg gtg aat      510
Ala Thr Arg Gly Ser Arg Leu Val Lys Arg Glu Tyr Leu Arg Val Asn
  22                      27                      32                      37

gtg gtg aaa acc tgc gag gaa atc ctc aat tac gtg ctg gta cga gtg      558
Val Val Lys Thr Cys Glu Glu Ile Leu Asn Tyr Val Leu Val Arg Val
  38                      43                      48                      53

caa ccc ccg cag ccc ggc ctg ccg cgg ccc cgc ttc tcc ctc tat ctc      606
Gln Pro Pro Gln Pro Gly Leu Pro Arg Pro Arg Phe Ser Leu Tyr Leu
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tca gcc caa ctt cag atc ggt gtg atc cgc gtc tat tct caa caa tgc      654
Ser Ala Gln Leu Gln Ile Gly Val Ile Arg Val Tyr Ser Gln Gln Cys
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cag tac ctc gtg gag gac atc cag cac atc ttg gag cgc ctc cac cgt      702
Gln Tyr Leu Val Glu Asp Ile Gln His Ile Leu Glu Arg Leu His Arg
  86                      91                      96                      101

gcc cag ctg cag atc cga ata gat atg gag act gag cta ccc agc ctg      750
Ala Gln Leu Gln Ile Arg Ile Asp Met Glu Thr Glu Leu Pro Ser Leu
 102                      107                      112                      117
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Asp Pro Phe Phe Gly Met Met Ser Val Asp Pro Arg Leu Pro Ser Pro	
134 139 144 149	
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Phe Asp Ile Pro Gln Ile Arg His Leu Leu Glu Ala Ala Ile Pro Glu	
150 155 160 165	
aga gtt gaa gag atc cct cct gaa gtt cct aca gag ccc agg gag cca	942
Arg Val Glu Glu Ile Pro Pro Glu Val Pro Thr Glu Pro Arg Glu Pro	
166 171 176 181	
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Glu Arg Ile Pro Val Thr Val Leu Pro Pro Glu Ala Ile Thr Ile Leu	
182 187 192 197	
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Glu Ala Glu Pro Ile Arg Met Leu Glu Ile Glu Gly Glu Arg Glu Leu	
198 203 208 213	
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Pro Glu Val Ser Arg Arg Glu Leu Asp Leu Leu Ile Ala Glu Glu Glu	
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Glu Ala Ile Leu Leu Glu Ile Pro Arg Leu Pro Pro Pro Ala Pro Ala	
230 235 240 245	
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Glu Val Glu Gly Ile Gly Glu Ala Leu Gly Pro Glu Glu Leu Arg Leu	
246 251 256 261	
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Thr Gly Trp Glu Pro Gly Ala Leu Leu Met Glu Val Thr Pro Pro Glu	
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Pro Pro Pro Pro Arg Arg Arg Arg Arg Arg Arg Leu Leu Phe Trp Asp	
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Ile Arg Gly Pro Ala Glu Leu Phe Arg Thr Pro Thr Leu Ser Gly Trp	
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Leu Pro Pro Glu Leu Leu Gly Leu Trp Thr His Cys Ala Gln Pro Pro	
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Ala Leu Glu Pro Ser Val Pro Leu Met Val Ser Leu Glu Ile Ser Leu	
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Glu Arg Trp Ala Trp Pro Glu Val Glu Ala Pro Glu Ala Pro Ala Leu	
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Pro Val Val Pro Glu Leu Pro Glu Val Pro Met Glu Met Pro Leu Val	
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Val Ala Leu Glu Leu Gln Ala Asn Arg Glu Pro Asp Phe Ser Ser Leu	
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Pro Tyr Gly Arg Leu Leu Ile Gln Pro Gly Pro Arg Phe His *	
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22 27 32 37

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Val Val Lys Thr Cys Glu Glu Ile Leu Asn Tyr Val Leu Val Arg Val
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Gln Pro Pro Gln Pro Gly Leu Pro Arg Pro Arg Phe Ser Leu Tyr Leu
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Ser Ala Gln Leu Gln Ile Gly Val Ile Arg Val Tyr Ser Gln Gln Cys	
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Gln Tyr Leu Val Glu Asp Ile Gln His Ile Leu Glu Arg Leu His Arg	
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Leu Leu Pro Asn His Leu Ala Met Met Glu Thr Leu Glu Asp Ala Pro	
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Asp Pro Phe Phe Gly Met Met Ser Val Asp Pro Arg Leu Pro Ser Pro	
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Phe Asp Ile Pro Gln Ile Arg His Leu Leu Glu Ala Ala Ile Pro Glu	
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Thr Gly Trp Glu Pro Gly Ala Leu Leu Met Glu Val Thr Pro Pro Glu	
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Glu Arg Arg Lys Ile Glu Val Pro Ser Glu Ile Glu Val Pro Arg Glu	
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Pro Val Val Pro Glu Leu Pro Glu Val Pro Met Glu Met Pro Leu Val	
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Leu Pro Pro Glu Leu Glu Leu Leu Ser Leu Glu Ala Val His Ser Pro	
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Arg Arg Met Ala Ala Arg Val Phe Tyr Leu Leu Leu Val Leu Ser Ala	
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Gln Gln Ile Leu His Val Lys Gln Glu Lys Pro Tyr Gly Arg Leu Leu	
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Ile Gln Pro Gly Pro Arg Phe His *

518 523

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Met Ala Ser Glu

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Asp Ile Ala Lys Leu Ala Glu Thr Leu Ala Lys Thr Gln Val Ala Gly

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Gly Gln Leu Ser Phe Lys Gly Lys Ser Leu Lys Leu Asn Thr Ala Glu

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Asp Ala Lys Asp Val Ile Lys Glu Ile Glu Asp Phe Asp Ser Leu Glu

37 42 47 52

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Ile Ala Lys Ala Leu Glu Lys Lys Ser Glu Leu Lys Arg Cys His Trp	
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Ser Asp Met Phe Thr Gly Arg Leu Arg Thr Glu Ile Pro Pro Ala Leu	
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Ile Ser Leu Gly Glu Gly Leu Ile Thr Ala Gly Ala Gln Leu Val Glu	
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Ala Leu Thr Glu Cys His Arg Lys Ser Ser Ala Gln Gly Lys Pro Leu	
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Ala Thr Ala Leu Ala Glu Ala Phe Arg Val Ile Gly Thr Leu Glu Glu	
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gac aac acc ttc act gag aag ggc gcc gtg gcc atg gcc gag acc ttg	1122
Asp Asn Thr Phe Thr Glu Lys Gly Ala Val Ala Met Ala Glu Thr Leu	
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Lys Thr Leu Arg Gln Val Glu Val Ile Asn Phe Gly Asp Cys Leu Val	
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Arg Ser Lys Gly Ala Val Ala Ile Ala Asp Ala Ile Arg Gly Gly Leu	
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Pro Lys Leu Lys Glu Leu Asn Leu Ser Phe Cys Glu Ile Lys Arg Asp	
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Lys Leu Asp Leu Asn Gly Asn Thr Leu Gly Glu Glu Gly Cys Glu Gln	
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Phe Leu Ala Phe Pro Ser Pro Glu Lys Leu Leu Arg Leu Gly Pro Lys	
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Ile Ala Lys Ala Leu Glu Lys Lys Ser Glu Leu Lys Arg Cys His Trp						
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Ser Asp Met Phe Thr Gly Arg Leu Arg Thr Glu Ile Pro Pro Ala Leu						
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Ile Ser Leu Gly Glu Gly Leu Ile Thr Ala Gly Ala Gln Leu Val Glu						
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Leu Asp Leu Ser Asp Asn Ala Phe Gly Pro Asp Gly Val Gln Gly Phe						

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Leu Asn Asn Cys Gly Met Gly Ile Gly Gly Gly Lys Ile Leu Ala Ala				
149	154	159	164	
gct ctg acc gaa tgt cac cgg aaa tcc agt gcc caa ggc aag cct ctg				882
Ala Leu Thr Glu Cys His Arg Lys Ser Ser Ala Gln Gly Lys Pro Leu				
165	170	175	180	
gcc ctg aag gtc ttt gtg gct ggc aga aac cgt ctg gag aat gat ggc				930
Ala Leu Lys Val Phe Val Ala Gly Arg Asn Arg Leu Glu Asn Asp Gly				
181	186	191	196	
gcc act gcc ttg gca gaa gct ttt agg gtc atc ggg acc ctg gag gag				978
Ala Thr Ala Leu Ala Glu Ala Phe Arg Val Ile Gly Thr Leu Glu Glu				
197	202	207	212	
gtc cac atg cca cag aat ggg atc aac cac cct ggc atc act gcc ctg				1026
Val His Met Pro Gln Asn Gly Ile Asn His Pro Gly Ile Thr Ala Leu				
213	218	223	228	
gcc cag gct ttc gct gtc aac ccc ctg ctg cgg gtc atc aac ctg aat				1074
Ala Gln Ala Phe Ala Val Asn Pro Leu Leu Arg Val Ile Asn Leu Asn				
229	234	239	244	
gac aac acc ttc act gag aag ggc gcc gtg gcc atg gcc gag acc ttg				1122
Asp Asn Thr Phe Thr Glu Lys Gly Ala Val Ala Met Ala Glu Thr Leu				
245	250	255	260	
aag acc ttg cgg cag gtg gag gtg att aat ttt ggg gac tgc ctg gtg				1170
Lys Thr Leu Arg Gln Val Glu Val Ile Asn Phe Gly Asp Cys Leu Val				
261	266	271	276	
cgc tcc aag ggt gca gtt gcc att gca gat gcc atc cgc ggc ggc ctg				1218
Arg Ser Lys Gly Ala Val Ala Ile Ala Asp Ala Ile Arg Gly Gly Leu				
277	282	287	292	
ccc aag cta aag gag ctg aac ttg tca ttc tgt gaa atc aag agg gat				1266
Pro Lys Leu Lys Glu Leu Asn Leu Ser Phe Cys Glu Ile Lys Arg Asp				
293	298	303	308	
gct gcc ctg gct gtt gct gag gcc atg gca gac aaa gct gag ctg gag				1314
Ala Ala Leu Ala Val Ala Glu Ala Met Ala Asp Lys Ala Glu Leu Glu				
309	314	319	324	
aag ctg gac ctg aat ggc aac acc ctg gga gaa gaa ggc tgt gaa cag				1362
Lys Leu Asp Leu Asn Gly Asn Thr Leu Gly Glu Glu Gly Cys Glu Gln				
325	330	335	340	
ctt cag gag gtg ctg gag ggc ttc aac atg gcc aag gtg ctg gcg tcc				1410
Leu Gln Glu Val Leu Glu Gly Phe Asn Met Ala Lys Val Leu Ala Ser				
341	346	351	356	

ctc agt gat gac gag gac gag gag gag gag gag gaa gaa gag cct cag	1458
Leu Ser Asp Asp Glu Asp Glu Glu Glu Glu Glu Glu Glu Glu Pro Gln	
357 362 367 372	
cag cga ggg cag gga gag aag tca gcc acg ccc tca cgg aag att ctg	1506
Gln Arg Gly Gln Gly Glu Lys Ser Ala Thr Pro Ser Arg Lys Ile Leu	
373 378 383 388	
gac cct aac act ggg gag cca gct ccc gtg ctg tcc tcc cca cct cct	1554
Asp Pro Asn Thr Gly Glu Pro Ala Pro Val Leu Ser Ser Pro Pro Pro	
389 394 399 404	
gca gac gtc tcc acc ttc ctg gct ttt ccc tct cca gag aag ctg ctg	1602
Ala Asp Val Ser Thr Phe Leu Ala Phe Pro Ser Pro Glu Lys Leu Leu	
405 410 415 420	
cgc cta ggg ccc aag agc tcc gtg ctg ata gcc cag cag act gac acg	1650
Arg Leu Gly Pro Lys Ser Ser Val Leu Ile Ala Gln Gln Thr Asp Thr	
421 426 431 436	
tct gac ccc gag aag gtg gtc tct gcc ttc cta aag gtg tca tct gtg	1698
Ser Asp Pro Glu Lys Val Val Ser Ala Phe Leu Lys Val Ser Ser Val	
437 442 447 452	
ttc aag gac gaa gct act gtg agg atg gca gtg cag gat gca gta gat	1746
Phe Lys Asp Glu Ala Thr Val Arg Met Ala Val Gln Asp Ala Val Asp	
453 458 463 468	
gcc ctg atg cag aag gct ttc aac tcc tcg tcc ttc aac tcc aac acc	1794
Ala Leu Met Gln Lys Ala Phe Asn Ser Ser Ser Phe Asn Ser Asn Thr	
469 474 479 484	
ttc ctc acc agg ctc ctc gtg cac atg ggt ctg ctc aag agt gaa gac	1842
Phe Leu Thr Arg Leu Leu Val His Met Gly Leu Leu Lys Ser Glu Asp	
485 490 495 500	
aag gtc aag gcc att gcc aac ctg tac ggc ccc ctg atg gcg ctg aac	1890
Lys Val Lys Ala Ile Ala Asn Leu Tyr Gly Pro Leu Met Ala Leu Asn	
501 506 511 516	
cac atg gtg cag cag gac tat ttc ccc aag gcc ctt gca ccc ctg ctg	1938
His Met Val Gln Gln Asp Tyr Phe Pro Lys Ala Leu Ala Pro Leu Leu	
517 522 527 532	
ctg gcg ttc gtg acc aag ccc aac agc gcc ctg gaa tcc tgc tcc ttc	1986
Leu Ala Phe Val Thr Lys Pro Asn Ser Ala Leu Glu Ser Cys Ser Phe	
533 538 543 548	
gcc cgc cac agt ctg ctg cag acg ctg tac aag gtc tag actcaaagcc	2035
Ala Arg His Ser Leu Leu Gln Thr Leu Tyr Lys Val *	
549 554 559	
tctcccatcc cttggcctgg accagtgagc tggggagggga ctcgatgaa ctgaggcgca	2095
gcctacgccca ttgccttggga caggactctg gccacaggca gggcgggtct gtgtcccatg	2155

tgctcctgtca	gtccccctgag	tatgtgtgtg	ggtgtggcgc	atgtgcaggt	ctgtgcctcc	2215
tgtcgggatt	tgggttttaa	cgtcttctgc	tggcccagcc	ctgctctgtt	gtggggagtt	2275
ggcccccagg	ggaaagggct	gtgagctgct	ccgccattaa	actcacctcc	acctgagggc	2335
gctctgctga	tctccgcctg	ggccctgatg	gccgtcccca	cccacctgcc	ttccggcccc	2395
gctccctggc	ggagccagaa	cccaaggagt	tgcccgcgtg	ctgtccttcc	cctctgtgtt	2455
gtgattgggt	tgtttcctgc	cctgcctggg	gctgcttctc	gtcaccaagc	cctggctcctg	2515
cggcagctgt	caccctacc	atccatacca	ctgtgctgac	cgctcagcct	gaagagcaga	2575
gaatgccatg	ggtgggactg	tgggggtcgg	atcgtggggg	tgttggcaga	gggcaaccct	2635
gggccccaca	ccgtgtggac	aggcagacac	cagattgtcc	aggagcagga	gctgctggga	2695
ctgcgctggc	cccggacctt	gtgggccttc	tcttggtgc	tgagatgtcg	tctgtgactg	2755
gcctggctgg	agggggagtg	ttgacaacct	aaagctgttc	tccagtctgg	ggaggagag	2815
gcaggggtccc	caatgtccga	gctgcatctg	gacgctgctc	ttaaaggacc	tctgggggca	2875
ggggagcggg	aggggtctga	ctgggcagat	gctgtatgac	ctccctgagc	accctgact	2935
gccccatgct	ttcccctttg	tgctctgtgt	gtgtctgggc	tgtgccggg	ggcttcacaa	2995
ataaagtcgt	gtggcagctt	caaaaaaaaa	aaa			3028

<210> 259
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (223)..(1149)

<400> 259						
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cggttctctc	ggccgtcctg	agtcccaaat	cccaagctgg	agccgttcag	ctcccctcca	120
ccgcttagag	atttgggggg	ctctggcccc	gtccttgccg	accattccga	ggggagtcca	180
gaggtgtcag	taattaacac	tgtggatacc	tcccatgagg	ac	atg att cac gac	234
					Met Ile His Asp	
					1	
gcc cag atg gac tac tat ggc acc cgc ctg gca acc tgc tca tca gac						282
Ala Gln Met Asp Tyr Tyr Gly Thr Arg Leu Ala Thr Cys Ser Ser Asp						
5		10		15	20	

agg tcc gtc aaa atc ttt gat gtg cgc aat gga ggg cag atc ctt atc	330
Arg Ser Val Lys Ile Phe Asp Val Arg Asn Gly Gly Gln Ile Leu Ile	
21 26 31 36	
gcc gac ctc agg ggt cat gag ggt cct gtg tgg caa gtg gcc tgg gct	378
Ala Asp Leu Arg Gly His Glu Gly Pro Val Trp Gln Val Ala Trp Ala	
37 42 47 52	
cac ccc atg tac ggc aac atc ctg gca tgc tgc tcc tat gac cgg aaa	426
His Pro Met Tyr Gly Asn Ile Leu Ala Ser Cys Ser Tyr Asp Arg Lys	
53 58 63 68	
gtc att atc tgg aga gag gaa aac ggc acc tgg gag aag agc cac gag	474
Val Ile Ile Trp Arg Glu Glu Asn Gly Thr Trp Glu Lys Ser His Glu	
69 74 79 84	
cat gcg gga cac gac tcc tca gtg aac tgc gtg tgc tgg gcc ccc cat	522
His Ala Gly His Asp Ser Ser Val Asn Ser Val Cys Trp Ala Pro His	
85 90 95 100	
gac tac ggc ctg atc ctg gcc tgt ggg agc tgc gat ggg gcc atc tcc	570
Asp Tyr Gly Leu Ile Leu Ala Cys Gly Ser Ser Asp Gly Ala Ile Ser	
101 106 111 116	
ctg ctg act tac acc ggg gaa ggc caa tgg gaa gta aag aag atc aac	618
Leu Leu Thr Tyr Thr Gly Glu Gly Gln Trp Glu Val Lys Lys Ile Asn	
117 122 127 132	
aac gct cac acc att ggc tgc aat gcc gtc agc tgg gcc cct gct gtt	666
Asn Ala His Thr Ile Gly Cys Asn Ala Val Ser Trp Ala Pro Ala Val	
133 138 143 148	
gta cct gga agc ctc ata gac cac cca tgc ggg cag aaa ccc aat tac	714
Val Pro Gly Ser Leu Ile Asp His Pro Ser Gly Gln Lys Pro Asn Tyr	
149 154 159 164	
atc aag agg ttt gca tca ggt ggc tgt gac aac ctc atc aag ctg tgg	762
Ile Lys Arg Phe Ala Ser Gly Gly Cys Asp Asn Leu Ile Lys Leu Trp	
165 170 175 180	
aag gag gag gag gac ggc cag tgg aag gag gag cag aag cta gaa gcg	810
Lys Glu Glu Glu Asp Gly Gln Trp Lys Glu Glu Gln Lys Leu Glu Ala	
181 186 191 196	
cac agt gac tgg gtt cga gat gtg gcc tgg gcc ccc tcc atc ggc ctg	858
His Ser Asp Trp Val Arg Asp Val Ala Trp Ala Pro Ser Ile Gly Leu	
197 202 207 212	
ccc acc agc acc atc gcc agc tgc tcc cag gat ggt cgt gtg ttc att	906
Pro Thr Ser Thr Ile Ala Ser Cys Ser Gln Asp Gly Arg Val Phe Ile	
213 218 223 228	
tgg acc tgt gat gat gcc tca agc aat acg tgg tcc cct aaa ttg ttg	954
Trp Thr Cys Asp Asp Ala Ser Ser Asn Thr Trp Ser Pro Lys Leu Leu	
229 234 239 244	
cac aag ttc aac gat gtg gtg tgg cat gtg agc tgg tcc atc aca gcc	1002

His Lys Phe Asn Asp Val Val Trp His Val Ser Trp Ser Ile Thr Ala	
245 250 255 260	
aac atc ctg gct gtc tct ggt gga gac aat aag gtg acc ctg tgg aag	1050
Asn Ile Leu Ala Val Ser Gly Gly Asp Asn Lys Val Thr Leu Trp Lys	
261 266 271 276	
gag tca gtt gat ggg cag tgg gtg tgc atc agt gat gtc aac aag ggc	1098
Glu Ser Val Asp Gly Gln Trp Val Cys Ile Ser Asp Val Asn Lys Gly	
277 282 287 292	
cag ggc tcc gta tca gca tca gtg aca gag ggc cag cag aac gag cag	1146
Gln Gly Ser Val Ser Ala Ser Val Thr Glu Gly Gln Gln Asn Glu Gln	
293 298 303 308	
tga caag acaggtgggg cctggctccc caccgcag ctccaggact gccccttct	1203
* 309	
gggccaacta accaaacaac tgggaagagc cccaactcc aacaggatta ttttcccagg	1263
aggagttaca gatgcagcca cagattgatc atctgcctta acgtgatcgg agatgctttg	1323
taatctactg tccagctgaa agcactcatg ttacgaggaa gaaactacaa gtgatgttca	1383
aatctatttt gggtcatttt tatgtacctt tgggttcagg cattatttgg ggggttttgt	1443
ttccaaagga actaaataaa gtcattattgc ttataaaaaa aaaaaa	1489

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gtcttaagag cccccactag ctcaaaaatg gtcttagttg tctccccca ttagcagcat	120
ggagagtcaa ggag atg act tct acc ttg cca aag gcc ttg gga aga aag	170
Met Thr Ser Thr Leu Pro Lys Ala Leu Gly Arg Lys	
1 5 10	
aca gca tca agg tct cac aca aca ctc cag gga ggc agc tgc tgc cca	218
Thr Ala Ser Arg Ser His Thr Thr Leu Gln Gly Gly Ser Cys Cys Pro	
13 18 23 28	
gtg ctg tgg aca gca aag ctt cgg tgc agg aaa tta aga ttc ccc ctg	266
Val Leu Trp Thr Ala Lys Leu Arg Cys Arg Lys Leu Arg Phe Pro Leu	
29 34 39 44	

cct ccc cct ccc cca tcc tca tca gct tgg cca tgg cag ggc tgg ggg 314
 Pro Pro Pro Pro Pro Ser Ser Ser Ala Trp Pro Trp Gln Gly Trp Gly
 45 50 55 60

atc aga ggt gaa cag gaa gca gaa gga ccc ctg ggg gag aca ggg cct 362
 Ile Arg Gly Glu Gln Glu Ala Glu Gly Pro Leu Gly Glu Thr Gly Pro
 61 66 71 76

cca gtg gga cca gag ctg agt ggc ctc agg cag tgg cgg aag ctg att 410
 Pro Val Gly Pro Glu Leu Ser Gly Leu Arg Gln Trp Arg Lys Leu Ile
 77 82 87 92

aaa gga agg tac ggg gag tgg agg gga agt gga caa aag aca gga cag 458
 Lys Gly Arg Tyr Gly Glu Trp Arg Gly Ser Gly Gln Lys Thr Gly Gln
 93 98 103 108

cca tct tag acaacaa tgcaaggggg agaaactgaa gaaaacagaa cagagaccac 514
 Pro Ser *
 109

tactggcaat aaacagagag aaagtgaagc cccatgggtg aggcacacct acattactta 574

agaaacgtga gcacattctt acgcctaggg caataaatac atccttgagc tacacaggct 634

aagcaagagt gaaattacag cac 657

<210> 261
 <211> 2078
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (199)..(1836)

<400> 261
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gcgactacct tgagagtagc gggttgaggt gtaagccctg aggaggcagc gttttctggg 120

cttctgtctg gttctctctc tccagaaggt tctgccggtt cccccagctc tgggtaccg 180

gctctgcac gcgtcgcc atg atg ggc cat cgt cca gtg ctc gtg ctc agc 231
 Met Met Gly His Arg Pro Val Leu Val Leu Ser
 1 5

cag aac aca aag cgt gaa tcc gga aga aaa gtt caa tct gga aac atc 279
 Gln Asn Thr Lys Arg Glu Ser Gly Arg Lys Val Gln Ser Gly Asn Ile
 12 17 22 27

aat gct gcc aag act att gca gat atc atc cga aca tgt ttg gga ccc 327
 Asn Ala Ala Lys Thr Ile Ala Asp Ile Ile Arg Thr Cys Leu Gly Pro
 28 33 38 43

aag tcc atg atg aag atg ctt ttg gac cca atg gga ggc att gtg atg	375
Lys Ser Met Met Lys Met Leu Leu Asp Pro Met Gly Gly Ile Val Met	
44 49 54 59	
acc aat gat ggc aat gcc att ctt cga gag att caa gtc cag cat cca	423
Thr Asn Asp Gly Asn Ala Ile Leu Arg Glu Ile Gln Val Gln His Pro	
60 65 70 75	
gcg gcc aag tcc atg atc gaa att agc cgg acc cag gat gaa gag gtt	471
Ala Ala Lys Ser Met Ile Glu Ile Ser Arg Thr Gln Asp Glu Glu Val	
76 81 86 91	
gga gat ggg acc aca tca gta att att ctt gca ggg gaa atg ctg tct	519
Gly Asp Gly Thr Thr Ser Val Ile Ile Leu Ala Gly Glu Met Leu Ser	
92 97 102 107	
gta gct gag cac ttc ctg gag cag cag atg cac cca aca gtg gtg atc	567
Val Ala Glu His Phe Leu Glu Gln Gln Met His Pro Thr Val Val Ile	
108 113 118 123	
agt gct tac cgc aag gca ttg gat gat atg atc agc acc cta aag aaa	615
Ser Ala Tyr Arg Lys Ala Leu Asp Asp Met Ile Ser Thr Leu Lys Lys	
124 129 134 139	
ata agt atc cca gtc gac atc agt gac agt gat atg atg ctg aac atc	663
Ile Ser Ile Pro Val Asp Ile Ser Asp Ser Asp Met Met Leu Asn Ile	
140 145 150 155	
atc aac agc tct att act acc aaa gcc atc agt cgg tgg tca tct ttg	711
Ile Asn Ser Ser Ile Thr Thr Lys Ala Ile Ser Arg Trp Ser Ser Leu	
156 161 166 171	
gct tgc aac att gcc ctg gat gct gtc aag atg gta cag ttt gag gag	759
Ala Cys Asn Ile Ala Leu Asp Ala Val Lys Met Val Gln Phe Glu Glu	
172 177 182 187	
aat ggt cgg aaa gag att gac ata aaa aaa tat gca aga gtg gaa aag	807
Asn Gly Arg Lys Glu Ile Asp Ile Lys Lys Tyr Ala Arg Val Glu Lys	
188 193 198 203	
ata cct gga ggc atc att gaa gac tcc tgt gtc ttg cgt gga gtc atg	855
Ile Pro Gly Gly Ile Ile Glu Asp Ser Cys Val Leu Arg Gly Val Met	
204 209 214 219	
att aac aag gat gtg acc cat cca cgt atg cgg cgc tat atc aag aac	903
Ile Asn Lys Asp Val Thr His Pro Arg Met Arg Arg Tyr Ile Lys Asn	
220 225 230 235	
cct cgc att gtg ctg ctg gat tct tct ctg gaa tac aag aaa gga gaa	951
Pro Arg Ile Val Leu Leu Asp Ser Ser Leu Glu Tyr Lys Lys Gly Glu	
236 241 246 251	
agc cag act gac att gag att aca cga gag gag gac ttc acc cga att	999
Ser Gln Thr Asp Ile Glu Ile Thr Arg Glu Glu Asp Phe Thr Arg Ile	
252 257 262 267	

ctc cag atg gag gaa gag tac atc cag cag ctc tgt gag gac att atc	1047
Leu Gln Met Glu Glu Glu Tyr Ile Gln Gln Leu Cys Glu Asp Ile Ile	
268 273 278 283	
caa ctg aag ccc gat gtg gtc atc act gaa aag ggc atc tca gat tta	1095
Gln Leu Lys Pro Asp Val Val Ile Thr Glu Lys Gly Ile Ser Asp Leu	
284 289 294 299	
gct cag cac tac ctt atg cgg gcc aat atc aca gcc atc cgc aga gtc	1143
Ala Gln His Tyr Leu Met Arg Ala Asn Ile Thr Ala Ile Arg Arg Val	
300 305 310 315	
cgg aag aca gac aat aat cgc att gct aga gcc tgt ggg gcc cgg ata	1191
Arg Lys Thr Asp Asn Asn Arg Ile Ala Arg Ala Cys Gly Ala Arg Ile	
316 321 326 331	
gtc agc cga cca gag gaa ctg aga gaa gat gat gtt gga aca gga gca	1239
Val Ser Arg Pro Glu Glu Leu Arg Glu Asp Asp Val Gly Thr Gly Ala	
332 337 342 347	
ggc ctg ttg gaa atc aag aaa att gga gat gaa tac ttt act ttc atc	1287
Gly Leu Leu Glu Ile Lys Lys Ile Gly Asp Glu Tyr Phe Thr Phe Ile	
348 353 358 363	
act gac tgc aaa gac ccc aag gcc tgc acc att ctc ctc cgg ggg gct	1335
Thr Asp Cys Lys Asp Pro Lys Ala Cys Thr Ile Leu Leu Arg Gly Ala	
364 369 374 379	
agc aaa gag att ctc tcg gaa gta gaa cgc aac ctc cag gat gcc atg	1383
Ser Lys Glu Ile Leu Ser Glu Val Glu Arg Asn Leu Gln Asp Ala Met	
380 385 390 395	
caa gtg tgt cgc aat gtt ctc ctg gac cct cag ctg gtg cca ggg ggt	1431
Gln Val Cys Arg Asn Val Leu Leu Asp Pro Gln Leu Val Pro Gly Gly	
396 401 406 411	
ggg gcc tcc gag atg gct gtg gcc cat gcc ttg aca gaa aaa tcc aag	1479
Gly Ala Ser Glu Met Ala Val Ala His Ala Leu Thr Glu Lys Ser Lys	
412 417 422 427	
gcc atg act ggt gtg gaa caa tgg cca tac agg gct gtt gcc cag gcc	1527
Ala Met Thr Gly Val Glu Gln Trp Pro Tyr Arg Ala Val Ala Gln Ala	
428 433 438 443	
cta gag gtc att cct cgt acc ctg atc cag aac tgt ggg gcc agc acc	1575
Leu Glu Val Ile Pro Arg Thr Leu Ile Gln Asn Cys Gly Ala Ser Thr	
444 449 454 459	
atc cgt cta ctt acc tcc ctt cgg gcc aag cac acc cag gag aac tgt	1623
Ile Arg Leu Leu Thr Ser Leu Arg Ala Lys His Thr Gln Glu Asn Cys	
460 465 470 475	
gag acc tgg ggt gta aat ggt gag acg ggt act ttg gtg gac atg aag	1671
Glu Thr Trp Gly Val Asn Gly Glu Thr Gly Thr Leu Val Asp Met Lys	
476 481 486 491	
gaa ctg ggc ata tgg gag cca ttg gct gtg aag ctg cag act tat aag	1719

Glu Leu Gly Ile Trp	Glu Pro Leu Ala Val	Lys Leu Gln Thr Tyr Lys	
492	497	502	507
aca gca gtg gag acg gca gtt ctg cta ctg cga att gat gac atc gtt		1767	
Thr Ala Val Glu Thr	Ala Val Leu Leu Leu Arg Ile Asp Asp Ile Val		
508	513	518	523
tca ggc cac aaa aag aaa ggc gat gac cag agc cgg caa ggc ggg gct		1815	
Ser Gly His Lys Lys Lys Gly Asp Asp Gln Ser Arg Gln Gly Gly Ala			
524	529	534	539
cct gat gct ggc cag gag tga gt gctaggcaag gctacttcaa tgcacagaac		1868	
Pro Asp Ala Gly Gln Glu *			
540	545		
cagcagagtc tccccttttc ctgagccaga gtgccaggaa cactgtggac gtctttgttc		1928	
agaagggatc aggttggggg gcagcccccga gtcccctttct gtcccagctc agttttccaa		1988	
aagacactga catgtaattc ttctctattg taagggtttcc atttagtttg cttccgatga		2048	
ttaaatttaa gtcatttgaa aaaaaaaaaa		2078	

<210> 262
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 <212> DNA
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<220>
 <221> CDS
 <222> (188)..(1108)

<400> 262		
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gacgcctaac cccgcgagaa ccctgcaaat tttcttcctc ataattggga gaagactcac		180
tggccga atg gca gca gta gat gac ttg caa ttt gaa gaa ttt ggc aat		229
Met Ala Ala Val Asp Asp Leu Gln Phe Glu Glu Phe Gly Asn		
1 5 10		
gca gcc act tct ctg aca gca aac cca gat gcc acc aca gta aac att		277
Ala Ala Thr Ser Leu Thr Ala Asn Pro Asp Ala Thr Thr Val Asn Ile		
15 20 25 30		
gag gat cct ggt gaa acc cca aaa cat cag cca gga tcc cca aga ggc		325
Glu Asp Pro Gly Glu Thr Pro Lys His Gln Pro Gly Ser Pro Arg Gly		
31 36 41 46		
tca gga aga gaa gaa gat gat gag tta ctg gga aat gat gac tct gac		373
Ser Gly Arg Glu Glu Asp Asp Glu Leu Leu Gly Asn Asp Asp Ser Asp		
47 52 57 62		

aaa act gag tta ctt gct gga cag aag aaa agc tcc ccc ttc tgg aca	421
Lys Thr Glu Leu Leu Ala Gly Gln Lys Lys Ser Ser Pro Phe Trp Thr	
63 68 73 78	
ttt gaa tac tac caa aca ttc ttt gat gtg gac acc tac cag gtc ttt	469
Phe Glu Tyr Tyr Gln Thr Phe Phe Asp Val Asp Thr Tyr Gln Val Phe	
79 84 89 94	
gac aga att aaa gga tct ctt ttg cca ata ccc ggg aaa aac ttt gtg	517
Asp Arg Ile Lys Gly Ser Leu Leu Pro Ile Pro Gly Lys Asn Phe Val	
95 100 105 110	
agg tta tat atc cgc agc aat cca gat ctc tat ggc ccc ttt tgg ata	565
Arg Leu Tyr Ile Arg Ser Asn Pro Asp Leu Tyr Gly Pro Phe Trp Ile	
111 116 121 126	
tgt gcc acg ttg gtc ttt gcc ata gca att agt ggg aat ctt tcc aac	613
Cys Ala Thr Leu Val Phe Ala Ile Ala Ile Ser Gly Asn Leu Ser Asn	
127 132 137 142	
ttc ttg atc cat ctg gga gag aag acg tac cat tat gtg ccc gaa ttc	661
Phe Leu Ile His Leu Gly Glu Lys Thr Tyr His Tyr Val Pro Glu Phe	
143 148 153 158	
cga aaa gtg tcc ata gca gct acc atc atc tat gcc tat gcc tgg ctg	709
Arg Lys Val Ser Ile Ala Ala Thr Ile Ile Tyr Ala Tyr Ala Trp Leu	
159 164 169 174	
gtt cct ctt gca ctc tgg ggt ttc ctc atg tgg aga aac agc aaa gtt	757
Val Pro Leu Ala Leu Trp Gly Phe Leu Met Trp Arg Asn Ser Lys Val	
175 180 185 190	
atg aac atc gtc tcc tat tca ttt ctg gag att gtg tgt gtc tat gga	805
Met Asn Ile Val Ser Tyr Ser Phe Leu Glu Ile Val Cys Val Tyr Gly	
191 196 201 206	
tat tcc ctc ttc att tat atc ccc acc gca ata ctg tgg att atc ccc	853
Tyr Ser Leu Phe Ile Tyr Ile Pro Thr Ala Ile Leu Trp Ile Ile Pro	
207 212 217 222	
cag aaa gct gtt cgt tgg att cta gtc atg att gcc ctg ggc atc tca	901
Gln Lys Ala Val Arg Trp Ile Leu Val Met Ile Ala Leu Gly Ile Ser	
223 228 233 238	
gga tct ctc ttg gca atg aca ttt tgg cca gct gtt cgt gag gat aac	949
Gly Ser Leu Leu Ala Met Thr Phe Trp Pro Ala Val Arg Glu Asp Asn	
239 244 249 254	
cga cgc gtt gca ttg gcc aca att gtg aca att gtg ttg ctc cat atg	997
Arg Arg Val Ala Leu Ala Thr Ile Val Thr Ile Val Leu Leu His Met	
255 260 265 270	
ctg ctt tct gtg ggc tgc ttg gca tac ttt ttt gat gca cca gag atg	1045
Leu Leu Ser Val Gly Cys Leu Ala Tyr Phe Phe Asp Ala Pro Glu Met	
271 276 281 286	

gac cat ctc cca aca act aca gct act cca aac caa aca gtt gct gca 1093
 Asp His Leu Pro Thr Thr Thr Ala Thr Pro Asn Gln Thr Val Ala Ala
 287 292 297 302

gcc aag tcc agc taa tgaggaaaga ctcaacttgag ataccctctc cttgctgaag 1148
 Ala Lys Ser Ser *
 303

tttttcttga cttctccagt tctcttttgt tttttggagc atgggtcttt gggaagtggc 1208

atccactgca ggaaagcaga atgagcagag ccagcagaac tgatggagtg gcacaaattc 1268

ccagtgtctg gatggtgcca cactggcgcc taatcacccg ttttaacaagc agaaattaa 1328

tggtgctcag cacatgtgtc tttcagctct tccttttcac ccatggatga tcattgctgag 1388

catgcgctga ttggactgaa atgccgggga atagggttagg catgctcagt gccgtccctt 1448

tgccaccaca gtcaaatgac atgcttcact gtggtacctt aatacctgaa atagaacat 1508

ggaaaattct gatgtcctct ctctgaatta tgtacagact acctggggga tcctcttctc 1568

tcctaatgtt agccatcctg aagtagccga acagtagaaa ctttggtggg gattaaccgg 1628

gagcttgaaa atttgtcttt ggtaacctga tactggacag ctgaactgaa tggctgcaaa 1688

ataaatacct cacatgatgt ctgtgtctgc aaaaaaaaaa aaa 1731

<210> 263
 <211> 1717
 <212> DNA
 <213> Homo sapiens

<220>
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<400> 263

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ctgcctgggc atcctgcgcc cggccc atg acg gcg cac tca ttc gcc ctc ccg 112
 Met Thr Ala His Ser Phe Ala Leu Pro
 1 5

gtc atc atc ttc acc acg ttc tgg ggc ctc gtc ggc atc gcc ggg ccc 160
 Val Ile Ile Phe Thr Thr Phe Trp Gly Leu Val Gly Ile Ala Gly Pro
 10 15 20 25

tgg ttc gtg ccg aag gga ccc aac cgc gga gtg atc atc acc atg ctg 208
 Trp Phe Val Pro Lys Gly Pro Asn Arg Gly Val Ile Ile Thr Met Leu
 26 31 36 41

gtc gcc acc gcc gtc tgc tgt tac ctc ttc tgg ctc atc gcc atc ctg 256
 Val Ala Thr Ala Val Cys Cys Tyr Leu Phe Trp Leu Ile Ala Ile Leu

42	47	52	57	
gcg cag ctg aac ccc ctg ttc ggg ccc cag ctg aag aat gag acc atc				304
Ala Gln Leu Asn Pro Leu Phe Gly Pro Gln Leu Lys Asn Glu Thr Ile				
58	63	68	73	
tggttacgtg cgc ttc ctg tgg gag tga cccgc ccccccgac ccaggtgccc				356
Trp Tyr Val Arg Phe Leu Trp Glu *				
74	79			
agctctcgga atgactgtgg ctccactgtc cctgacaacc ccttcgtccg gaccctcccc				416
cacacaacta tgtctggtca ccagctccct cctgctggca ccagagacc cggacccgca				476
gggcctgcct gggtcctgga agtcttccca gtcttccag ccagccggg ccctggggag				536
ccctgggcac agcagcggcc gaggggatgt cctgctccaa taccgcact gctctggagt				596
ttgccctctt tccaaggag atgctgctgg ggagctggta tgggtgggggt ctttcccttt				656
acagacgggg cagatgccag gactcagccc atcctgagga ggacacgtgt cctcatggag				716
aggggtgctcc ggcccaggcg ggggagtcgg tgcccagtca gcagctctgc caccatcctg				776
ctgggaactg ggggggcctc tattgggtta taggcaaggc cttttctctg gcatggaatt				836
gttaattttc tgacacgtct agatgtgaaa tttctgaaaa tgttgaagca gagaaacatt				896
cacacacaaa aagcaacata gtcatgtggg tccagatggc ctcagtccta gatgttgga				956
ccctttgctg tgtctcctca gagtatcctg ttccgctcc tgccacctgg acctccctca				1016
gtggatgtct tccctcccc gacccagcc tgtcagtccg agcacagtgc aggtttggct				1076
ctgacttggg cctttggctg cagtgggggt ggatttcaga gcctctcatg gcagcatcta				1136
agtgaccaga gctgggatga gagaggggaa ggggcaatgt gagtggcgct atgggacggg				1196
ccagccctgc tcctgagcca gcccgcct ctgccccctg gccctgggct ctgtgctagg				1256
gatggtgaag aatgggggag tgccagcctg gcaggagtgg gaagcaacac gcaggggtcc				1316
cggacctctc cagccttgcc ctcacgctta cccagactcc cagtgtggtt agcacagagc				1376
tcaccacact tgcttggtc ccagctgggg cctgtcctca ctggtgctcc aggggaagaa				1436
acgacagcct cacttctgta tggactgctg atgtggcctg ccatcctgtt cagcgggcat				1496
tgtctttgga gcagcaggag aataggatgc ctctcactca catgccagtt cctggctggc				1556
cagctgctca gggctcaggc tggggcctcc cattgacatc cccccctac actccctctc				1616
tgagcctccg tcgccccctc tgttgggtaa ggggtgttgag tgtgacttgt gctgaaaacc				1676
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<210> 264
 <211> 2215
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (6)..(1160)

<400> 264

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	Met Met Tyr Ile Thr Ile Tyr Ser Met Met Lys Ile Pro His	
	1 5 10	
caa acc caa aaa aag aga tct ctc gag gat ccg aat tcg cgg ccg cgt	95	
Gln Thr Gln Lys Lys Arg Ser Leu Glu Asp Pro Asn Ser Arg Pro Arg		
15 20 25 30		
cga ccg cgg tct atg gct gcg act tct cta atg tct gct ttg gct gcc	143	
Arg Pro Arg Ser Met Ala Ala Thr Ser Leu Met Ser Ala Leu Ala Ala		
31 36 41 46		
cgg ctg ctg cag ccc gcg cac agc tgc tcc ctt cgc ctt cgc cct ttc	191	
Arg Leu Leu Gln Pro Ala His Ser Cys Ser Leu Arg Leu Arg Pro Phe		
47 52 57 62		
cac ctc gcg gca gtt cga aat gaa gct gtt gtc att tct gga agg aaa	239	
His Leu Ala Ala Val Arg Asn Glu Ala Val Val Ile Ser Gly Arg Lys		
63 68 73 78		
ctg gcc cag cag atc aag cag gaa gtg cgg cag gag gta gaa gag tgg	287	
Leu Ala Gln Gln Ile Lys Gln Glu Val Arg Gln Glu Val Glu Glu Trp		
79 84 89 94		
gtg gcc tca ggc aac aaa cgg cca cac ctg agt gtg atc ctg gtt ggc	335	
Val Ala Ser Gly Asn Lys Arg Pro His Leu Ser Val Ile Leu Val Gly		
95 100 105 110		
gag aat cct gca agt cac tcc tat gtc ctc aac aaa acc agg gca gct	383	
Glu Asn Pro Ala Ser His Ser Tyr Val Leu Asn Lys Thr Arg Ala Ala		
111 116 121 126		
gca gtt gtg gga atc aac agt gag aca att atg aaa cca gct tca att	431	
Ala Val Val Gly Ile Asn Ser Glu Thr Ile Met Lys Pro Ala Ser Ile		
127 132 137 142		
tca gag gaa gaa ttg ttg aat tta atc aat aaa ctg aat aat gat gat	479	
Ser Glu Glu Glu Leu Leu Asn Leu Ile Asn Lys Leu Asn Asn Asp Asp		
143 148 153 158		
aat gta gat ggc ctc ctt gtt cag ttg cct ctt cca gag cat att gat	527	
Asn Val Asp Gly Leu Leu Val Gln Leu Pro Leu Pro Glu His Ile Asp		
159 164 169 174		
gag aga agg atc tgc aat gct gtt tct cca gac aag gat gtt gat ggc	575	

Glu	Arg	Arg	Ile	Cys	Asn	Ala	Val	Ser	Pro	Asp	Lys	Asp	Val	Asp	Gly		
175					180					185					190		
ttt	cat	gta	att	aat	gta	gga	cga	atg	tgt	ttg	gat	cag	tat	tcc	atg		623
Phe	His	Val	Ile	Asn	Val	Gly	Arg	Met	Cys	Leu	Asp	Gln	Tyr	Ser	Met		
191					196					201					206		
tta	ccg	gct	act	cca	tgg	ggt	gtg	tgg	gaa	ata	atc	aag	cga	act	ggc		671
Leu	Pro	Ala	Thr	Pro	Trp	Gly	Val	Trp	Glu	Ile	Ile	Lys	Arg	Thr	Gly		
207					212					217					222		
att	cca	acc	cta	ggg	aag	aat	gtg	gtt	gtg	gct	gga	agg	tca	aaa	aac		719
Ile	Pro	Thr	Leu	Gly	Lys	Asn	Val	Val	Val	Ala	Gly	Arg	Ser	Lys	Asn		
223					228					233					238		
gtt	gga	atg	ccc	att	gca	atg	tta	ctg	cac	aca	gat	ggg	gcg	cat	gaa		767
Val	Gly	Met	Pro	Ile	Ala	Met	Leu	Leu	His	Thr	Asp	Gly	Ala	His	Glu		
239					244					249					254		
cgt	ccc	gga	ggt	gat	gcc	act	gtt	aca	ata	tct	cat	cga	tat	act	ccc		815
Arg	Pro	Gly	Gly	Asp	Ala	Thr	Val	Thr	Ile	Ser	His	Arg	Tyr	Thr	Pro		
255					260					265					270		
aaa	gag	cag	ttg	aag	aaa	cat	aca	att	ctt	gca	gat	att	gta	ata	tct		863
Lys	Glu	Gln	Leu	Lys	Lys	His	Thr	Ile	Leu	Ala	Asp	Ile	Val	Ile	Ser		
271					276					281					286		
gct	gca	ggt	att	cca	aat	ctg	atc	aca	gca	gat	atg	atc	aag	gaa	gga		911
Ala	Ala	Gly	Ile	Pro	Asn	Leu	Ile	Thr	Ala	Asp	Met	Ile	Lys	Glu	Gly		
287					292					297					302		
gca	gca	gtc	att	gat	gtg	gga	ata	aat	aga	gtt	cac	gat	cct	gta	act		959
Ala	Ala	Val	Ile	Asp	Val	Gly	Ile	Asn	Arg	Val	His	Asp	Pro	Val	Thr		
303					308					313					318		
gcc	aaa	ccc	aag	ttg	gtt	gga	gat	gtg	gat	ttt	gaa	gga	gtc	aga	caa		1007
Ala	Lys	Pro	Lys	Leu	Val	Gly	Asp	Val	Asp	Phe	Glu	Gly	Val	Arg	Gln		
319					324					329					334		
aaa	gct	ggg	tat	atc	act	cca	gtt	cct	gga	ggt	gtt	ggc	ccc	atg	aca		1055
Lys	Ala	Gly	Tyr	Ile	Thr	Pro	Val	Pro	Gly	Gly	Val	Gly	Pro	Met	Thr		
335					340					345					350		
gtg	gca	atg	cta	atg	aag	aat	acc	att	att	gct	gca	aaa	aag	gtg	ctg		1103
Val	Ala	Met	Leu	Met	Lys	Asn	Thr	Ile	Ile	Ala	Ala	Lys	Lys	Val	Leu		
351					356					361					366		
agg	ctt	gaa	gag	cga	gaa	gtg	ctg	aag	tct	aaa	gag	ctt	ggg	gta	gcc		1151
Arg	Leu	Glu	Glu	Arg	Glu	Val	Leu	Lys	Ser	Lys	Glu	Leu	Gly	Val	Ala		
367					372					377					382		
act	aat	taa	ctactgt	gtcttctgtg	tcacaaacag	cactccaggc	cagctcaaga										1207
Thr	Asn	*															
383																	
agcaaagcag	gccaatagaa	atgcaatatt	tttaatttat	tctactgaaa	tggtttaaaa												1267

tgatgccttg tatttattga aagcttaa at ggggtgggtgt ttctgcacat acctctgcag 1327
 tacctcacca gggagcattc cagtatcatg cagggctctg tgatctagcc aggagcagcc 1387
 attaacctag tgattaatat gggagacatt accatatgga ggatggatgc ttcactttgt 1447
 caagcacctc agttacacat tcgccttttc taggattgca tttcccaagt gctattgcaa 1507
 taacagttga tactcatttt aggtacccaaa ccttttgagt tcaactgatc aaaccaaagg 1567
 aaaagtgttg ctagagaaaa ttagggaaaa ggtgaaaaag aaaaaatggg agtaattgag 1627
 cagaaaaaaa ttaatttata tatgtattga ttggcaacca gatttatcta agtagaactg 1687
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 gcttagtcag tttattggga aaatgtttag gattattcct tgctattagt actcatttta 1807
 tgtatgttac ccttcagtaa gttctcccca ttttagtttt ctaggactga aaggattcct 1867
 ttctacatta tacatgtgtg ttgtcatatt tggcctttgc tatatacttt aacttcattg 1927
 ttaaattttt gtattgtata gtttctttgg tgtatcttaa aacctatttt tgaaaaacaa 1987
 acttggttg ataatcattt gggcagcttg ggtaagtacg caacttactt ttccaccaa 2047
 gaactgtcag cagctgcctg cttttctgtg atgtatgtat cctgttgact tttccagaaa 2107
 ttttttaaga gtttgagtta ctattgaatt taatcagact ttctgattaa aggggtttct 2167
 ttctttttta ataaaacaca tctgtctggg atggtatgaa aaaaaaaa 2215

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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (100)..(1161)

<400> 265
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 cggagaaacg tttctctttc ctctcagttt gcgcacacc atg gcg gcc cct gcc 114
 Met Ala Ala Pro Ala
 1
 cag cag act act cag cct ggc ggc ggg aag cgc aaa ggc aag gct cag 162
 Gln Gln Thr Thr Gln Pro Gly Gly Gly Lys Arg Lys Gly Lys Ala Gln
 6 11 16 21
 tat gtg ctg gcc aag cgc gct cgg cgc tgc gac gct ggc ggg ccc cgt 210
 Tyr Val Leu Ala Lys Arg Ala Arg Arg Cys Asp Ala Gly Gly Pro Arg

22	27	32	37	
cag cta gag ccc ggg cta cag ggc atc ctc atc acc tgc aat atg aac				258
Gln Leu Glu Pro Gly Leu Gln Gly Ile Leu Ile Thr Cys Asn Met Asn				
38	43	48	53	
gag cgc aag tgc gtg gag gag gcc tac agc ctc ctc aac gaa tac ggc				306
Glu Arg Lys Cys Val Glu Glu Ala Tyr Ser Leu Leu Asn Glu Tyr Gly				
54	59	64	69	
gac gac atg tat ggg cca gaa aag ttt aca gac aag gat cag cag ccc				354
Asp Asp Met Tyr Gly Pro Glu Lys Phe Thr Asp Lys Asp Gln Gln Pro				
70	75	80	85	
tct gga agt gag gga gag gat gat gat gcg gag gct gcc ttg aag aaa				402
Ser Gly Ser Glu Gly Glu Asp Asp Asp Ala Glu Ala Ala Leu Lys Lys				
86	91	96	101	
gaa gtt ggt gac att aag gca tct aca gag atg agg tta aga aga ttc				450
Glu Val Gly Asp Ile Lys Ala Ser Thr Glu Met Arg Leu Arg Arg Phe				
102	107	112	117	
cag tca gtg gaa agt gga gca aat aac gtt gtc ttc atc agg aca ctt				498
Gln Ser Val Glu Ser Gly Ala Asn Asn Val Val Phe Ile Arg Thr Leu				
118	123	128	133	
ggg ata gag cct gag aaa ttg gtg cat cat att ctc cag gat atg tac				546
Gly Ile Glu Pro Glu Lys Leu Val His His Ile Leu Gln Asp Met Tyr				
134	139	144	149	
aaa acc aag aaa aag aag act cga gtt att ttg cga atg tta ccc atc				594
Lys Thr Lys Lys Lys Lys Thr Arg Val Ile Leu Arg Met Leu Pro Ile				
150	155	160	165	
tca ggc aca tgc aag gct ttt tta gaa gat atg aaa aaa tat gca gaa				642
Ser Gly Thr Cys Lys Ala Phe Leu Glu Asp Met Lys Lys Tyr Ala Glu				
166	171	176	181	
aca ttt ttg gaa ccc tgg ttt aaa gct cca aac aaa ggg aca ttt cag				690
Thr Phe Leu Glu Pro Trp Phe Lys Ala Pro Asn Lys Gly Thr Phe Gln				
182	187	192	197	
att gtg tac aaa tct cga aat aac agt cat gtg aat aga gaa gaa gtt				738
Ile Val Tyr Lys Ser Arg Asn Asn Ser His Val Asn Arg Glu Glu Val				
198	203	208	213	
atc aga gaa ttg gca gga ata gtg tgc acc ctc aat tca gaa aat aaa				786
Ile Arg Glu Leu Ala Gly Ile Val Cys Thr Leu Asn Ser Glu Asn Lys				
214	219	224	229	
gtg gat ctc acc aat cca cag tac aca gtg gta gta gaa atc atc aaa				834
Val Asp Leu Thr Asn Pro Gln Tyr Thr Val Val Val Glu Ile Ile Lys				
230	235	240	245	
gct gtc tgt tgc ctg agt gtt gtg aaa gat tac atg ttg ttt aga aaa				882
Ala Val Cys Cys Leu Ser Val Val Lys Asp Tyr Met Leu Phe Arg Lys				
246	251	256	261	

tac aat ctc cag gag gtg gtg aag agc cct aag gat ccg tca cag ctt	930
Tyr Asn Leu Gln Glu Val Val Lys Ser Pro Lys Asp Pro Ser Gln Leu	
262 267 272 277	

aac tca aag cag gga aat ggg aaa gaa gct aaa ctg gaa tct gcg gac	978
Asn Ser Lys Gln Gly Asn Gly Lys Glu Ala Lys Leu Glu Ser Ala Asp	
278 283 288 293	

aaa tca gac caa aac aac aca gca gaa gga aaa aat aac cag cag gta	1026
Lys Ser Asp Gln Asn Asn Thr Ala Glu Gly Lys Asn Asn Gln Gln Val	
294 299 304 309	

cca gag aat act gag gag ctg ggg cag aca aaa cca acg tct aat cca	1074
Pro Glu Asn Thr Glu Glu Leu Gly Gln Thr Lys Pro Thr Ser Asn Pro	
310 315 320 325	

cag gtg gta aat gag gga gga gcc aaa cct gaa ctt gca agt caa gcc	1122
Gln Val Val Asn Glu Gly Gly Ala Lys Pro Glu Leu Ala Ser Gln Ala	
326 331 336 341	

aca gaa gga tcc aag tca aat gaa aat gac ttc tca tag gaagtcattt	1171
Thr Glu Gly Ser Lys Ser Asn Glu Asn Asp Phe Ser *	
342 347 352	

ggtgttggag ctgacagtcc agtgtcgcaa ttttgggaagg caagatgtga gagagacgag	1231
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aaccattttta ggcatagaac tacagacatt tctgaaaagg ttggtgatga agaacttcag	1291
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tcttctgagt atac	1305
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 <212> DNA
 <213> Homo sapiens

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Met	
1	

agg gca gac gag atc aaa gat gcc atc tac gtg acc atg gag atc ctg	166
Arg Ala Asp Glu Ile Lys Asp Ala Ile Tyr Val Thr Met Glu Ile Leu	
2 7 12 17	

tcc aac tgg ggc aac tcg tgg tgg gtg ggt ctc aca gaa gtc gag ttc	214
Ser Asn Trp Gly Asn Ser Trp Trp Val Gly Leu Thr Glu Val Glu Phe	
18 23 28 33	

ttt gac ttg aat gac aca aag ctt tat gtg tgc ccc cac gat gtg gat	262
Phe Asp Leu Asn Asp Thr Lys Leu Tyr Val Ser Pro His Asp Val Asp	
34 39 44 49	
atc cgg aac aca gcc acg cct ggg gag ctg ggc cgc ctc gtc aac agg	310
Ile Arg Asn Thr Ala Thr Pro Gly Glu Leu Gly Arg Leu Val Asn Arg	
50 55 60 65	
aac tta gct ggc aag aaa gac tcc tcc ccg tgg acc tgc ccc ttc cac	358
Asn Leu Ala Gly Lys Lys Asp Ser Ser Pro Trp Thr Cys Pro Phe His	
66 71 76 81	
cca cca ctc cag ctg ttt ttt gtt att cga aac aca aga cag ctg ggg	406
Pro Pro Leu Gln Leu Phe Phe Val Ile Arg Asn Thr Arg Gln Leu Gly	
82 87 92 97	
gac ttc cat ctg gcc aag atc aag gtt cgg aat tac tgg aca gct gat	454
Asp Phe His Leu Ala Lys Ile Lys Val Arg Asn Tyr Trp Thr Ala Asp	
98 103 108 113	
ggc gat ctt gac att ggt gcc aag aac gtg aag ctt tac gtc aac aga	502
Gly Asp Leu Asp Ile Gly Ala Lys Asn Val Lys Leu Tyr Val Asn Arg	
114 119 124 129	
aac ctc atc ttc aat ggc aag tta gac aaa gga gat agg gag gcc cca	550
Asn Leu Ile Phe Asn Gly Lys Leu Asp Lys Gly Asp Arg Glu Ala Pro	
130 135 140 145	
gct gac cac agc atc ctg gtt gac cag aag aac gag aag agc gag caa	598
Ala Asp His Ser Ile Leu Val Asp Gln Lys Asn Glu Lys Ser Glu Gln	
146 151 156 161	
cta gag gag gcc atg aac gct cac tgc gaa gaa agc aaa ggc acc cat	646
Leu Glu Glu Ala Met Asn Ala His Ser Glu Glu Ser Lys Gly Thr His	
162 167 172 177	
gag atg gct ggt gcc agc ggg gac aag gag ctt ggt ctc ggt tgc tca	694
Glu Met Ala Gly Ala Ser Gly Asp Lys Glu Leu Gly Leu Gly Cys Ser	
178 183 188 193	
ccg cca gct gaa aca tta gcg gat gca aag ctt tct tca caa gga aat	742
Pro Pro Ala Glu Thr Leu Ala Asp Ala Lys Leu Ser Ser Gln Gly Asn	
194 199 204 209	
gtg tct ggc aaa aga aag aat tct act aat tgc agg aaa gac agt ttg	790
Val Ser Gly Lys Arg Lys Asn Ser Thr Asn Cys Arg Lys Asp Ser Leu	
210 215 220 225	
tcc cag tta gag gaa tat ttg aga ctg tgc gca gtc ccc act tgc atg	838
Ser Gln Leu Glu Glu Tyr Leu Arg Leu Ser Ala Val Pro Thr Ser Met	
226 231 236 241	
ggt gac atg ccc agt gct cct gcc act tcc cca cct gtg aag tgc cct	886
Gly Asp Met Pro Ser Ala Pro Ala Thr Ser Pro Pro Val Lys Cys Pro	
242 247 252 257	

cct gtc cat gag gag ccc tct ctc atc caa caa ctg gaa aac ctc atg	934
Pro Val His Glu Glu Pro Ser Leu Ile Gln Gln Leu Glu Asn Leu Met	
258 263 268 273	
ggc aga aaa atc tgt gag cca ccc ggg aaa acc cca tcc tgg tta caa	982
Gly Arg Lys Ile Cys Glu Pro Pro Gly Lys Thr Pro Ser Trp Leu Gln	
274 279 284 289	
cct tct ccc acc ggc aag gac agg aag cag gga ggc agg aag cca aaa	1030
Pro Ser Pro Thr Gly Lys Asp Arg Lys Gln Gly Gly Arg Lys Pro Lys	
290 295 300 305	
ccc ctc tgg ctt agt ccc gag aag ccc ctg gcc tgg aag ggc agg ctc	1078
Pro Leu Trp Leu Ser Pro Glu Lys Pro Leu Ala Trp Lys Gly Arg Leu	
306 311 316 321	
cca tca gac gat gtc atc ggt gag ggt cct gga gag acc gag gcc agg	1126
Pro Ser Asp Asp Val Ile Gly Glu Gly Pro Gly Glu Thr Glu Ala Arg	
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 atg gcg gac ttc gac acc tac gac gat cgg gcc tac agc agc ttc ggc 168
 Met Ala Asp Phe Asp Thr Tyr Asp Asp Arg Ala Tyr Ser Ser Phe Gly
 1 5 10 15
 ggc ggc aga ggg tcc cgc ggc agt gct ggt ggc cat ggt tcc cgt agc 216
 Gly Gly Arg Gly Ser Arg Gly Ser Ala Gly Gly His Gly Ser Arg Ser
 17 22 27 32
 cag aag gag ttg ccc aca gag ccc ccc tac aca gca tac gta gga aat 264
 Gln Lys Glu Leu Pro Thr Glu Pro Pro Tyr Thr Ala Tyr Val Gly Asn
 33 38 43 48
 cta cct ttc aat acg gtt cag ggc gac ata gat gct atc ttt aag gat 312
 Leu Pro Phe Asn Thr Val Gln Gly Asp Ile Asp Ala Ile Phe Lys Asp
 49 54 59 64
 ctc agc ata agg agt gta cgg cta gtc aga gac aaa gac aca gat aaa 360
 Leu Ser Ile Arg Ser Val Arg Leu Val Arg Asp Lys Asp Thr Asp Lys
 65 70 75 80
 ttt aaa gga ttc tgc tat gta gaa ttc gat gaa gtg gat tcc ctt aag 408
 Phe Lys Gly Phe Cys Tyr Val Glu Phe Asp Glu Val Asp Ser Leu Lys
 81 86 91 96
 gaa gcc ttg aca tac gat ggt gca ctg ttg ggc gat cgg tca ctt cgt 456
 Glu Ala Leu Thr Tyr Asp Gly Ala Leu Leu Gly Asp Arg Ser Leu Arg
 97 102 107 112
 gtg gac att gca gaa ggc aga aaa caa gat aaa ggt ggc ttt gga ttc 504
 Val Asp Ile Ala Glu Gly Arg Lys Gln Asp Lys Gly Gly Phe Gly Phe

113	118	123	128	
aga aaa ggt gga cca gat gac aga gga atg ggt agc tct cga gaa tct				552
Arg Lys Gly Gly Pro Asp Asp Arg Gly Met Gly Ser Ser Arg Glu Ser				
129	134	139	144	
aga ggt gga tgg gat tcc cgg gat gac ttc aat tct ggc ttc agg gat				600
Arg Gly Gly Trp Asp Ser Arg Asp Asp Phe Asn Ser Gly Phe Arg Asp				
145	150	155	160	
gac ttc tta ggg ggc agg gga ggt agt cgc cca ggc gac cgg cga aca				648
Asp Phe Leu Gly Gly Arg Gly Gly Ser Arg Pro Gly Asp Arg Arg Thr				
161	166	171	176	
ggc ccc ccc atg ggc agc cgc ttc aga gat ggc cct ccc ctc cgt gga				696
Gly Pro Pro Met Gly Ser Arg Phe Arg Asp Gly Pro Pro Leu Arg Gly				
177	182	187	192	
tcc aac atg gat ttc aga gaa ccc aca gaa gag gaa aga gca cag aga				744
Ser Asn Met Asp Phe Arg Glu Pro Thr Glu Glu Glu Arg Ala Gln Arg				
193	198	203	208	
cca cga ctc cag ctt aaa cct cga aca gtc gcg acg ccc ctc aat caa				792
Pro Arg Leu Gln Leu Lys Pro Arg Thr Val Ala Thr Pro Leu Asn Gln				
209	214	219	224	
gta gcc aat ccc aac tct gct atc ttc ggg ggt gcc agg cct aga gag				840
Val Ala Asn Pro Asn Ser Ala Ile Phe Gly Gly Ala Arg Pro Arg Glu				
225	230	235	240	
gaa gtc gtt caa aag gag caa gaa tga gcctg cgggtgggag ggaatggggc				892
Glu Val Val Gln Lys Glu Gln Glu *				
241	246			
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cgactttttt	tttttttttt	aattcttcag	ctaaaacagc	ggaagaggtg	atttattata	180
tggttgttac	actcggccac	aaataaacac	agaaatagtc	cagaatgtca	caggtccagg	240

gcagaggacc aacatgggca ttttgtttat gagcaaggtg ggtctcagag gtgatcggcg 300

atcagagggc gatgaagttc tagatccatt gagacaagct ctagacagta gcatgcagtc 360

ccacaacttg taccagcatc cccagcgtct ggcattcc atg ttt ctg ctc ctg 413
Met Phe Leu Leu Leu
1

tgg cct cca cgg tgc aac aag cta gcg gtt tac ttg gac ctc tgc ctc 461
Trp Pro Pro Arg Cys Asn Lys Leu Ala Val Tyr Leu Asp Leu Cys Leu
6 11 16 21

atc ttt ctt ctt ttg cgc ttc agc ctg cgc att cgc ttc ttc ctc cac 509
Ile Phe Leu Leu Leu Arg Phe Ser Leu Arg Ile Arg Phe Phe Leu His
22 27 32 37

ttg gct ctc atg gcg cag agg ttt cca aaa aaa tgg cgc tac cca cgc 557
Leu Ala Leu Met Ala Gln Arg Phe Pro Lys Lys Trp Arg Tyr Pro Arg
38 43 48 53

gtc cgc cca cgc gtc cgc gga cgc gtg ggt ttt ttt gga aac ctc tgc 605
Val Arg Pro Arg Val Arg Gly Arg Val Gly Phe Phe Gly Asn Leu Cys
54 59 64 69

gcc atg aga gcc aag tgg agg aag aag cga atg cgc agg ctg aag cgc 653
Ala Met Arg Ala Lys Trp Arg Lys Lys Arg Met Arg Arg Leu Lys Arg
70 75 80 85

aaa aga aga aag atg agg cag agg tcc aag taa accgctag cttgttgac 704
Lys Arg Arg Lys Met Arg Gln Arg Ser Lys *
86 91 96

cgtggaggcc acaggagcag aaacatggaa tgccagacgc tggggatgct ggtacaagtt 764

gtgggactgc atgctactgt ctagagcttg tctcaatgga tctagaactt catcgccctc 824

tgatcgccga tcacctctga gacccacctt gtcataaac aaaatgccca tgttggtcct 884

ctgccctgga cctgtgacat tctggactat ttctgtgttt atttgtggcc gagtgttaaca 944

accatataat aaatcacctc ttccgctggt ttagctgaag aattaaaaaa aaaaaaaa 1002

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<212> DNA
<213> Homo sapiens

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atccactagt ccagtgtggt ggaattccct ccgccacatc ctccacctct cttggtccag	120
cgagcgttgc cgggccaggg tcaagcggag ggctccgacg gcgcggacgg agcgaagcgc	180
cgagcc atg gcg cac caa acg ggc atc cac gcc acg gaa gag ctg aag Met Ala His Gln Thr Gly Ile His Ala Thr Glu Glu Leu Lys	228
1 5 10	
gaa ttc ttt gcc aag gca cgg gct ggc tct gtg cgg ctc atc aag gtt Glu Phe Phe Ala Lys Ala Arg Ala Gly Ser Val Arg Leu Ile Lys Val	276
15 20 25 30	
gtg att gag gac gag cag ctc gtg ctg ggt gcc tcg cag gag cca gta Val Ile Glu Asp Glu Gln Leu Val Leu Gly Ala Ser Gln Glu Pro Val	324
31 36 41 46	
ggc cgc tgg gat cag gac tat gac agg gcc gtg ctg cca ctg ctg gac Gly Arg Trp Asp Gln Asp Tyr Asp Arg Ala Val Leu Pro Leu Leu Asp	372
47 52 57 62	
gcc cag cag ccc tgc tac ctg ctc tac cgc ctc gac tca cag aat gct Ala Gln Gln Pro Cys Tyr Leu Leu Tyr Arg Leu Asp Ser Gln Asn Ala	420
63 68 73 78	
cag ggc ttc gaa tgg ctc ttc ctc gcc tgg tcg cct gat aac tcc ccc Gln Gly Phe Glu Trp Leu Phe Leu Ala Trp Ser Pro Asp Asn Ser Pro	468
79 84 89 94	
gtg cgg ctg aag atg ctg tac gcg gcc acg cgg gcc aca gtg aaa aag Val Arg Leu Lys Met Leu Tyr Ala Ala Thr Arg Ala Thr Val Lys Lys	516
95 100 105 110	
gag ttt gga ggt ggc cac atc aag gat gag ctc ttc ggg act gtg aag Glu Phe Gly Gly Gly His Ile Lys Asp Glu Leu Phe Gly Thr Val Lys	564
111 116 121 126	
gat gac ctc tct ttt gct ggg tac cag aaa cac ctg tcg tcc tgt gcg Asp Asp Leu Ser Phe Ala Gly Tyr Gln Lys His Leu Ser Ser Cys Ala	612
127 132 137 142	
gca cct gcc ccg ctg acc tcg gct gag aga gag ctc cag cag atc cgc Ala Pro Ala Pro Leu Thr Ser Ala Glu Arg Glu Leu Gln Gln Ile Arg	660
143 148 153 158	
att aac gag gtg aag aca gag atc agt gtg gaa agc aag cac cag acc Ile Asn Glu Val Lys Thr Glu Ile Ser Val Glu Ser Lys His Gln Thr	708
159 164 169 174	
ctg cag ggc ctc gcc ttc ccc ctg cag cct gag gcc cag cgg gca ctc Leu Gln Gly Leu Ala Phe Pro Leu Gln Pro Glu Ala Gln Arg Ala Leu	756
175 180 185 190	
cag cag ctc aag cag aaa atg gtc aac tac atc cag atg aag ctg gac Gln Gln Leu Lys Gln Lys Met Val Asn Tyr Ile Gln Met Lys Leu Asp	804
191 196 201 206	

cta gag cgg gaa acc att gag ctg gtg cac aca gag ccc acg gat gtg	852
Leu Glu Arg Glu Thr Ile Glu Leu Val His Thr Glu Pro Thr Asp Val	
207 212 217 222	
gcc cag ctg ccc tcc cgg gtg ccc cga gat gct gcc cgc tac cac ttc	900
Ala Gln Leu Pro Ser Arg Val Pro Arg Asp Ala Ala Arg Tyr His Phe	
223 228 233 238	
ttc ctc tac aag cac acc cat gag ggc gac ccc ctt gag tct gta gtg	948
Phe Leu Tyr Lys His Thr His Glu Gly Asp Pro Leu Glu Ser Val Val	
239 244 249 254	
ttc atc tac tcc atg ccg ggg tac aag tgc agc atc aag gag cga atg	996
Phe Ile Tyr Ser Met Pro Gly Tyr Lys Cys Ser Ile Lys Glu Arg Met	
255 260 265 270	
ctc tac tcc agc tgc aag agc cgc ctc ctc gac tcc gtg gag cag gac	1044
Leu Tyr Ser Ser Cys Lys Ser Arg Leu Leu Asp Ser Val Glu Gln Asp	
271 276 281 286	
ttc cat ctg gag atc gcc aag aaa att gag att ggc gat ggg gca gag	1092
Phe His Leu Glu Ile Ala Lys Lys Ile Glu Ile Gly Asp Gly Ala Glu	
287 292 297 302	
ctg acg gca gag ttc ctc tac gac gag gtg cac ccc aag caa cac gcc	1140
Leu Thr Ala Glu Phe Leu Tyr Asp Glu Val His Pro Lys Gln His Ala	
303 308 313 318	
ttc aag cag gcc ttc gcc aag ccc aag ggc cca ggg ggc aag cgg ggc	1188
Phe Lys Gln Ala Phe Ala Lys Pro Lys Gly Pro Gly Gly Lys Arg Gly	
319 324 329 334	
cat aag cgc ctc atc cgc ggc ccg ggt gaa aat ggg gat gac agc tag	1236
His Lys Arg Leu Ile Arg Gly Pro Gly Glu Asn Gly Asp Asp Ser *	
335 340 345 350	
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aaaaaaaaaa aa	1668

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Met Val Leu Leu His Val Leu Phe Glu His
1 5

gcg gtc ggc tac gcg ctg ctg gcg ctg aag gaa gtg gag gag atc agt 159
Ala Val Gly Tyr Ala Leu Leu Ala Leu Lys Glu Val Glu Glu Ile Ser
11 16 21 26

ctg ctg cag ccg cag gtg gag gag tcc gtg ctc aac ctg ggc aaa ttc 207
Leu Leu Gln Pro Gln Val Glu Glu Ser Val Leu Asn Leu Gly Lys Phe
27 32 37 42

cac agc atc gtt cgt ctg gtg gcc ttt tgt ccc ttt gcc tca tcc cag 255
His Ser Ile Val Arg Leu Val Ala Phe Cys Pro Phe Ala Ser Ser Gln
43 48 53 58

gtt gcc ttg gaa aat gcc aac gcc gtg tct gaa ggg gtt gtt cat gag 303
Val Ala Leu Glu Asn Ala Asn Ala Val Ser Glu Gly Val Val His Glu
59 64 69 74

gac ctc cgc ctg ctc ttg gag acc cac ctg ccg tcc aaa aag aag aaa 351
Asp Leu Arg Leu Leu Leu Glu Thr His Leu Pro Ser Lys Lys Lys Lys
75 80 85 90

gta ctc ttg gga gtt ggg gat ccc aag att ggt gcc gca ata cag gag 399
Val Leu Leu Gly Val Gly Asp Pro Lys Ile Gly Ala Ala Ile Gln Glu
91 96 101 106

gag tta ggg tac aac tgc cag act gga gga gtc ata gct gag atc ctg 447
Glu Leu Gly Tyr Asn Cys Gln Thr Gly Gly Val Ile Ala Glu Ile Leu
107 112 117 122

cga gga gtt cgt ctg cac ttc cac aat ctg gtg aag ggt ctg acc gat 495
Arg Gly Val Arg Leu His Phe His Asn Leu Val Lys Gly Leu Thr Asp
123 128 133 138

ctg tca gct tgt aaa gca cag ctg ggg ctg gga cac agc tat tcc cgt 543
Leu Ser Ala Cys Lys Ala Gln Leu Gly Leu Gly His Ser Tyr Ser Arg
139 144 149 154

gcc aaa gtt aag ttt aat gtg aac cgg gtg gac aat atg atc atc cag 591
Ala Lys Val Lys Phe Asn Val Asn Arg Val Asp Asn Met Ile Ile Gln

155	160	165	170	
tcc att agc ctc ctg gac cag ctg gat aag gac atc aat acc ttc tct				639
Ser Ile Ser Leu Leu Asp Gln Leu Asp Lys Asp Ile Asn Thr Phe Ser				
171	176	181	186	
atg cgt gtc agg gag tgg tac ggg tat cac ttt ccg gag ctg gtg aag				687
Met Arg Val Arg Glu Trp Tyr Gly Tyr His Phe Pro Glu Leu Val Lys				
187	192	197	202	
atc atc aac gac aat gcc aca tac tgc cgt ctt gcc cag ttt att gga				735
Ile Ile Asn Asp Asn Ala Thr Tyr Cys Arg Leu Ala Gln Phe Ile Gly				
203	208	213	218	
aac cga agg gaa ctg aat gag gac aag ctg gag aag ctg gag gag ctg				783
Asn Arg Arg Glu Leu Asn Glu Asp Lys Leu Glu Lys Leu Glu Glu Leu				
219	224	229	234	
aca atg gat ggg gcc aag gct aag gct att ctg gat gcc tca cgg tcc				831
Thr Met Asp Gly Ala Lys Ala Lys Ala Ile Leu Asp Ala Ser Arg Ser				
235	240	245	250	
tcc atg ggc atg gac ata tct gcc att gac ttg ata aac atc gag agc				879
Ser Met Gly Met Asp Ile Ser Ala Ile Asp Leu Ile Asn Ile Glu Ser				
251	256	261	266	
ttc tcc agt cgt gtg gtg tct tta tct gaa tac cgc cag agc cta cac				927
Phe Ser Ser Arg Val Val Ser Leu Ser Glu Tyr Arg Gln Ser Leu His				
267	272	277	282	
act tac ctg cgc tcc aag atg agc caa gta gcc ccc agc ctg tca gcc				975
Thr Tyr Leu Arg Ser Lys Met Ser Gln Val Ala Pro Ser Leu Ser Ala				
283	288	293	298	
cta att ggg gaa gcg gta ggt gca cgt ctc atc gca cat gct ggc agc				1023
Leu Ile Gly Glu Ala Val Gly Ala Arg Leu Ile Ala His Ala Gly Ser				
299	304	309	314	
ctc acc aac ctg gcc aag tat cca gca tcc aca gtg cag atc ctt ggg				1071
Leu Thr Asn Leu Ala Lys Tyr Pro Ala Ser Thr Val Gln Ile Leu Gly				
315	320	325	330	
gct gaa aag gcc ctg ttc aga gcc ctg aag aca agg ggt aac act cca				1119
Ala Glu Lys Ala Leu Phe Arg Ala Leu Lys Thr Arg Gly Asn Thr Pro				
331	336	341	346	
aaa tat gga ctc att ttc cac tcc acc ttc att ggc cga gca gct gcc				1167
Lys Tyr Gly Leu Ile Phe His Ser Thr Phe Ile Gly Arg Ala Ala Ala				
347	352	357	362	
aag aac aaa ggc cgc atc tcc cga tac ctg gca aac aaa tgc agt att				1215
Lys Asn Lys Gly Arg Ile Ser Arg Tyr Leu Ala Asn Lys Cys Ser Ile				
363	368	373	378	
gcc tca cga atc gat tgc ttc tct gag gtg ccc acg agt gta ttc ggg				1263
Ala Ser Arg Ile Asp Cys Phe Ser Glu Val Thr Ser Val Phe Gly				
379	384	389	394	

gag aag ctt cga gaa caa gtt gaa gag cga ctg tcc ttc tat gag act	1311
Glu Lys Leu Arg Glu Gln Val Glu Glu Arg Leu Ser Phe Tyr Glu Thr	
395 400 405 410	
gga gag ata cca cga aag aat ctg gat gtc atg aag gaa gca atg gtt	1359
Gly Glu Ile Pro Arg Lys Asn Leu Asp Val Met Lys Glu Ala Met Val	
411 416 421 426	
cag gca gag gca gag gaa gcg gct gct gag att act agg aag ctg gag	1407
Gln Ala Glu Ala Glu Glu Ala Ala Ala Glu Ile Thr Arg Lys Leu Glu	
427 432 437 442	
aaa cag gag aag aaa cgc tta aag aag gaa aag aaa cgg ctg gct gca	1455
Lys Gln Glu Lys Lys Arg Leu Lys Lys Glu Lys Lys Arg Leu Ala Ala	
443 448 453 458	
ctt gcc ctc gcg tct tca gaa aac agc agt agt act cca gag gag tgt	1503
Leu Ala Leu Ala Ser Ser Glu Asn Ser Ser Ser Thr Pro Glu Glu Cys	
459 464 469 474	
gag gag atg agt gaa aaa ccc aaa aag aag aaa aag caa aag ccc cag	1551
Glu Glu Met Ser Glu Lys Pro Lys Lys Lys Lys Lys Gln Lys Pro Gln	
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Glu Val Pro Gln Glu Asn Gly Met Glu Asp Pro Ser Ile Ser Phe Ser	
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Lys Pro Lys Lys Lys Lys Ser Phe Ser Lys Glu Glu Leu Met Ser Ser	
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Asp Leu Glu Glu Thr Ala Gly Ser Thr Ser Ile Pro Lys Arg Lys Lys	
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Lys Lys Phe His Lys Ala Ser Gln Glu Asp *	
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                                   Met Pro Gln Ala Ser
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Glu His Arg Leu Gly Arg Thr Arg Glu Pro Pro Val Asn Ile Gln Pro
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cga gtg gga tcc aag cta cca ttt gcc ccc agg gcc cgc agc aag gag      449
Arg Val Gly Ser Lys Leu Pro Phe Ala Pro Arg Ala Arg Ser Lys Glu
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Arg Arg Asn Pro Ala Ser Gly Pro Asn Pro Met Leu Arg Pro Leu Pro
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ccc cgg cca ggt ctg cct gat gaa cgg ctc aag aaa ctg gag ctg gga      545
Pro Arg Pro Gly Leu Pro Asp Glu Arg Leu Lys Lys Leu Glu Leu Gly
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cgg gga cgg acc tca ggc cct cgt ccc aga ggc ccc ctt cga gca gat      593
Arg Gly Arg Thr Ser Gly Pro Arg Pro Arg Gly Pro Leu Arg Ala Asp
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cat ggg gtt ccc ctg cct ggc tca cca ccc cca aca gtg gct ttg cct      641
His Gly Val Pro Leu Pro Gly Ser Pro Pro Pro Thr Val Ala Leu Pro
  86                91                96                101

ctc cca tct cgg acc aac tta gcc cgt tcc aag tct gtg agc agt ggg      689
Leu Pro Ser Arg Thr Asn Leu Ala Arg Ser Lys Ser Val Ser Ser Gly
  102                107                112                117

gac ttg cgt cca atg ggg att gcc ttg gga ggg cac cgt ggc acc gga      737
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Thr Leu Arg Arg Ser	Thr Ser Leu Arg Arg	Leu Gly Gly Phe Pro	Gly				
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ccc cct acc ctg ttc	agc ata cgg aca gag	ccc cct gct tcc cat	ggc	881			
Pro Pro Thr Leu Phe	Ser Ile Arg Thr Glu	Pro Pro Ala Ser His	Gly				
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Ser Phe His Met Ile	Ser Ala Arg Ser Ser	Glu Pro Phe Tyr Ser	Asp				
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Asp Lys Met Ala His	His Thr Leu Leu Leu	Gly Ser Gly His Val	Gly				
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Val Asn Pro Thr Arg	Phe Arg Ala Val Phe	Gln Lys Tyr Val Pro	Ser				
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Pro Ile Leu Ala Asn	Gly Pro Val Pro Ser	Pro Pro Arg Arg Gly	Gly				
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342	347	352	357				

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Phe Val Gly Gln Leu Lys Ser Cys Leu Lys Cys Gln Ala Cys Gly Tyr	
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Arg Ser Thr Thr Phe Glu Val Phe Cys Asp Leu Ser Leu Pro Ile Pro	
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Lys Lys Gly Phe Ala Gly Gly Lys Val Ser Leu Arg Asp Cys Phe Asn	
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Leu Phe Thr Lys Glu Glu Glu Leu Glu Ser Glu Asn Ala Pro Val Cys	
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His Tyr Thr Ala Leu Cys Arg Cys Gln Thr Gly Trp His Val Tyr Asn	
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Asn Gln Glu Pro Gly Ile Leu Gln Gln Lys Asn Ala Val Gln Ile Ile	
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Thr Phe Val Leu Gly Asp Val Gln Lys Thr Asp Ala Phe Val Pro Val	
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Tyr Ser Asp Ser Thr Ile Gln Glu Ala Ser Pro Asn Phe Glu Lys Ala	
253 258 263 268	
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Tyr Thr Leu Pro Val Leu Pro Ser Glu Lys Asp Phe Asn Gly Ser Asp	
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Ala Ser Thr Gln Leu Asn Thr His Tyr Ala Phe Ser Lys Leu Thr Tyr	
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Lys Ser Ser Ser Gly His Glu Val Glu Asn Ser Thr Thr Asp Thr Gln	
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Val Ile Ser His Glu Lys Glu Asn Lys Leu Glu Ser Leu Val Leu Thr	
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80 85 90 95	
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Gln Glu Ile Thr Asp Asn Leu Thr Lys Lys Glu Ile Gln Ile Glu Lys	
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atc cat ttg gac aca tcc tcc ttc gtg gag gag ctg cct gga gag aag	1042
Ile His Leu Asp Thr Ser Ser Phe Val Glu Glu Leu Pro Gly Glu Lys	
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gac ctt gcc cac gtg gta gag atc tat gac ttt gaa cca gcg ctc aag	1090
Asp Leu Ala His Val Val Glu Ile Tyr Asp Phe Glu Pro Ala Leu Lys	
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Thr Glu Asp Leu Leu Ala Thr Phe Ser Glu Phe Gln Glu Lys Gly Phe	
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Arg Ile Gln Trp Val Asp Asp Thr His Ala Leu Gly Ile Phe Pro Cys	
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Leu Ala Ser Ala Ala Glu Ala Leu Thr Arg Glu Phe Ser Val Leu Lys	
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Ile Arg Pro Leu Thr Gln Gly Thr Lys Gln Ser Lys Leu Lys Ala Leu	
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Gln Arg Pro Lys Leu Leu Arg Leu Val Lys Glu Arg Pro Gln Thr Asn	
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gcg act gtg gcc cgg cgg ctg gtg gcc cgg gcc ctg gga ctc caa cac	1378
Ala Thr Val Ala Arg Arg Leu Val Ala Arg Ala Leu Gly Leu Gln His	
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Lys Lys Lys Glu Arg Pro Ala Val Arg Gly Ser Val Pro Pro *	
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Pro Leu Gln Phe Arg Asp Val Ala Ile Glu Phe Ser Leu Glu Glu Trp
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cat tgc ctg gac act gca cag cgg aat cta tat agg aat gtg atg tta      331
His Cys Leu Asp Thr Ala Gln Arg Asn Leu Tyr Arg Asn Val Met Leu
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gag aac tac agt aac ctg gtc ttc ctt ggt att gtt gtc tct aag cca      379
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gac ctg atc gcc cat ctg gag caa gga aaa aaa cct ttg act atg aag      427
Asp Leu Ile Ala His Leu Glu Gln Gly Lys Lys Pro Leu Thr Met Lys
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aga cat gag atg gta gcc aac ccc tca ggg cca gtt ata tgt tct cat      475
Arg His Glu Met Val Ala Asn Pro Ser Gly Pro Val Ile Cys Ser His
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ttt gcc caa gat ctt tgg cca gag cag aac ata aaa gat tct ttc caa      523
Phe Ala Gln Asp Leu Trp Pro Glu Gln Asn Ile Lys Asp Ser Phe Gln
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aaa gtg ata ctg aga aga tat gaa aaa cgt gga cat gga aat tta cag      571
Lys Val Ile Leu Arg Arg Tyr Glu Lys Arg Gly His Gly Asn Leu Gln
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tta ata aaa agg tgt gaa agt gta gat gag tgt aag gtg cac aca gga      619
Leu Ile Lys Arg Cys Glu Ser Val Asp Glu Cys Lys Val His Thr Gly
  115              120             125             130

ggt tat aat gga ctt aac cag tgt agt aca act acc cag agc aaa gta      667
Gly Tyr Asn Gly Leu Asn Gln Cys Ser Thr Thr Thr Gln Ser Lys Val
  131              136             141             146

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Phe Gln Cys Asp Lys Tyr Gly Lys Val Phe His Lys Phe Ser Asn Ser	
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aat aga cat aat ata aga cat act gaa aaa aaa cct ttc aaa tgc ata	763
Asn Arg His Asn Ile Arg His Thr Glu Lys Lys Pro Phe Lys Cys Ile	
163 168 173 178	
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aaa att cat act gga gag aaa ccc tac att tgt gaa gaa tgt ggc aaa	859
Lys Ile His Thr Gly Glu Lys Pro Tyr Ile Cys Glu Glu Cys Gly Lys	
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Ser Ser Thr Leu Ser Lys His Glu Ile Ile His Thr Gly Lys Lys Pro	
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Tyr Lys Cys Glu Glu Cys Gly Lys Ala Phe Asn Gln Ser Ser Thr Leu	
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Thr Lys His Lys Lys Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Glu	
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Glu Cys Gly Lys Ala Phe Asn Gln Ser Ser Thr Leu Thr Lys His Lys	
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Lys Ile His Thr Gly Glu Lys Pro Tyr Val Cys Glu Glu Cys Gly Lys	
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323 328 333 338	
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Gly Glu Lys Pro Tyr Lys Cys Asn Lys Cys Gly Lys Ala Phe Ile Ala	
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Ser Ser Thr Leu Ser Arg His Glu Phe Ile His Met Gly Lys Lys His	
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Thr	Arg	His	Lys	Arg	Val	His	Thr	Gly	Glu	Lys	Pro	Tyr	Lys	Cys	Glu	
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Glu	Cys	Gly	Lys	Ala	Phe	Lys	Tyr	Ser	Ser	Thr	Leu	Ser	Ser	His	Lys	
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Ala	Phe	Val	Ala	Ser	Ser	Thr	Leu	Ser	Lys	His	Glu	Ile	Ile	His	Thr	
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Ser	Ser	Ser	Leu	Thr	Lys	His	Lys	Lys	Ile	His	Thr	Gly	Glu	Lys	Pro	
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Tyr	Lys	Cys	Glu	Glu	Cys	Gly	Lys	Ala	Phe	Asn	Gln	Ser	Ser	Ser	Leu	
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Glu	Cys	Gly	Lys	Ala	Phe	Asn	Gln	Ser	Ser	Thr	Leu	Ile	Lys	His	Lys	
515					520					525					530	
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Lys	Ile	His	Thr	Arg	Glu	Lys	Pro	Tyr	Lys	Cys	Glu	Glu	Cys	Gly	Lys	
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gct	ttt	cac	cta	tcc	aca	cac	ctt	act	aca	cat	aag	ata	ctt	cat	act	1915
Ala	Phe	His	Leu	Ser	Thr	His	Leu	Thr	Thr	His	Lys	Ile	Leu	His	Thr	
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Gly	Glu	Lys	Pro	Tyr	Arg	Cys	Arg	Glu	Cys	Gly	Lys	Ala	Phe	Asn	His	
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Tyr	Glu	Cys	Asp	Lys	Cys	Gly	Lys	Ala	Phe	Ile	Ser	Pro	Ser	Ser	Leu	

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Ser Arg His Glu Ile Ile His Thr Gly Glu Lys Pro *				
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Met Phe Pro Arg Val Ser Thr Phe Leu Pro Leu	
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Lys Glu Asn Thr Lys Lys Asp Leu Leu Gly Ile Ile Lys Gly Met Lys				
92	97	102	107	
gtt gaa tta agc aca gta aat gta cga aca aca aag ccc ccc aaa aga				688
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Thr Glu Tyr Ala Pro Lys Lys Arg Ile Glu Pro Leu Ser Pro Glu Leu				
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Val Ala Ala Ala Ser Ala Val Ala Asp Ser Leu Pro Phe Asp Lys Gln				
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Pro Gly Gln Glu Lys Thr Asp Asp Leu Lys Lys Arg Lys Asn Ile Phe				
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aca aca aag ccc ccc aaa aga aga cca ctt aaa agt ttg gaa gct aca	688
Thr Thr Lys Pro Pro Lys Arg Arg Pro Leu Lys Ser Leu Glu Ala Thr	
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Ser Leu Pro Phe Asp Lys Gln Thr Thr Lys Ser Glu Leu Leu Ser Gln	
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Pro	Lys	Ile	Ser	Phe	Ser	Asn	Ile	Ile	Ser	Asp	Met	Lys	Val	Ala	Arg	
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Met	Met	Ala	Val	Thr	Lys	Glu	Ala	Pro	Glu	Thr	Asp	Thr	Ser	Pro	Ser	
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Pro	Leu	Gln	Asn	Gly	Phe	Glu	Glu	Leu	Ile	Gln	Trp	Thr	Lys	Glu	Gly	
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Lys	Leu	Trp	Glu	Phe	Pro	Ile	Asn	Asn	Glu	Ala	Gly	Phe	Asp	Asp	Asp	
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ggg	tca	gaa	ttt	cat	gaa	cat	ata	ttt	ctg	gag	aaa	cac	ctg	gag	agc	1312
Gly	Ser	Glu	Phe	His	Glu	His	Ile	Phe	Leu	Glu	Lys	His	Leu	Glu	Ser	
316					321					326					331	
ttt	cca	aaa	caa	gga	cca	att	cgc	cac	ttc	atg	gag	ctg	gtg	act	tgt	1360
Phe	Pro	Lys	Gln	Gly	Pro	Ile	Arg	His	Phe	Met	Glu	Leu	Val	Thr	Cys	
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Gly	Leu	Ser	Lys	Asn	Pro	Tyr	Leu	Ser	Val	Lys	Gln	Lys	Val	Glu	His	
348					353					358					363	
ata	gag	tgg	ttt	aga	aat	tat	ttt	aat	gaa	aaa	aag	gat	att	cta	aaa	1456
Ile	Glu	Trp	Phe	Arg	Asn	Tyr	Phe	Asn	Glu	Lys	Lys	Asp	Ile	Leu	Lys	
364					369					374					379	
gaa	agt	aac	ata	cag	ttc	aat	taa	gaccatggaa	attttttattt	caaacaatta						1510
Glu	Ser	Asn	Ile	Gln	Phe	Asn	*									
380					385											
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accacgtgcg gccggaaggg aagtaacgtc agcctgagaa ctgagtagct gtactgtgtg 180
gcgccttatt ctaggcactt gttgggcaga atg tca cac ctg ccg atg aaa 231
Met Ser His Leu Pro Met Lys
1 5
ctc ctg cgt aag aag atc gag aag cgg aac ctc aaa ttg cgg cag cgg 279
Leu Leu Arg Lys Lys Ile Glu Lys Arg Asn Leu Lys Leu Arg Gln Arg
8 13 18 23
aac cta aag ttt cag ggg gcc tca aat ctg acc cta tcg gaa act caa 327
Asn Leu Lys Phe Gln Gly Ala Ser Asn Leu Thr Leu Ser Glu Thr Gln
24 29 34 39
aat gga gat gta tct gaa gaa aca atg gga agt aga aag gtt aaa aaa 375
Asn Gly Asp Val Ser Glu Glu Thr Met Gly Ser Arg Lys Val Lys Lys
40 45 50 55
tca aaa caa aag ccc atg aat gtg ggc tta tca gaa act caa aat gga 423
Ser Lys Gln Lys Pro Met Asn Val Gly Leu Ser Glu Thr Gln Asn Gly
56 61 66 71
ggc atg tct caa gaa gca gtg gga aat ata aaa gtt aca aag tct ccc 471
Gly Met Ser Gln Glu Ala Val Gly Asn Ile Lys Val Thr Lys Ser Pro
72 77 82 87

cag	aaa	tcc	act	gta	tta	agc	aat	gga	gaa	gca	gca	atg	cag	tct	tcc	519
Gln	Lys	Ser	Thr	Val	Leu	Ser	Asn	Gly	Glu	Ala	Ala	Met	Gln	Ser	Ser	
88					93					98					103	
aat	tca	gaa	tca	aaa	aag	aaa	aag	aag	aaa	aag	aga	aaa	atg	gtg	aat	567
Asn	Ser	Glu	Ser	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Arg	Lys	Met	Val	Asn	
104					109					114					119	
gat	gct	gag	cct	gat	acg	aaa	aaa	gca	aaa	act	gaa	aac	aaa	ggg	aaa	615
Asp	Ala	Glu	Pro	Asp	Thr	Lys	Lys	Ala	Lys	Thr	Glu	Asn	Lys	Gly	Lys	
120					125					130					135	
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Ser	Glu	Glu	Glu	Ser	Ala	Glu	Thr	Thr	Lys	Glu	Thr	Glu	Asn	Asn	Val	
136					141					146					151	
gag	aag	cca	gat	aat	gat	gaa	gat	gag	agt	gag	gtg	ccc	agt	ctg	ccc	711
Glu	Lys	Pro	Asp	Asn	Asp	Glu	Asp	Glu	Ser	Glu	Val	Pro	Ser	Leu	Pro	
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Leu	Gly	Leu	Thr	Gly	Ala	Phe	Glu	Asp	Thr	Ser	Phe	Ala	Ser	Leu	Cys	
168					173					178					183	
aat	ctt	gtc	aat	gaa	aac	act	ctg	aag	gca	ata	aaa	gaa	atg	ggg	ttt	807
Asn	Leu	Val	Asn	Glu	Asn	Thr	Leu	Lys	Ala	Ile	Lys	Glu	Met	Gly	Phe	
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aca	aac	atg	act	gaa	att	cag	cat	aaa	agt	atc	aga	cca	ctt	ctg	gaa	855
Thr	Asn	Met	Thr	Glu	Ile	Gln	His	Lys	Ser	Ile	Arg	Pro	Leu	Leu	Glu	
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ccc	agg	aat	gga	aca	gga	gtc	ctt	att	ctc	tca	cct	act	aga	gaa	cta	999
Pro	Arg	Asn	Gly	Thr	Gly	Val	Leu	Ile	Leu	Ser	Pro	Thr	Arg	Glu	Leu	
248					253					258					263	
gcc	atg	caa	acc	ttt	ggg	gtt	ctt	aag	gag	ctg	atg	act	cac	cac	gtg	1047
Ala	Met	Gln	Thr	Phe	Gly	Val	Leu	Lys	Glu	Leu	Met	Thr	His	His	Val	
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cat	acc	tat	ggc	ttg	ata	atg	ggg	ggc	agt	aac	aga	tct	gct	gaa	gca	1095
His	Thr	Tyr	Gly	Leu	Ile	Met	Gly	Gly	Ser	Asn	Arg	Ser	Ala	Glu	Ala	
280					285					290					295	
cag	aaa	ctt	ggg	aat	ggg	atc	aac	atc	att	gtg	gcc	aca	cca	ggc	cgt	1143
Gln	Lys	Leu	Gly	Asn	Gly	Ile	Asn	Ile	Ile	Val	Ala	Thr	Pro	Gly	Arg	
296					301					306					311	

ctg ctg gac cat atg cag aat acc cca gga ttt atg tat aaa aac ctg	1191
Leu Leu Asp His Met Gln Asn Thr Pro Gly Phe Met Tyr Lys Asn Leu	
312 317 322 327	
cag tgt ctg gtt att gat gaa gct gat cgt atc ttg gat gtg ggg ttt	1239
Gln Cys Leu Val Ile Asp Glu Ala Asp Arg Ile Leu Asp Val Gly Phe	
328 333 338 343	
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Glu Glu Glu Leu Lys Gln Ile Ile Lys Leu Leu Pro Thr Arg Arg Gln	
344 349 354 359	
act atg ctc ttt tct gcc acc caa act cga aaa gtt gaa gac ctg gca	1335
Thr Met Leu Phe Ser Ala Thr Gln Thr Arg Lys Val Glu Asp Leu Ala	
360 365 370 375	
agg att tct ctg aaa aag gag cca ttg tat gtt ggc gtt gat gat gat	1383
Arg Ile Ser Leu Lys Lys Glu Pro Leu Tyr Val Gly Val Asp Asp Asp	
376 381 386 391	
aaa gcg aat gca aca gtg gat ggt ctt gaa cag gga tat gtt gtt tgt	1431
Lys Ala Asn Ala Thr Val Asp Gly Leu Glu Gln Gly Tyr Val Val Cys	
392 397 402 407	
cct tct gaa aag aga ttc ctt ctg ctc ttt aca ttc ctt aag aag aac	1479
Pro Ser Glu Lys Arg Phe Leu Leu Leu Phe Thr Phe Leu Lys Lys Asn	
408 413 418 423	
cga aag aag aag ctt atg gtc ttc ttt tca tct tgt atg tct gtg aaa	1527
Arg Lys Lys Lys Leu Met Val Phe Phe Ser Ser Cys Met Ser Val Lys	
424 429 434 439	
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Tyr His Tyr Glu Leu Leu Asn Tyr Ile Asp Leu Pro Val Leu Ala Ile	
440 445 450 455	
cat gga aag caa aag caa aat aag cgt aca acc aca ttc ttc cag ttc	1623
His Gly Lys Gln Lys Gln Asn Lys Arg Thr Thr Thr Phe Phe Gln Phe	
456 461 466 471	
tgc aat gca gat tcg gga aca cta ttg tgt acg gat gtg gca gcg aga	1671
Cys Asn Ala Asp Ser Gly Thr Leu Leu Cys Thr Asp Val Ala Ala Arg	
472 477 482 487	
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Gly Leu Asp Ile Pro Glu Val Asp Trp Ile Val Gln Tyr Asp Pro Pro	
488 493 498 503	
gat gac cct aag gaa tat att cat cgt gtg ggt aga aca gcc aga ggc	1767
Asp Asp Pro Lys Glu Tyr Ile His Arg Val Gly Arg Thr Ala Arg Gly	
504 509 514 519	
cta aat ggg aga ggg cat gcc ttg ctc att ttg cgc cca gaa gaa ttg	1815
Leu Asn Gly Arg Gly His Ala Leu Leu Ile Leu Arg Pro Glu Glu Leu	
520 525 530 535	
ggg ttt ctt cgt tac ttg aaa caa tcc aag gtt cca tta agt gaa ttt	1863

Gly Phe Leu Arg Tyr Leu Lys Gln Ser Lys Val Pro Leu Ser Glu Phe	
536 541 546 551	
gac ttt tcc tgg tct aaa att tct gac att cag tct cag ctt gag aaa	1911
Asp Phe Ser Trp Ser Lys Ile Ser Asp Ile Gln Ser Gln Leu Glu Lys	
552 557 562 567	
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Leu Ile Glu Lys Asn Tyr Phe Leu His Lys Ser Ala Gln Glu Ala Tyr	
568 573 578 583	
aag tca tac ata cga gcc tat gat tcc cat tct ctg aaa cag atc ttt	2007
Lys Ser Tyr Ile Arg Ala Tyr Asp Ser His Ser Leu Lys Gln Ile Phe	
584 589 594 599	
aat gtt aat aac cta aat ttg cct cag gtt gct ctg tca ttt ggt ttc	2055
Asn Val Asn Asn Leu Asn Leu Pro Gln Val Ala Leu Ser Phe Gly Phe	
600 605 610 615	
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Lys Val Pro Pro Phe Val Asp Leu Asn Val Asn Ser Asn Glu Gly Lys	
616 621 626 631	
cag aaa aag cga gga ggt ggt ggt gga ttt ggc tac cag aaa acc aag	2151
Gln Lys Lys Arg Gly Gly Gly Gly Phe Gly Tyr Gln Lys Thr Lys	
632 637 642 647	
aaa gtt gag aaa tcc aaa atc ttt aaa cac att agc aag aaa tca tct	2199
Lys Val Glu Lys Ser Lys Ile Phe Lys His Ile Ser Lys Lys Ser Ser	
648 653 658 663	
gac agc agg cag ttc tct cac tga acacatgcct tcctttcatc ttgaataact	2253
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 Met Ser His His Pro His
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 Ser Leu Arg Asn Ser Cys Leu Ile Arg Met Asp Leu Leu Tyr Trp Gln
 7 12 17 22
 ttc acc ata tat acc att aca ttt tgt ttc tcc cat ctc tca ggt aga 270
 Phe Thr Ile Tyr Thr Ile Thr Phe Cys Phe Ser His Leu Ser Gly Arg
 23 28 33 38
 ctt aca ctt tcg gcc cag cac atc agt cat cgc cct tgc ttg ctt tcc 318
 Leu Thr Leu Ser Ala Gln His Ile Ser His Arg Pro Cys Leu Leu Ser
 39 44 49 54
 tat tca ctc ctg ttc tgg aag gtg cac cac ctt ttc ttg gaa ggc ttc 366
 Tyr Ser Leu Leu Phe Trp Lys Val His His Leu Phe Leu Glu Gly Phe
 55 60 65 70

cct tgc tct ccc agg cta gat gag atg tcc ttc cat cag ttc cca cag	414
Pro Cys Ser Pro Arg Leu Asp Glu Met Ser Phe His Gln Phe Pro Gln	
71 76 81 86	
cac cct gtg cat gta tct gtt gtg cac tta cca ata gta tac aag gga	462
His Pro Val His Val Ser Val Val His Leu Pro Ile Val Tyr Lys Gly	
87 92 97 102	
tct atg acc caa gtc tct ccc cac tag cttgt aagctcctca cagacaggaa	514
Ser Met Thr Gln Val Ser Pro His *	
103 108	
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taccagggtg ttatctgtct attacagccc cttcacttct gggctcctgg ccctttgcga	1114
agtacttcag aaagcctaga gagaagagag ggccctcaaa tcccattcca gccctaaat	1174
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<400> 281

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Val Leu Ser Ser Leu Ala Val Tyr Ala Glu Asp Ser Glu Pro Glu Ser		
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gat ggc gag gct gga atc gag gcg gtg ggc agc gcg gct gag gag aaa		150
Asp Gly Glu Ala Gly Ile Glu Ala Val Gly Ser Ala Ala Glu Glu Lys		
23 28 33 38		
ggc gga ttg gta tct gat gcc tat ggg gag gat gac ttt tct cgt cta		198
Gly Gly Leu Val Ser Asp Ala Tyr Gly Glu Asp Asp Phe Ser Arg Leu		
39 44 49 54		
ggg ggt gat gaa gat ggt tat gaa gaa gaa gaa gat gag aac agt aga		246
Gly Gly Asp Glu Asp Gly Tyr Glu Glu Glu Glu Asp Glu Asn Ser Arg		
55 60 65 70		
cag tcg gaa gat gac gat tca gag act gaa aaa cct gag gct gat gac		294
Gln Ser Glu Asp Asp Asp Ser Glu Thr Glu Lys Pro Glu Ala Asp Asp		
71 76 81 86		
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Pro Lys Asp Asn Thr Glu Ala Glu Lys Arg Asp Pro Gln Glu Leu Val		
87 92 97 102		
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Ala Ser Phe Ser Glu Arg Val Arg Asn Met Ser Pro Asp Glu Ile Lys		
103 108 113 118		
atc ccg cca gaa ccc cct ggc aga tgt tca aat cac ttg caa gac aag		438
Ile Pro Pro Glu Pro Pro Gly Arg Cys Ser Asn His Leu Gln Asp Lys		
119 124 129 134		
atc cag aag ctt tat gaa cga aag ata aag gag gga atg gat atg aac		486
Ile Gln Lys Leu Tyr Glu Arg Lys Ile Lys Glu Gly Met Asp Met Asn		
135 140 145 150		
tac att atc caa agg aag aaa gaa ttt cgg aac cct agc atc tac gag		534
Tyr Ile Ile Gln Arg Lys Lys Glu Phe Arg Asn Pro Ser Ile Tyr Glu		
151 156 161 166		

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Lys Leu Ile Gln Phe Cys Ala Ile Asp Glu Leu Gly Thr Asn Tyr Pro	
167 172 177 182	
aag gat atg ttt gat ccc cat ggc tgg tct gag gac tcc tac tat gag	630
Lys Asp Met Phe Asp Pro His Gly Trp Ser Glu Asp Ser Tyr Tyr Glu	
183 188 193 198	
gca tta gcc aag gcc cag aaa att gag atg gac aaa ttg gaa aag gcc	678
Ala Leu Ala Lys Ala Gln Lys Ile Glu Met Asp Lys Leu Glu Lys Ala	
199 204 209 214	
aaa aag gag cga aca aaa att gag ttt gtg acg ggc acc aaa aaa ggc	726
Lys Lys Glu Arg Thr Lys Ile Glu Phe Val Thr Gly Thr Lys Lys Gly	
215 220 225 230	
acc acg acc aac gcc acg tcc acc acc act acc act gcc agc aca gct	774
Thr Thr Thr Asn Ala Thr Ser Thr Thr Thr Thr Thr Ala Ser Thr Ala	
231 236 241 246	
gtt gca gat gct cag aag aga aag agc aag tgg gat tcg gct atc cca	822
Val Ala Asp Ala Gln Lys Arg Lys Ser Lys Trp Asp Ser Ala Ile Pro	
247 252 257 262	
gtg aca acg ata gcc cag ccc acc atc ctc acc acc aca gcc acc ctg	870
Val Thr Thr Ile Ala Gln Pro Thr Ile Leu Thr Thr Thr Ala Thr Leu	
263 268 273 278	
cca gct gtt gtc acg gtc acc acc agc gcc agc ggc tcc aag acc acc	918
Pro Ala Val Val Thr Val Thr Thr Ser Ala Ser Gly Ser Lys Thr Thr	
279 284 289 294	
gtc atc tct gct gtg ggc acc att gtg aag aag gcc aag cag tga cct	966
Val Ile Ser Ala Val Gly Thr Ile Val Lys Lys Ala Lys Gln *	
295 300 305	
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gcattctcaga tgcaactggc tctcctgcat tctgtttgca ggcaaagtct tcagctcaca	1266
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<400> 282

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ggt ctg tct tct ctc gca gtt tac gcg gaa gat tca gag ccc gag tct		102
Val Leu Ser Ser Leu Ala Val Tyr Ala Glu Asp Ser Glu Pro Glu Ser		
7 12 17 22		
gat ggc gag gct gga atc gag gcg gtg ggc agc gcg gct gag gag aaa		150
Asp Gly Glu Ala Gly Ile Glu Ala Val Gly Ser Ala Ala Glu Glu Lys		
23 28 33 38		
ggc gga ttg gta tct gat gcc tat ggg gag gat gac ttt tct cgt cta		198
Gly Gly Leu Val Ser Asp Ala Tyr Gly Glu Asp Asp Phe Ser Arg Leu		
39 44 49 54		
ggg ggt gat gaa gat ggt tat gaa gaa gaa gaa gat gag aac agt aga		246
Gly Gly Asp Glu Asp Gly Tyr Glu Glu Glu Glu Asp Glu Asn Ser Arg		
55 60 65 70		
cag tct aga cgg tgt ttc act atg ttt ccc agt ctg gtt tca aac ttc		294
Gln Ser Arg Arg Cys Phe Thr Met Phe Pro Ser Leu Val Ser Asn Phe		
71 76 81 86		
tgg cct caa gca att ccc ctg cct cac cct ccc aaa gtg ctg gga tta		342
Trp Pro Gln Ala Ile Pro Leu Pro His Pro Pro Lys Val Leu Gly Leu		
87 92 97 102		
cag gaa gat gac gat tca gag act gaa aaa cct gag gct gat gac cca		390
Gln Glu Asp Asp Asp Ser Glu Thr Glu Lys Pro Glu Ala Asp Asp Pro		
103 108 113 118		
aag gat aat aca gaa gca gaa aag cga gac ccc cag gaa ctc gtg gcc		438
Lys Asp Asn Thr Glu Ala Glu Lys Arg Asp Pro Gln Glu Leu Val Ala		
119 124 129 134		
tcc ttt tct gaa aga gtt cgg aac atg tct cct gat gaa atc aag atc		486
Ser Phe Ser Glu Arg Val Arg Asn Met Ser Pro Asp Glu Ile Lys Ile		
135 140 145 150		
ccg cca gaa ccc cct ggc aga tgt tca aat cac ttg caa gac aag atc		534
Pro Pro Glu Pro Pro Gly Arg Cys Ser Asn His Leu Gln Asp Lys Ile		
151 156 161 166		
cag aag ctt tat gaa cga aag ata aag gag gga atg gat atg aac tac		582
Gln Lys Leu Tyr Glu Arg Lys Ile Lys Glu Gly Met Asp Met Asn Tyr		
167 172 177 182		

att atc caa agg aag aaa gaa ttt cgg aac cct agc atc tac gag aag	630
Ile Ile Gln Arg Lys Lys Glu Phe Arg Asn Pro Ser Ile Tyr Glu Lys	
183 188 193 198	
ctg atc cag ttc tgt gcc att gac gag ctt ggc acc aac tac cca aag	678
Leu Ile Gln Phe Cys Ala Ile Asp Glu Leu Gly Thr Asn Tyr Pro Lys	
199 204 209 214	
gat atg ttt gat ccc cat ggc tgg tct gag gac tcc tac tat gag gca	726
Asp Met Phe Asp Pro His Gly Trp Ser Glu Asp Ser Tyr Tyr Glu Ala	
215 220 225 230	
tta gcc aag gcc cag aaa att gag atg gac aaa ttg gaa aag gcc aaa	774
Leu Ala Lys Ala Gln Lys Ile Glu Met Asp Lys Leu Glu Lys Ala Lys	
231 236 241 246	
aag gag cga aca aaa gct tgt tgc agg gac gtg tct gca gcg cct ggg	822
Lys Glu Arg Thr Lys Ala Cys Cys Arg Asp Val Ser Ala Ala Pro Gly	
247 252 257 262	
gaa ccg agc tgt cct tcc cct gtg cgg gcg ggc acc gcc tcc tcc tgg	870
Glu Pro Ser Cys Pro Ser Pro Val Arg Ala Gly Thr Ala Ser Ser Trp	
263 268 273 278	
att gag ttt gtg acg ggc acc aaa aaa ggc acc acg acc aac gcc acg	918
Ile Glu Phe Val Thr Gly Thr Lys Lys Gly Thr Thr Thr Asn Ala Thr	
279 284 289 294	
tcc acc acc act acc act gcc agc aca gct gtt gca gat gct cag aag	966
Ser Thr Thr Thr Thr Thr Ala Ser Thr Ala Val Ala Asp Ala Gln Lys	
295 300 305 310	
aga aag agc aag tgg gat tcg gct atc cca gtg aca acg ata gcc cag	1014
Arg Lys Ser Lys Trp Asp Ser Ala Ile Pro Val Thr Thr Ile Ala Gln	
311 316 321 326	
ccc acc atc ctc acc acc aca gcc acc ctg cca gct gtt gtc acg gtc	1062
Pro Thr Ile Leu Thr Thr Thr Ala Thr Leu Pro Ala Val Val Thr Val	
327 332 337 342	
acc acc agc gcc agc ggc tcc aag acc acc gtc atc tct gct gtg ggc	1110
Thr Thr Ser Ala Ser Gly Ser Lys Thr Thr Val Ile Ser Ala Val Gly	
343 348 353 358	
acc att gtg aag aag gcc aag cag tga cctga ggggccaccc taggacttga	1162
Thr Ile Val Lys Lys Ala Lys Gln *	
359 364	
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tcctgcattc tgtttgcagg caaatgcttc agctcacatg tcccccaaga ctcaatagtc	1462

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<213> Homo sapiens

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Met Ala Glu Arg Gln Glu Glu Gln Arg Gly Ser Pro
1 5 10
ccc ttg agg gcg gaa ggc aag gcc gac gcg gag gtt aag ctc att ctg 159
Pro Leu Arg Ala Glu Gly Lys Ala Asp Ala Glu Val Lys Leu Ile Leu
13 18 23 28
tac cat tgg acg cat tcc ttc agc tct caa aag gtg cgc ttg gta att 207
Tyr His Trp Thr His Ser Phe Ser Ser Gln Lys Val Arg Leu Val Ile
29 34 39 44
gct gaa aag gca ttg aag tgc gag gaa cat gat gta agt ctg ccc ttg 255
Ala Glu Lys Ala Leu Lys Cys Glu Glu His Asp Val Ser Leu Pro Leu
45 50 55 60
agt gag cac aat gag cct tgg ttt atg cgt ttg aac tca act gga gaa 303
Ser Glu His Asn Glu Pro Trp Phe Met Arg Leu Asn Ser Thr Gly Glu
61 66 71 76
gtg cct gtc ctt atc cac ggg gaa aac ata att tgt gag gcc act cag 351
Val Pro Val Leu Ile His Gly Glu Asn Ile Ile Cys Glu Ala Thr Gln
77 82 87 92
atc att gat tat ctt gaa cag act ttc ctg gat gaa aga aca ccc agg 399
Ile Ile Asp Tyr Leu Glu Gln Thr Phe Leu Asp Glu Arg Thr Pro Arg
93 98 103 108
tta atg cct gat aaa gaa agc atg tat tac cca cgg gta caa cat tac 447
Leu Met Pro Asp Lys Glu Ser Met Tyr Tyr Pro Arg Val Gln His Tyr
109 114 119 124
cga gag ctg ctt gac tcc ttg cca atg gat gcc tat aca cat ggc tgc 495
Arg Glu Leu Leu Asp Ser Leu Pro Met Asp Ala Tyr Thr His Gly Cys
125 130 135 140
att tta cat cct gag tta act gtg gac tcc atg atc ccg gct tat gca 543

Ile	Leu	His	Pro	Glu	Leu	Thr	Val	Asp	Ser	Met	Ile	Pro	Ala	Tyr	Ala	
141					146					151					156	
act	aca	agg	att	cgt	agc	caa	att	gga	aac	aca	gag	tct	gag	ctg	aag	591
Thr	Thr	Arg	Ile	Arg	Ser	Gln	Ile	Gly	Asn	Thr	Glu	Ser	Glu	Leu	Lys	
157					162					167					172	
aaa	ctt	gct	gaa	gaa	aac	cca	gat	tta	caa	gaa	gca	tac	att	gca	aaa	639
Lys	Leu	Ala	Glu	Glu	Asn	Pro	Asp	Leu	Gln	Glu	Ala	Tyr	Ile	Ala	Lys	
173					178					183					188	
cag	aaa	cga	ctt	aaa	tca	aag	ctg	ctt	gat	cat	gac	aat	gtc	aag	tat	687
Gln	Lys	Arg	Leu	Lys	Ser	Lys	Leu	Leu	Asp	His	Asp	Asn	Val	Lys	Tyr	
189					194					199					204	
ttg	aag	aaa	att	ctt	gat	gag	ttg	gag	aaa	gtc	ttg	gat	cag	gtt	gaa	735
Leu	Lys	Lys	Ile	Leu	Asp	Glu	Leu	Glu	Lys	Val	Leu	Asp	Gln	Val	Glu	
205					210					215					220	
act	gaa	ttg	caa	aga	aga	aat	gaa	gaa	acc	cca	gaa	gag	ggc	cag	caa	783
Thr	Glu	Leu	Gln	Arg	Arg	Asn	Glu	Glu	Thr	Pro	Glu	Glu	Gly	Gln	Gln	
221					226					231					236	
cct	tgg	ctc	tgc	ggc	gaa	tcc	ttc	acc	ctg	gca	gac	gtc	tca	ctc	gct	831
Pro	Trp	Leu	Cys	Gly	Glu	Ser	Phe	Thr	Leu	Ala	Asp	Val	Ser	Leu	Ala	
237					242					247					252	
gtc	aca	ttg	cat	cga	ctg	aag	ttc	ctg	ggg	ttt	gca	agg	aga	aac	tgg	879
Val	Thr	Leu	His	Arg	Leu	Lys	Phe	Leu	Gly	Phe	Ala	Arg	Arg	Asn	Trp	
253					258					263					268	
gga	aac	gga	aag	cga	cca	aac	ttg	gaa	acc	tat	tac	gag	cgt	gtc	ttg	927
Gly	Asn	Gly	Lys	Arg	Pro	Asn	Leu	Glu	Thr	Tyr	Tyr	Glu	Arg	Val	Leu	
269					274					279					284	
aag	aga	aaa	aca	ttt	aac	aag	gtt	tta	gga	cat	gtc	aac	aat	ata	tta	975
Lys	Arg	Lys	Thr	Phe	Asn	Lys	Val	Leu	Gly	His	Val	Asn	Asn	Ile	Leu	
285					290					295					300	
atc	tct	gca	gtg	ctg	cca	aca	gca	ttc	cgg	gtg	gcc	aag	aaa	agg	gcc	1023
Ile	Ser	Ala	Val	Leu	Pro	Thr	Ala	Phe	Arg	Val	Ala	Lys	Lys	Arg	Ala	
301					306					311					316	
cca	aaa	gtt	ctt	ggc	acg	acc	ctt	gtg	gtt	ggc	ttg	ctt	gca	gga	gtg	1071
Pro	Lys	Val	Leu	Gly	Thr	Thr	Leu	Val	Val	Gly	Leu	Leu	Ala	Gly	Val	
317					322					327					332	
gga	tat	ttt	gct	ttt	atg	ctt	ttc	aga	aag	aga	ctt	ggc	agc	atg	ata	1119
Gly	Tyr	Phe	Ala	Phe	Met	Leu	Phe	Arg	Lys	Arg	Leu	Gly	Ser	Met	Ile	
333					338					343					348	
tta	gca	ctt	aga	ccc	aga	cca	aat	tat	ttc	tag						1152
Leu	Ala	Leu	Arg	Pro	Arg	Pro	Asn	Tyr	Phe	*						
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 Pro Arg Ala Ala Arg Ala Pro Ala Thr Leu Leu Leu Ala Leu Gly Ala
 3 8 13 18

gtg ctg tgg cct gcg gct ggc gcc tgg gag ctt acg att ttg cac acc 151
 Val Leu Trp Pro Ala Ala Gly Ala Trp Glu Leu Thr Ile Leu His Thr
 19 24 29 34

aac gac gtg cac agc cgg ctg gag cag acc agc gag gac tcc agc aag 199
 Asn Asp Val His Ser Arg Leu Glu Gln Thr Ser Glu Asp Ser Ser Lys
 35 40 45 50

tgc gtc aac gcc agc cgc tgc atg ggt ggc gtg gct cgg ctc ttc acc 247
 Cys Val Asn Ala Ser Arg Cys Met Gly Gly Val Ala Arg Leu Phe Thr
 51 56 61 66

aag gtt cag cag atc cgc cgc gcc gaa ccc aac gtg ctg ctg ctg gac 295
 Lys Val Gln Gln Ile Arg Arg Ala Glu Pro Asn Val Leu Leu Leu Asp
 67 72 77 82

gcc gcc gac cag tac cag gcc act atc tgg ttc acc gtg tac aag gcc 343
 Ala Gly Asp Gln Tyr Gln Gly Thr Ile Trp Phe Thr Val Tyr Lys Gly
 83 88 93 98

gcc gag gtg gcg cac ttc atg aac gcc ctg cgc tac gat gcc atg gca 391
 Ala Glu Val Ala His Phe Met Asn Ala Leu Arg Tyr Asp Ala Met Ala
 99 104 109 114

ctg gga aat cat gaa ttt gat aat ggt gtg gaa gga ctg atc gag cca 439
 Leu Gly Asn His Glu Phe Asp Asn Gly Val Glu Gly Leu Ile Glu Pro
 115 120 125 130

ctc ctc aaa gag gcc aaa ttt cca att ctg agt gca aac att aaa gca 487
 Leu Leu Lys Glu Ala Lys Phe Pro Ile Leu Ser Ala Asn Ile Lys Ala
 131 136 141 146

aag ggg cca cta gca tct caa ata tca gga ctt tat ttg cca tat aaa 535
 Lys Gly Pro Leu Ala Ser Gln Ile Ser Gly Leu Tyr Leu Pro Tyr Lys
 147 152 157 162

gtt ctt cct gtt ggt gat gaa gtt gtg gga atc gtt gga tac act tcc 583

Val	Leu	Pro	Val	Gly	Asp	Glu	Val	Val	Gly	Ile	Val	Gly	Tyr	Thr	Ser		
163					168					173					178		
aaa	gaa	acc	cct	ttt	ctc	tca	aat	cca	ggg	aca	aat	tta	gtg	ttt	gaa	631	
Lys	Glu	Thr	Pro	Phe	Leu	Ser	Asn	Pro	Gly	Thr	Asn	Leu	Val	Phe	Glu		
179					184					189					194		
gat	gaa	atc	act	gca	tta	caa	cct	gaa	gta	gat	aag	tta	aaa	act	cta	679	
Asp	Glu	Ile	Thr	Ala	Leu	Gln	Pro	Glu	Val	Asp	Lys	Leu	Lys	Thr	Leu		
195					200					205					210		
aat	gtg	aac	aaa	att	att	gca	ctg	gga	cat	tcg	ggg	ttt	gaa	atg	gat	727	
Asn	Val	Asn	Lys	Ile	Ile	Ala	Leu	Gly	His	Ser	Gly	Phe	Glu	Met	Asp		
211					216					221					226		
aaa	ctc	atc	gct	cag	aaa	gtg	agg	ggg	gtg	gac	gtc	gtg	gtg	gga	gga	775	
Lys	Leu	Ile	Ala	Gln	Lys	Val	Arg	Gly	Val	Asp	Val	Val	Val	Gly	Gly		
227					232					237					242		
cac	tcc	aac	aca	ttt	ctt	tac	aca	ggc	aat	cca	cct	tcc	aaa	gag	gtg	823	
His	Ser	Asn	Thr	Phe	Leu	Tyr	Thr	Gly	Asn	Pro	Pro	Ser	Lys	Glu	Val		
243					248					253					258		
cct	gct	ggg	aag	tac	cca	ttc	ata	gtc	act	tct	gat	gat	ggg	cgg	aag	871	
Pro	Ala	Gly	Lys	Tyr	Pro	Phe	Ile	Val	Thr	Ser	Asp	Asp	Gly	Arg	Lys		
259					264					269					274		
gtt	cct	gta	gtc	cag	gcc	tat	gct	ttt	ggc	aaa	tac	cta	ggc	tat	ctg	919	
Val	Pro	Val	Val	Gln	Ala	Tyr	Ala	Phe	Gly	Lys	Tyr	Leu	Gly	Tyr	Leu		
275					280					285					290		
aag	atc	gag	ttt	gat	gaa	aga	gga	aac	gtc	atc	tct	tcc	cat	gga	aat	967	
Lys	Ile	Glu	Phe	Asp	Glu	Arg	Gly	Asn	Val	Ile	Ser	Ser	His	Gly	Asn		
291					296					301					306		
ccc	att	ctt	cta	aac	agc	agc	att	cct	gaa	gat	cca	agc	ata	aaa	gca	1015	
Pro	Ile	Leu	Leu	Asn	Ser	Ser	Ile	Pro	Glu	Asp	Pro	Ser	Ile	Lys	Ala		
307					312					317					322		
gac	att	aac	aaa	tgg	agg	ata	aaa	ttg	gat	aat	tat	tct	acc	cag	gaa	1063	
Asp	Ile	Asn	Lys	Trp	Arg	Ile	Lys	Leu	Asp	Asn	Tyr	Ser	Thr	Gln	Glu		
323					328					333					338		
tta	ggg	aaa	aca	att	gtc	tat	ctg	gat	ggc	tcc	tct	caa	tca	tgc	cgc	1111	
Leu	Gly	Lys	Thr	Ile	Val	Tyr	Leu	Asp	Gly	Ser	Ser	Gln	Ser	Cys	Arg		
339					344					349					354		
ttt	aga	gaa	tgc	aac	atg	ggc	aac	ctg	att	tgt	gat	gca	atg	att	aac	1159	
Phe	Arg	Glu	Cys	Asn	Met	Gly	Asn	Leu	Ile	Cys	Asp	Ala	Met	Ile	Asn		
355					360					365					370		
aac	aac	ctg	aga	cac	acg	gat	gaa	atg	ttc	tgg	aac	cac	gta	tcc	atg	1207	
Asn	Asn	Leu	Arg	His	Thr	Asp	Glu	Met	Phe	Trp	Asn	His	Val	Ser	Met		
371					376					381					386		
tgc	att	tta	aat	gga	ggg	ggg	atc	cgg	tcg	ccc	att	gat	gaa	cgc	aac	1255	
Cys	Ile	Leu	Asn	Gly	Gly	Gly	Ile	Arg	Ser	Pro	Ile	Asp	Glu	Arg	Asn		

387	392	397	402	
aat ggc aca att acc tgg gag aac ctg gct gct gta ttg ccc ttt gga				1303
Asn Gly Thr Ile Thr Trp Glu Asn Leu Ala Val Leu Pro Phe Gly				
403	408	413	418	
ggc aca ttt gac cta gtc cag tta aaa ggt tcc acc ctg aag aag gcc				1351
Gly Thr Phe Asp Leu Val Gln Leu Lys Gly Ser Thr Leu Lys Lys Ala				
419	424	429	434	
ttt gag cat agc gtg cac cgc tac ggc cag tcc act gga gag ttc ctg				1399
Phe Glu His Ser Val His Arg Tyr Gly Gln Ser Thr Gly Glu Phe Leu				
435	440	445	450	
cag gtg ggc gga atc cat gtg gtg tat gat ctt tcc cga aaa cct gga				1447
Gln Val Gly Gly Ile His Val Val Tyr Asp Leu Ser Arg Lys Pro Gly				
451	456	461	466	
gac aga gta gtc aaa tta gat gtt ctt tgc acc aag tgt cga gtg ccc				1495
Asp Arg Val Val Lys Leu Asp Val Leu Cys Thr Lys Cys Arg Val Pro				
467	472	477	482	
agt tat gac cct ctc aaa atg gac gag gta tat aag gtg atc ctc cca				1543
Ser Tyr Asp Pro Leu Lys Met Asp Glu Val Tyr Lys Val Ile Leu Pro				
483	488	493	498	
aac ttc ctg gcc aat ggt gga gat ggg ttc cag atg ata aaa gat gaa				1591
Asn Phe Leu Ala Asn Gly Gly Asp Gly Phe Gln Met Ile Lys Asp Glu				
499	504	509	514	
tta tta aga cat gac tct ggt gac caa gat atc aac gtg gtt tct aca				1639
Leu Leu Arg His Asp Ser Gly Asp Gln Asp Ile Asn Val Val Ser Thr				
515	520	525	530	
tat atc tcc aaa atg aaa gta att tat cca gca gtt gaa ggt cgg atc				1687
Tyr Ile Ser Lys Met Lys Val Ile Tyr Pro Ala Val Glu Gly Arg Ile				
531	536	541	546	
aag ttt tcc aca gga agt cac tgc cat gga agc ttt tct tta ata ttt				1735
Lys Phe Ser Thr Gly Ser His Cys His Gly Ser Phe Ser Leu Ile Phe				
547	552	557	562	
ctt tca ctt tgg gca gtg atc ttt gtt tta tac caa tag ccaaaaattc				1784
Leu Ser Leu Trp Ala Val Ile Phe Val Leu Tyr Gln *				
563	568	573		
tccttgccctt taatgtgtga aactgcattt tttcaagtga gattcaaatac tgccttttag				1844
gacctggcctt tgtgacagca aaaaccatct ttacaggctc ctagaagctg aagggttagag				1904
cattataaaaa tgaagagaca gacatgatta ctcagggtca gcaacctagt gagttagaaa				1964
aaaaattaac atagggccct ataaggagaa agccaactat gttaagttaa cgtgtccaaa				2024
ttttaatgaa attttactaa caattttaaa ccatatTTTT cttcttcata tccattttcta				2084
atccatcaaa cagcttatgt ttacataaaaa ttttatcatt cacaaggaag ttttaagcac				2144

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agatccaaga cctagaccta ggtcttttga actcaagtcc agcattctca actatatcaa	2324
gttactgttc agaatactta atatctcttc tcttcataat tatcaatagc cccaagctca	2384
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tatagaaaag caagagctaa agagcattta cacatgttaa acagatactt gttaagcata	2684
gtgcctgaca cacggcatta gctgttattt tatgagattc catcagctct gcctctgtcc	2744
tctttcttct aacatgaagg tatcatgaga agagaacctt ctaacataag ctgtaattct	2804
aaacctgcac ttgtccctct ccagcaagag gctagcactg aattcattct actcatacta	2864
cacaccaggt tatggaatgt ccagagttct cgaagaaaat aatgacttt aggaagaggt	2924
atacattttt taagtcgctc tgctccaaa tctgaacagt cactgtaaat cattcttaag	2984
cccagatatg agaacttctg ctggaaagtg ggaccctctg agtgggtggt cagaaaatac	3044
ccatgctgat gaaatgacct atgcccaaag aacaaatact taacgtggga gtggaaccca	3104
catgagcctg ctcagctctg cataagtaat tcaagaaatg ggaggcttca ccttaaaaac	3164
agtgtgcaaa tggcagctag aggttttgat aggaagtatg tttgtttctt agtgtttaca	3224
aatattaagt actcttgata caaaatatac ttttaaactt cataaccttt ttataaaagt	3284
tgttgagca aaataatagc ctcggttcta tgcatatatg gattagctat aaaaaatgtc	3344
aataagattg tacaaggaaa attagagaaa gtcacattta ggggtttattt tttacacttg	3404
gccagtaaaa tagggtaaact cctattagaa ttttttaaag aacttttttt aagtttccta	3464
aatctgtgtg tgtattgtga agtgggtataa gaaatgactt tgaaccactt tgcaattgta	3524
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<210> 285
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 <213> Homo sapiens

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tct gga aag aca ggt gaa cag gaa ggt tcc ctt tca acg ctc ttc agt 276
Ser Gly Lys Thr Gly Glu Gln Glu Gly Ser Leu Ser Thr Leu Phe Ser
14 19 24 29

aga ctt tat gca ttt gtg atg tct gtt att tca gat gac aga ttt gaa 324
Arg Leu Tyr Ala Phe Val Met Ser Val Ile Ser Asp Asp Arg Phe Glu
30 35 40 45

gat ctg gaa gag gca aat cca ttc tct ttt aga gag ttt ctg aag acc 372
Asp Leu Glu Glu Ala Asn Pro Phe Ser Phe Arg Glu Phe Leu Lys Thr
46 51 56 61

aag aac ctc ggc ctc tcg aaa gag gat ccg gcc agc aga att tat gca 420
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62 67 72 77

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Lys Glu Ala Ser Arg His Ser Leu Gly Leu Asp His Asn Ser Pro Pro
78 83 88 93

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Ser Gln Thr Gly Gly Tyr Gly Leu Glu Tyr Gln Gln Pro Phe Phe Glu
94 99 104 109

gat ccg aca ggg gct ggt gac ctc ctg gat gag gag gag gat gag gac 564
Asp Pro Thr Gly Ala Gly Asp Leu Leu Asp Glu Glu Glu Asp Glu Asp
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acc gga tgg agt ggg gcc tac ctg ccg tcc gcc atc gag cag act cac 612
Thr Gly Trp Ser Gly Ala Tyr Leu Pro Ser Ala Ile Glu Gln Thr His
126 131 136 141

ccc gag agg gtc cct gcc ggc acg tcg ccc tgc agc aca tac ctt tcc 660
Pro Glu Arg Val Pro Ala Gly Thr Ser Pro Cys Ser Thr Tyr Leu Ser
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Ala Gln Thr Glu Met Val Arg Thr Leu Glu	Arg Lys Leu Glu Ala Lys			
238	243 248 253			
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Gln Val Glu Gln Asn Leu Glu Leu Met Thr	Lys Arg Ala Val Lys Ala			
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Gln Val Ser Asn Phe Gln Arg Glu Asn Glu	Ala Leu Arg Cys Gly Gln			
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Val Ser Gly Ala Glu Thr Leu Asn Leu Val	Ala Glu Ile Leu Lys Ser			
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ata gac aga att tct gaa gtt aaa gac gag	gag gaa gac tct tga gga	1332		
Ile Asp Arg Ile Ser Glu Val Lys Asp Glu	Glu Glu Glu Asp Ser *			
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tcgccatcct actctcctc cctcgtcatc ctcccccttc gtctctctcg ccttctctct 180
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Met Ala Ala Pro Arg Pro
1
ccg cct gcc agg ctg tcg ggc gtc atg gtg ccg gcg ccc atc caa gac 280
Pro Pro Ala Arg Leu Ser Gly Val Met Val Pro Ala Pro Ile Gln Asp
7 12 17 22
ctg gag gcc ctg cgc gcg ctc acg gcg ctc ttc aaa gag cag cgg aac 328
Leu Glu Ala Leu Arg Ala Leu Thr Ala Leu Phe Lys Glu Gln Arg Asn
23 28 33 38
cga gaa aca gca ccc agg act atc ttc caa aga gtt ctg gat atc cta 376
Arg Glu Thr Ala Pro Arg Thr Ile Phe Gln Arg Val Leu Asp Ile Leu
39 44 49 54

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Lys Lys Ser Ser His Ala Val Glu Leu Ala Cys Arg Asp Pro Ser Gln	
55 60 65 70	
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Val Glu Asn Leu Ala Ser Ser Leu Gln Leu Ile Thr Glu Cys Phe Arg	
71 76 81 86	
tgt ctt cgc aat gct tgc ata gag tgt tct gtg aac cag aat tca atc	520
Cys Leu Arg Asn Ala Cys Ile Glu Cys Ser Val Asn Gln Asn Ser Ile	
87 92 97 102	
agg aac ttg gat acg att ggt gtt gct gtt gat ttg att ctt ctg ttt	568
Arg Asn Leu Asp Thr Ile Gly Val Ala Val Asp Leu Ile Leu Leu Phe	
103 108 113 118	
cgt gaa ctg cga gtg gaa cag gaa tct ctg ttg aca gct ttt cgc tgt	616
Arg Glu Leu Arg Val Glu Gln Glu Ser Leu Leu Thr Ala Phe Arg Cys	
119 124 129 134	
ggc ctg cag ttt tta ggc aac att gcc tca cgg aat gaa gat tcc cag	664
Gly Leu Gln Phe Leu Gly Asn Ile Ala Ser Arg Asn Glu Asp Ser Gln	
135 140 145 150	
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Ser Ile Val Trp Val His Ala Phe Pro Glu Leu Phe Leu Ser Cys Leu	
151 156 161 166	
aat cat ccg gac aaa aaa att gtt gcc tac tct tca atg att ttg ttt	760
Asn His Pro Asp Lys Lys Ile Val Ala Tyr Ser Ser Met Ile Leu Phe	
167 172 177 182	
aca tcc ctt aat cat gaa aga atg aaa gaa ctg gag gag aac ctc aat	808
Thr Ser Leu Asn His Glu Arg Met Lys Glu Leu Glu Glu Asn Leu Asn	
183 188 193 198	
att gca att gat gtc ata gat gct tac caa aaa cat cct gaa tca gaa	856
Ile Ala Ile Asp Val Ile Asp Ala Tyr Gln Lys His Pro Glu Ser Glu	
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Trp Pro Phe Leu Ile Ile Thr Asp Leu Phe Leu Lys Ser Pro Glu Leu	
215 220 225 230	
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Val Gln Ala Met Phe Pro Lys Leu Asn Asn Gln Glu Arg Val Thr Leu	
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Leu Asp Leu Met Ile Ala Lys Ile Thr Ser Asp Glu Pro Leu Thr Lys	
247 252 257 262	
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Asp Asp Ile Pro Val Phe Leu Arg His Ala Glu Leu Ile Ala Ser Thr	
263 268 273 278	

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Phe Val Asp Gln Cys Lys Thr Val Leu Lys Leu Ala Ser Glu Glu Pro	
279 284 289 294	
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Pro Asp Asp Glu Glu Ala Leu Ala Thr Ile Arg Leu Leu Asp Val Leu	
295 300 305 310	
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Cys Glu Met Thr Val Asn Thr Glu Leu Leu Gly Tyr Leu Gln Val Phe	
311 316 321 326	
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Pro Gly Leu Leu Glu Arg Val Ile Asp Leu Leu Arg Val Ile His Val	
327 332 337 342	
gct gga aaa gaa acc aca aac atc ttc agt aat tgt ggt tgc gtg aga	1288
Ala Gly Lys Glu Thr Thr Asn Ile Phe Ser Asn Cys Gly Cys Val Arg	
343 348 353 358	
gca gaa ggt gac atc tcc aat gtg gcc aat ggg ttt aag tct cat ctc	1336
Ala Glu Gly Asp Ile Ser Asn Val Ala Asn Gly Phe Lys Ser His Leu	
359 364 369 374	
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Ile Arg Leu Ile Gly Asn Leu Cys Tyr Lys Asn Lys Asp Asn Gln Asp	
375 380 385 390	
aag gta aat gag ctg gat ggt atc ccg ttg atc ctg gac aac tgc aac	1432
Lys Val Asn Glu Leu Asp Gly Ile Pro Leu Ile Leu Asp Asn Cys Asn	
391 396 401 406	
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Ile Ser Asp Ser Asn Pro Phe Leu Thr Gln Trp Val Ile Tyr Ala Ile	
407 412 417 422	
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Arg Asn Leu Thr Glu Asp Asn Ser Gln Asn Gln Asp Leu Ile Ala Lys	
423 428 433 438	
atg gag gaa cag ggg ctg gca gat gca tcc cta ctt aaa aaa gtg ggt	1576
Met Glu Glu Gln Gly Leu Ala Asp Ala Ser Leu Leu Lys Lys Val Gly	
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Phe Glu Val Glu Lys Lys Gly Glu Lys Leu Ile Leu Lys Ser Thr Arg	
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Asp Thr Pro Lys Pro *	
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agtgaaagta actgagtgtt ctcttgtttc tttgcattaa tgtaactgtg tggtttgcc	1858

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Ser Asp Leu Glu Thr Thr Ser His Met Pro Arg Ser Gly Ala Pro
9 14 19 24

aaa gag cgc cct gcg gag cct ctc acc cct ccc cca tcc tat ggc cac 149
Lys Glu Arg Pro Ala Glu Pro Leu Thr Pro Pro Pro Ser Tyr Gly His
25 30 35 40

cag cca cag aca ggg tct ggg gag tct tca gga gcc tcg ggg gac aag 197
Gln Pro Gln Thr Gly Ser Gly Glu Ser Ser Gly Ala Ser Gly Asp Lys
41 46 51 56

gac cac ctg tac agc acg gta tgc aag cct cgg tcc cca aag cct gca 245
Asp His Leu Tyr Ser Thr Val Cys Lys Pro Arg Ser Pro Lys Pro Ala
57 62 67 72

gcc ccg gcg gcc cct cca ttc tcc tct tcc agc ggt gtc ttg ggt acc 293
Ala Pro Ala Ala Pro Pro Phe Ser Ser Ser Ser Gly Val Leu Gly Thr
73 78 83 88

ggg ctc tgt gag cta gat cgg ttg ctt cag gaa ctt aat gcc act cag 341
Gly Leu Cys Glu Leu Asp Arg Leu Leu Gln Glu Leu Asn Ala Thr Gln
89 94 99 104

ttc aac atc aca gat gaa atc atg tct cag ttc cca tct agc aag gtg 389
Phe Asn Ile Thr Asp Glu Ile Met Ser Gln Phe Pro Ser Ser Lys Val
105 110 115 120

gct tca gga gag cag aag gag gac cag tct gaa gat aag aaa aga ccc 437
Ala Ser Gly Glu Gln Lys Glu Asp Gln Ser Glu Asp Lys Lys Arg Pro
121 126 131 136

agc ctc cct tcc agc ccg tct cct ggc ctc cca aag gct tct gcc acc 485
Ser Leu Pro Ser Ser Pro Ser Pro Gly Leu Pro Lys Ala Ser Ala Thr
137 142 147 152

tca gcc act ctg gag ctg gat aga ctg atg gcc tca ctc tct gac ttc	533
Ser Ala Thr Leu Glu Leu Asp Arg Leu Met Ala Ser Leu Ser Asp Phe	
153 158 163 168	
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Arg Val Gln Asn His Leu Pro Ala Ser Gly Pro Thr Gln Pro Pro Val	
169 174 179 184	
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Val Ser Ser Thr Asn Glu Gly Ser Pro Ser Pro Pro Glu Pro Thr Gly	
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Lys Gly Ser Leu Asp Thr Met Leu Gly Leu Leu Gln Ser Asp Leu Ser	
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217 222 227 232	
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Lys Pro Ile Ala Gly Gln Val Val Thr Ala Leu Gly Arg Ala Trp His	
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Pro Glu His Phe Val Cys Gly Gly Cys Ser Thr Ala Leu Gly Gly Ser	
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Ser Phe Phe Glu Lys Asp Gly Ala Pro Phe Cys Pro Glu Cys Tyr Phe	
265 270 275 280	
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Glu Arg Phe Ser Pro Arg Cys Gly Phe Cys Asn Gln Pro Ile Arg His	
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Lys Met Val Thr Ala Leu Gly Thr His Trp His Pro Glu His Phe Cys	
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Cys Val Ser Cys Gly Glu Pro Phe Gly Asp Glu Gly Phe His Glu Arg	
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Glu Gly Arg Pro Tyr Cys Arg Arg Asp Phe Leu Gln Leu Phe Ala Pro	
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Arg Cys Gln Gly Cys Gln Gly Pro Ile Leu Asp Asn Tyr Ile Ser Ala	
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Leu Ser Ala Leu Trp His Pro Asp Cys Phe Val Cys Arg Glu Cys Phe	
361 366 371 376	

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Ala Pro Phe Ser Gly Gly Ser Phe Phe Glu His Glu Gly Arg Pro Leu	
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tgc gag aac cac ttc cac gca cga cgc ggc tcg ctg tgc gcc acg tgt	1253
Cys Glu Asn His Phe His Ala Arg Arg Gly Ser Leu Cys Ala Thr Cys	
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Gly Leu Pro Val Thr Gly Arg Cys Val Ser Ala Leu Gly Arg Arg Phe	
409 414 419 424	
cac ccg gac cac ttc aca tgc acc ttc tgc ctg cgc ccg ctc acc aag	1349
His Pro Asp His Phe Thr Cys Thr Phe Cys Leu Arg Pro Leu Thr Lys	
425 430 435 440	
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Gly Ser Phe Gln Glu Arg Ala Gly Lys Pro Tyr Cys Gln Pro Cys Phe	
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atattg atg gag atg cct aga aaa cct cgc ctg aca ctc ttt gtc caa	228
Met Glu Met Pro Arg Lys Pro Arg Leu Thr Leu Phe Val Gln	

1

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10

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Phe Tyr Tyr Leu Leu Glu Ala Ala Glu Gly His Ala Lys Glu Gly Gln	
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Gly Ile Lys Thr Asp Ile Pro Arg Tyr Ile Ile Ser Gln Leu Gly Leu	
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Asn Lys Asp Pro Leu Glu Glu Met Ala His Leu Gly Asn Tyr Asp Ser	
63 68 73 78	
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Gly Thr Ala Glu Thr Pro Glu Thr Asp Glu Ser Val Ser Ser Ser Asn	
79 84 89 94	
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Ala Ser Leu Lys Leu Arg Arg Lys Pro Arg Glu Ser Asp Phe Glu Thr	
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Ile Lys Leu Ile Ser Asn Gly Ala Tyr Gly Ala Val Tyr Phe Val Arg	
111 116 121 126	
cat aaa gaa tcc cgg cag agg ttt gcc atg aag aag att aat aaa cag	612
His Lys Glu Ser Arg Gln Arg Phe Ala Met Lys Lys Ile Asn Lys Gln	
127 132 137 142	
aac ctc atc ctt cga aac cag atc cag cag gcc ttt gtg gag cgg gat	660
Asn Leu Ile Leu Arg Asn Gln Ile Gln Gln Ala Phe Val Glu Arg Asp	
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Ile Leu Thr Phe Ala Glu Asn Pro Phe Val Val Ser Met Tyr Cys Ser	
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Phe Glu Thr Arg Arg His Leu Cys Met Val Met Glu Tyr Val Glu Gly	
175 180 185 190	
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Gly Asp Cys Ala Thr Leu Met Lys Asn Met Gly Pro Leu Pro Val Asp	
191 196 201 206	
atg gcc aga atg tac ttt gct gag acg gtc ttg gcc ttg gaa tat tta	852
Met Ala Arg Met Tyr Phe Ala Glu Thr Val Leu Ala Leu Glu Tyr Leu	
207 212 217 222	
cat aat tat gga att gta cac agg gat ttg aaa cca gac aac ttg ttg	900
His Asn Tyr Gly Ile Val His Arg Asp Leu Lys Pro Asp Asn Leu Leu	
223 228 233 238	

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239 244 249 254	
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Val Gly Leu Met Ser Met Thr Thr Asn Leu Tyr Glu Gly His Ile Glu	
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Tyr Ile Ala Pro Glu Val Ile Leu Arg Gln Gly Tyr Gly Lys Pro Val	
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303 308 313 318	
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Ser Asp Glu Ile Asn Trp Pro Glu Lys Asp Glu Ala Pro Pro Pro Asp	
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351 356 361 366	
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Gln Leu Glu Ser Glu Asp Asp Thr Ser Tyr Phe Asp Thr Arg Ser Glu	
399 404 409 414	
aag tat cat cat atg gaa acg gag gaa gaa gat gac aca aat gat gaa	1476
Lys Tyr His His Met Glu Thr Glu Glu Glu Asp Asp Thr Asn Asp Glu	
415 420 425 430	
gac ttt aat gtg gaa ata agg cag ttt tct tca tgt tca cac agg ttt	1524
Asp Phe Asn Val Glu Ile Arg Gln Phe Ser Ser Cys Ser His Arg Phe	
431 436 441 446	
tca aaa gtt ttc agc agt ata gat cga atc act cag aat tca gca gaa	1572
Ser Lys Val Phe Ser Ser Ile Asp Arg Ile Thr Gln Asn Ser Ala Glu	
447 452 457 462	

gag aag gaa gac tct gtg gac aaa acc aaa agc acc acc ttg cca tcc	1620
Glu Lys Glu Asp Ser Val Asp Lys Thr Lys Ser Thr Thr Leu Pro Ser	
463 468 473 478	
aca gaa aca ctg agc tgg agt tca gaa tat tct gaa atg caa cag cta	1668
Thr Glu Thr Leu Ser Trp Ser Ser Glu Tyr Ser Glu Met Gln Gln Leu	
479 484 489 494	
tca aca tcc aac tct tca gat act gaa agc aac aga cat aaa ctc agt	1716
Ser Thr Ser Asn Ser Ser Asp Thr Glu Ser Asn Arg His Lys Leu Ser	
495 500 505 510	
tct ggc cta ctt ccc aaa ctg gct att tca aca gag gga gag caa gat	1764
Ser Gly Leu Leu Pro Lys Leu Ala Ile Ser Thr Glu Gly Glu Gln Asp	
511 516 521 526	
gaa gct gcc tcc tgc cct gga gac ccc cat gag gag cca gga aag cca	1812
Glu Ala Ala Ser Cys Pro Gly Asp Pro His Glu Glu Pro Gly Lys Pro	
527 532 537 542	
gcc ctt cct cct gaa gag tgt gcc cag gag gag cct gag gtc acc acc	1860
Ala Leu Pro Pro Glu Glu Cys Ala Gln Glu Glu Pro Glu Val Thr Thr	
543 548 553 558	
cca gcc agc acc atc agc agc tcc acc ctg tca gtt ggc agt ttt tca	1908
Pro Ala Ser Thr Ile Ser Ser Ser Thr Leu Ser Val Gly Ser Phe Ser	
559 564 569 574	
gag cac ttg gat cag ata aat gga cga agc gag tgt gtg gac agt aca	1956
Glu His Leu Asp Gln Ile Asn Gly Arg Ser Glu Cys Val Asp Ser Thr	
575 580 585 590	
gat aat tcc tca aag cca tcc agt gaa ccc gct tct cac atg gct cgg	2004
Asp Asn Ser Ser Lys Pro Ser Ser Glu Pro Ala Ser His Met Ala Arg	
591 596 601 606	
cag cga tta gaa agc aca gaa aaa aaa aaa atc tcg ggg aaa gtc aca	2052
Gln Arg Leu Glu Ser Thr Glu Lys Lys Lys Ile Ser Gly Lys Val Thr	
607 612 617 622	
aag tcc ctc tct gcc agt gct ctt tcc ctc atg atc cca gga gat atg	2100
Lys Ser Leu Ser Ala Ser Ala Leu Ser Leu Met Ile Pro Gly Asp Met	
623 628 633 638	
ttt gct gtt tcc cct ctg gga agt cca atg tct ccc cat tcc ctg tcc	2148
Phe Ala Val Ser Pro Leu Gly Ser Pro Met Ser Pro His Ser Leu Ser	
639 644 649 654	
tcg gac cct tct tct tca cga gat tcc tct ccc agc cga gat tcc tca	2196
Ser Asp Pro Ser Ser Ser Arg Asp Ser Ser Pro Ser Arg Asp Ser Ser	
655 660 665 670	
gca gct tct gcc agt cca cat cag ccg att gtg atc cac agt tcg ggg	2244
Ala Ala Ser Ala Ser Pro His Gln Pro Ile Val Ile His Ser Ser Gly	
671 676 681 686	
aag aac tac ggc ttt acc atc cga gcc atc cgg gtg tat gtg gga gac	2292

Lys	Asn	Tyr	Gly	Phe	Thr	Ile	Arg	Ala	Ile	Arg	Val	Tyr	Val	Gly	Asp	
687					692					697					702	
agt	gac	atc	tat	aca	gtg	cac	cat	atc	gtc	tgg	aat	gta	gaa	gaa	gga	2340
Ser	Asp	Ile	Tyr	Thr	Val	His	His	Ile	Val	Trp	Asn	Val	Glu	Glu	Gly	
703					708					713					718	
agt	ccg	gca	tgc	cag	gca	gga	ctg	aag	gct	gga	gat	ctt	atc	act	cac	2388
Ser	Pro	Ala	Cys	Gln	Ala	Gly	Leu	Lys	Ala	Gly	Asp	Leu	Ile	Thr	His	
719					724					729					734	
atc	aat	gga	gaa	cca	gtg	cat	gga	ctt	gtc	cac	aca	gaa	gtt	ata	gaa	2436
Ile	Asn	Gly	Glu	Pro	Val	His	Gly	Leu	Val	His	Thr	Glu	Val	Ile	Glu	
735					740					745					750	
ctc	cta	ctg	aag	agt	ggg	aat	aag	gtg	tca	atc	act	act	acc	cca	ttt	2484
Leu	Leu	Leu	Lys	Ser	Gly	Asn	Lys	Val	Ser	Ile	Thr	Thr	Thr	Pro	Phe	
751					756					761					766	
gaa	aac	aca	tca	atc	aaa	act	gga	cca	gcc	agg	aga	aac	agc	tat	aag	2532
Glu	Asn	Thr	Ser	Ile	Lys	Thr	Gly	Pro	Ala	Arg	Arg	Asn	Ser	Tyr	Lys	
767					772					777					782	
agc	cgg	atg	gtg	agg	cgg	agc	aag	aaa	tcc	aag	aag	aaa	gaa	agt	ctc	2580
Ser	Arg	Met	Val	Arg	Arg	Ser	Lys	Lys	Ser	Lys	Lys	Lys	Glu	Ser	Leu	
783					788					793					798	
gaa	agg	agg	aga	tct	ctt	ttc	aaa	aag	cta	gcc	aag	cag	cct	tct	cct	2628
Glu	Arg	Arg	Arg	Ser	Leu	Phe	Lys	Lys	Leu	Ala	Lys	Gln	Pro	Ser	Pro	
799					804					809					814	
tta	ctc	cac	acc	agc	cga	agt	ttc	tcc	tgc	ttg	aac	aga	tcc	ctg	tca	2676
Leu	Leu	His	Thr	Ser	Arg	Ser	Phe	Ser	Cys	Leu	Asn	Arg	Ser	Leu	Ser	
815					820					825					830	
tcg	ggg	gag	agc	ctc	cca	ggg	tcc	ccc	act	cat	agc	ttg	tct	ccc	cgg	2724
Ser	Gly	Glu	Ser	Leu	Pro	Gly	Ser	Pro	Thr	His	Ser	Leu	Ser	Pro	Arg	
831					836					841					846	
tct	cca	aca	cca	agc	tac	cgc	tcc	acc	cct	gac	ttc	cca	tct	ggg	act	2772
Ser	Pro	Thr	Pro	Ser	Tyr	Arg	Ser	Thr	Pro	Asp	Phe	Pro	Ser	Gly	Thr	
847					852					857					862	
aat	tcc	tcc	cag	agc	agc	tcc	cct	agt	tct	agt	gcc	ccc	aat	tcc	cca	2820
Asn	Ser	Ser	Gln	Ser	Ser	Ser	Pro	Ser	Ser	Ser	Ala	Pro	Asn	Ser	Pro	
863					868					873					878	
gca	ggg	tcc	ggg	cac	atc	cgg	ccc	agc	act	ctc	cac	ggg	ctt	gca	ccc	2868
Ala	Gly	Ser	Gly	His	Ile	Arg	Pro	Ser	Thr	Leu	His	Gly	Leu	Ala	Pro	
879					884					889					894	
aaa	ctc	ggc	ggg	cag	cgg	tac	cgg	tcc	gga	agg	cga	aag	tcc	gcc	ggc	2916
Lys	Leu	Gly	Gly	Gln	Arg	Tyr	Arg	Ser	Gly	Arg	Arg	Lys	Ser	Ala	Gly	
895					900					905					910	
aac	atc	cca	ctg	tcc	ccg	ctg	gcc	cgg	acg	ccc	tct	cca	acc	ccg	caa	2964
Asn	Ile	Pro	Leu	Ser	Pro	Leu	Ala	Arg	Thr	Pro	Ser	Pro	Thr	Pro	Gln	

911	916	921	926	
ccc acc tcc ccg cag cgg tca cca tcc cct ctt ctg gga cac tca ctg				3012
Pro Thr Ser Pro Gln Arg Ser Pro Ser Pro Leu Leu Gly His Ser Leu				
927	932	937	942	
ggc aat tcc aag atc gcg caa gcc ttt ccc agc aag atg cac tcc ccg				3060
Gly Asn Ser Lys Ile Ala Gln Ala Phe Pro Ser Lys Met His Ser Pro				
943	948	953	958	
ccc acc atc gtc aga cac atc gtg agg ccc aag agt gcg gag ccc ccc				3108
Pro Thr Ile Val Arg His Ile Val Arg Pro Lys Ser Ala Glu Pro Pro				
959	964	969	974	
agg tcc ccg ctg ctc aag cgc gtg cag tcc gag gag aag ctg tcg ccc				3156
Arg Ser Pro Leu Leu Lys Arg Val Gln Ser Glu Glu Lys Leu Ser Pro				
975	980	985	990	
tct tac ggc agt gac aag aag cac ctg tgc tcc cgc aag cac agc ctg				3204
Ser Tyr Gly Ser Asp Lys Lys His Leu Cys Ser Arg Lys His Ser Leu				
991	996	1001	1006	
gag gtg acc caa gag gag gtg cag cgg gag cag tcc cag cgg gag gcg				3252
Glu Val Thr Gln Glu Glu Val Gln Arg Glu Gln Ser Gln Arg Glu Ala				
1007	1012	1017	1022	
ccg ctg cag agc ctg gat gag aac gtg tgc gac gtg ccg ccg ctc agc				3300
Pro Leu Gln Ser Leu Asp Glu Asn Val Cys Asp Val Pro Pro Leu Ser				
1023	1028	1033	1038	
cgc gcc cgg cca gtg gag caa ggc tgc ctg aaa cgc cca gtc tcc ccg				3348
Arg Ala Arg Pro Val Glu Gln Gly Cys Leu Lys Arg Pro Val Ser Arg				
1039	1044	1049	1054	
aag gtg ggc cgc cag gag tct gtg gac gac ctg gac cgc gac aag ctg				3396
Lys Val Gly Arg Gln Glu Ser Val Asp Asp Leu Asp Arg Asp Lys Leu				
1055	1060	1065	1070	
aag gcc aag gtg gtg gtg aag aaa gca gac ggc ttc cca gag aaa cag				3444
Lys Ala Lys Val Val Lys Lys Ala Asp Gly Phe Pro Glu Lys Gln				
1071	1076	1081	1086	
gaa tcc cac cag aaa tcc cat gga ccc ggg agt gat ttg gaa aac ttt				3492
Glu Ser His Gln Lys Ser His Gly Pro Gly Ser Asp Leu Glu Asn Phe				
1087	1092	1097	1102	
gct ctg ttt aag ctg gaa gag aga gag aag aaa gtc tat ccg aag gct				3540
Ala Leu Phe Lys Leu Glu Glu Arg Glu Lys Lys Val Tyr Pro Lys Ala				
1103	1108	1113	1118	
gtg gaa agg tca agt act ttt gaa aac aaa gcg tct atg cag gag gcg				3588
Val Glu Arg Ser Ser Thr Phe Glu Asn Lys Ala Ser Met Gln Glu Ala				
1119	1124	1129	1134	
cca ccg ctg ggc agc ctg ctg aag gat gct ctt cac aag cag gcc agc				3636
Pro Pro Leu Gly Ser Leu Leu Lys Asp Ala Leu His Lys Gln Ala Ser				
1135	1140	1145	1150	

gtg cgc gcc agc gag ggt gcg atg tcg gat ggc ccg gtg cct gcg gag	3684
Val Arg Ala Ser Glu Gly Ala Met Ser Asp Gly Pro Val Pro Ala Glu	
1151 1156 1161 1166	
cac cgc cag ggt ggc ggg gac ttc aga cgg gcc ccc gct cct ggc acc	3732
His Arg Gln Gly Gly Gly Asp Phe Arg Arg Ala Pro Ala Pro Gly Thr	
1167 1172 1177 1182	
ctc cag gat ggt ctc tgc cac tcc ctc gac agg ggc atc tct ggg aag	3780
Leu Gln Asp Gly Leu Cys His Ser Leu Asp Arg Gly Ile Ser Gly Lys	
1183 1188 1193 1198	
ggg gaa ggc acg gag aag tcc tcc cag gcc aag gag ctt ctc cga tgt	3828
Gly Glu Gly Thr Glu Lys Ser Ser Gln Ala Lys Glu Leu Leu Arg Cys	
1199 1204 1209 1214	
gaa aag tta gac agc aag ctg gcc aac atc gat tac ctc cga aag aaa	3876
Glu Lys Leu Asp Ser Lys Leu Ala Asn Ile Asp Tyr Leu Arg Lys Lys	
1215 1220 1225 1230	
atg tca ctt gag gac aaa gag gac aac ctc tgc cct gtg ctg aag ccc	3924
Met Ser Leu Glu Asp Lys Glu Asp Asn Leu Cys Pro Val Leu Lys Pro	
1231 1236 1241 1246	
aag atg aca gct ggc tcc cac gaa tgc ctg cca ggg aac cca gtc cga	3972
Lys Met Thr Ala Gly Ser His Glu Cys Leu Pro Gly Asn Pro Val Arg	
1247 1252 1257 1262	
ccc acg ggt ggg cag cag gag ccc ccg ccg gct tct gag agc cga gct	4020
Pro Thr Gly Gly Gln Gln Glu Pro Pro Pro Ala Ser Glu Ser Arg Ala	
1263 1268 1273 1278	
ttt gtc agc agc acc cat gca gct cag atg agt gcc gtc tct ttt gtt	4068
Phe Val Ser Ser Thr His Ala Ala Gln Met Ser Ala Val Ser Phe Val	
1279 1284 1289 1294	
ccc ctc aag gcc tta aca ggc cgg gtg gac agt gga acg gag aag cct	4116
Pro Leu Lys Ala Leu Thr Gly Arg Val Asp Ser Gly Thr Glu Lys Pro	
1295 1300 1305 1310	
ggc ttg gtt gct cct gag tcc cct gtt agg aag agc ccc tcc gag tat	4164
Gly Leu Val Ala Pro Glu Ser Pro Val Arg Lys Ser Pro Ser Glu Tyr	
1311 1316 1321 1326	
aag ctg gaa ggt agg tct gtc tca tgc ctg gag ccg atc gag ggc act	4212
Lys Leu Glu Gly Arg Ser Val Ser Cys Leu Glu Pro Ile Glu Gly Thr	
1327 1332 1337 1342	
ctg gac att gct ctc ctg tcc gga cct cag gcc tcc aag aca gaa ctg	4260
Leu Asp Ile Ala Leu Leu Ser Gly Pro Gln Ala Ser Lys Thr Glu Leu	
1343 1348 1353 1358	
cct tcc cca gag tct gca cag agc ccc agc cca agt ggt gac gtg agg	4308
Pro Ser Pro Glu Ser Ala Gln Ser Pro Ser Pro Ser Gly Asp Val Arg	
1359 1364 1369 1374	

gcc tct gtg cca cca gtt ctc ccc agc agc agt ggg aaa aag aac gat	4356
Ala Ser Val Pro Pro Val Leu Pro Ser Ser Ser Gly Lys Lys Asn Asp	
1375 1380 1385 1390	
acc acc agt gca aga gag ctt tct cct tcc agc tta aag atg aat aaa	4404
Thr Thr Ser Ala Arg Glu Leu Ser Pro Ser Ser Leu Lys Met Asn Lys	
1391 1396 1401 1406	
tcc tac ctg ctg gag cct tgg ttc ctg ccc ccc agc cga ggt ctc cag	4452
Ser Tyr Leu Leu Glu Pro Trp Phe Leu Pro Pro Ser Arg Gly Leu Gln	
1407 1412 1417 1422	
aat tca cca gca gtt tcc ctg cct gac cca gag ttc aag agg gac agg	4500
Asn Ser Pro Ala Val Ser Leu Pro Asp Pro Glu Phe Lys Arg Asp Arg	
1423 1428 1433 1438	
aaa ggt ccc cat cct act gcc agg agc cct gga aca gtc atg gaa agc	4548
Lys Gly Pro His Pro Thr Ala Arg Ser Pro Gly Thr Val Met Glu Ser	
1439 1444 1449 1454	
aat ccc caa cag aga gag ggc agc tcc cct aaa cac caa gac cac acc	4596
Asn Pro Gln Gln Arg Glu Gly Ser Ser Pro Lys His Gln Asp His Thr	
1455 1460 1465 1470	
act gac ccc aag ctt ctg acc tgc ctg ggg cag aac ctc cac agc cct	4644
Thr Asp Pro Lys Leu Leu Thr Cys Leu Gly Gln Asn Leu His Ser Pro	
1471 1476 1481 1486	
gac ctg gcc agg cca cgc tgc ccg ctc cca cct gaa gct tcc ccc tca	4692
Asp Leu Ala Arg Pro Arg Cys Pro Leu Pro Pro Glu Ala Ser Pro Ser	
1487 1492 1497 1502	
agg gag aag cca ggc ctg agg gaa tcg tct gaa aga ggc cct ccc aca	4740
Arg Glu Lys Pro Gly Leu Arg Glu Ser Ser Glu Arg Gly Pro Pro Thr	
1503 1508 1513 1518	
gcc aga agc gag cgc tct gct gcg agg gct gac aca tgc aga gag ccc	4788
Ala Arg Ser Glu Arg Ser Ala Ala Arg Ala Asp Thr Cys Arg Glu Pro	
1519 1524 1529 1534	
tcc atg gaa ctg tgc ttt cca gaa act gcg aaa acc agt gac aac tcc	4836
Ser Met Glu Leu Cys Phe Pro Glu Thr Ala Lys Thr Ser Asp Asn Ser	
1535 1540 1545 1550	
aaa aat ctc ctc tct gtg gga agg acc cac cca gat ttc tat aca cag	4884
Lys Asn Leu Leu Ser Val Gly Arg Thr His Pro Asp Phe Tyr Thr Gln	
1551 1556 1561 1566	
acc cag gcc atg gag aaa gca tgg gcg ccg ggt ggg aaa acg aac cac	4932
Thr Gln Ala Met Glu Lys Ala Trp Ala Pro Gly Gly Lys Thr Asn His	
1567 1572 1577 1582	
aaa gat ggc cca ggt gag gcg agg ccc ccg ccc aga gac aac tcc tct	4980
Lys Asp Gly Pro Gly Glu Ala Arg Pro Pro Pro Arg Asp Asn Ser Ser	
1583 1588 1593 1598	
ctg cac tca gct gga att ccc tgt gag aag gag ctg ggc aag gtg agg	5028

Leu His Ser Ala Gly Ile Pro Cys Glu Lys Glu Leu Gly Lys Val Arg	
1599	1604 1609 1614
cgt ggc gtg gaa ccc aag ccc gaa gcg ctt ctt gcc agg cgg tct ctg	5076
Arg Gly Val Glu Pro Lys Pro Glu Ala Leu Leu Ala Arg Arg Ser Leu	
1615	1620 1625 1630
cag cca cct gga att gag agt gag aag agt gaa aag ctc tcc agt ttc	5124
Gln Pro Pro Gly Ile Glu Ser Glu Lys Ser Glu Lys Leu Ser Ser Phe	
1631	1636 1641 1646
cca tct ttg cag aaa gat ggt gcc aag gaa cct gaa agg aag gag cag	5172
Pro Ser Leu Gln Lys Asp Gly Ala Lys Glu Pro Glu Arg Lys Glu Gln	
1647	1652 1657 1662
cct cta caa agg cat ccc agc agc atc cct ccg ccc cct ctg acg gcc	5220
Pro Leu Gln Arg His Pro Ser Ser Ile Pro Pro Pro Pro Leu Thr Ala	
1663	1668 1673 1678
aaa gac ctg tcc agc ccg gct gcc agg cag cat tgc agt tcc cca agc	5268
Lys Asp Leu Ser Ser Pro Ala Ala Arg Gln His Cys Ser Ser Pro Ser	
1679	1684 1689 1694
cac gct tct ggc aga gag ccg ggg gcc aag ccc agc act gca gag ccc	5316
His Ala Ser Gly Arg Glu Pro Gly Ala Lys Pro Ser Thr Ala Glu Pro	
1695	1700 1705 1710
agc tcg agc ccc cag gac cct ccc aag cct gtt gct gcg cac agt gaa	5364
Ser Ser Ser Pro Gln Asp Pro Pro Lys Pro Val Ala Ala His Ser Glu	
1711	1716 1721 1726
agc agc agc cac aag ccc ccg cct ggc cct gac ccg ggc cct cca aag	5412
Ser Ser Ser His Lys Pro Arg Pro Gly Pro Asp Pro Gly Pro Pro Lys	
1727	1732 1737 1742
act aag cac ccc gac ccg tcc ctc tcc tct cag aaa cca agt gtc ggg	5460
Thr Lys His Pro Asp Arg Ser Leu Ser Ser Gln Lys Pro Ser Val Gly	
1743	1748 1753 1758
gcc aca aag ggc aaa gag cct gcc act cag tcc ctc ggt ggc tct agc	5508
Ala Thr Lys Gly Lys Glu Pro Ala Thr Gln Ser Leu Gly Gly Ser Ser	
1759	1764 1769 1774
aga gag ggg aag ggc cac agt aag agt ggg ccg gat gtg ttt cct gct	5556
Arg Glu Gly Lys Gly His Ser Lys Ser Gly Pro Asp Val Phe Pro Ala	
1775	1780 1785 1790
acc cca ggc tcc cag aac aaa gcc agc gat ggg att ggc cag gga gaa	5604
Thr Pro Gly Ser Gln Asn Lys Ala Ser Asp Gly Ile Gly Gln Gly Glu	
1791	1796 1801 1806
ggt ggg ccc tct gtc cca ctg cac act gac agg gct cct cta gac gcc	5652
Gly Gly Pro Ser Val Pro Leu His Thr Asp Arg Ala Pro Leu Asp Ala	
1807	1812 1817 1822
aag cca caa ccc acc agt ggt ggg ccg ccc ctg gag gtg ctg gag aag	5700
Lys Pro Gln Pro Thr Ser Gly Gly Arg Pro Leu Glu Val Leu Glu Lys	

1823	1828	1833	1838	
cct gtg cat ttg cca agg ccg gga cac cca ggg cct agt gag cca gcg				5748
Pro Val His Leu Pro Arg Pro Gly His Pro Gly Pro Ser Glu Pro Ala				
1839	1844	1849	1854	
gac cag aaa ctg tcc gct gtt ggt gaa aag caa acc ctg tct cca aag				5796
Asp Gln Lys Leu Ser Ala Val Gly Glu Lys Gln Thr Leu Ser Pro Lys				
1855	1860	1865	1870	
cac ccc aaa cca tcc act gtg aaa gat tgc ccc acc ctg tgc aaa cag				5844
His Pro Lys Pro Ser Thr Val Lys Asp Cys Pro Thr Leu Cys Lys Gln				
1871	1876	1881	1886	
aca gac aac aga cag aca gac aaa agc ccg agt cag ccg gcc gcc aac				5892
Thr Asp Asn Arg Gln Thr Asp Lys Ser Pro Ser Gln Pro Ala Ala Asn				
1887	1892	1897	1902	
acc gac aga agg gcg gaa ggg aag aaa tgc act gaa gca ctt tat gct				5940
Thr Asp Arg Arg Ala Glu Gly Lys Lys Cys Thr Glu Ala Leu Tyr Ala				
1903	1908	1913	1918	
cca gca gag ggc gac aag ctc gag gcc ggc ctt tcc ttt gtg cat agc				5988
Pro Ala Glu Gly Asp Lys Leu Glu Ala Gly Leu Ser Phe Val His Ser				
1919	1924	1929	1934	
gag aac cgg ttg aaa ggc gcg gag cgg cca gcc gcg ggg gtg ggg aag				6036
Glu Asn Arg Leu Lys Gly Ala Glu Arg Pro Ala Ala Gly Val Gly Lys				
1935	1940	1945	1950	
ggc ttc cct gag gcc aga ggg aaa ggg ccc ggt ccc cag aag cca ccg				6084
Gly Phe Pro Glu Ala Arg Gly Lys Gly Pro Gly Pro Gln Lys Pro Pro				
1951	1956	1961	1966	
acg gag gca gac aag ccc aat ggc atg aaa cgg tcc ccc tca gcc act				6132
Thr Glu Ala Asp Lys Pro Asn Gly Met Lys Arg Ser Pro Ser Ala Thr				
1967	1972	1977	1982	
ggg cag agt tct ttc cga tcc acg gcc ctc ccg gaa aag tct ctg agc				6180
Gly Gln Ser Ser Phe Arg Ser Thr Ala Leu Pro Glu Lys Ser Leu Ser				
1983	1988	1993	1998	
tgc tcc tcc agc ttc cct gaa acc agg gcc gga gtt aga gag gcc tct				6228
Cys Ser Ser Ser Phe Pro Glu Thr Arg Ala Gly Val Arg Glu Ala Ser				
1999	2004	2009	2014	
gca gcc agc agc gac acc tct tct gcc aag gcc gcc ggg ggc atg ctg				6276
Ala Ala Ser Ser Asp Thr Ser Ser Ala Lys Ala Ala Gly Gly Met Leu				
2015	2020	2025	2030	
gag ctt cca gcc ccc agc aac agg gac cat agg aag gct cag cct gcc				6324
Glu Leu Pro Ala Pro Ser Asn Arg Asp His Arg Lys Ala Gln Pro Ala				
2031	2036	2041	2046	
ggg gag ggc cga acc cac atg aca aag agt gac tcc ctg ccc tcc ttc				6372
Gly Glu Gly Arg Thr His Met Thr Lys Ser Asp Ser Leu Pro Ser Phe				
2047	2052	2057	2062	

cg	g	t	c	a	c	t	g	a	c	a	c	c	a	a	a	c	c		6420
Arg	Val	Ser	Thr	Leu	Pro	Leu	Glu	Ser	His	His	Pro	Asp	Pro	Asn	Thr				
2063					2068				2073					2078					
at	g	g	c	a	c	c	g	a	a	g	g	c	t	c	t	c	a	6468	
Met	Gly	Gly	Ala	Ser	His	Arg	Asp	Arg	Ala	Leu	Ser	Val	Thr	Ala	Thr				
2079				2084					2089					2094					
g	t	a	g	a	a	a	a	a	a	a	a	a	a	a	a	a	6516		
Val	Gly	Glu	Thr	Lys	Gly	Lys	Asp	Pro	Ala	Pro	Ala	Gln	Pro	Pro	Pro				
2095				2100					2105					2110					
g	c	t	a	a	a	a	a	a	a	a	a	a	a	a	a	a	6564		
Ala	Arg	Lys	Gln	Asn	Val	Gly	Arg	Asp	Val	Thr	Lys	Pro	Ser	Pro	Ala				
2111				2116					2121					2126					
c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	6612		
Pro	Asn	Thr	Asp	Arg	Pro	Ile	Ser	Leu	Ser	Asn	Glu	Lys	Asp	Phe	Val				
2127				2132					2137					2142					
g	t	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	6660		
Val	Arg	Gln	Arg	Arg	Gly	Lys	Glu	Ser	Leu	Arg	Ser	Ser	Pro	His	Lys				
2143				2148					2153					2158					
a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	6715		
Lys	Ala	Leu	*																
2159																			
g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	6775		
gag	c	t	c	a	t	t	a	a	a	a	a	a	a	a	a	a			
gag	c	t	c	a	t	t	a	a	a	a	a	a	a	a	a	a	6835		
at	g	c	t	t	c	c	c	c	c	c	c	c	c	c	c	c	6895		
at	g	c	t	t	c	c	c	c	c	c	c	c	c	c	c	c			
a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	6899		
a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a			

<210> 289
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)..(1872)

<400> 289

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Met	Pro	Ala	Ser	Phe	Pro	Leu	Ser	Arg	Asn	Ala	Gly	Thr	Arg	Gly	Gly		
1					5				10								
a	a	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	96
Asn	Pro	Ala	Pro	Ser	Pro	Pro	Leu	Arg	Ser	Pro	Gly	Lys	Gly	Arg	Leu		
17					22				27					32			

gcc agc ccc atc cta cct caa cgc agc ggc aac ata ccg gag gcc cca	144
Ala Ser Pro Ile Leu Pro Gln Arg Ser Gly Asn Ile Pro Glu Ala Pro	
33 38 43 48	
cgt cga tac gac cca ggc gtc cgc att gga ttg ggc ggt gcg gcg gcg	192
Arg Arg Tyr Asp Pro Gly Val Arg Ile Gly Leu Gly Gly Ala Ala Ala	
49 54 59 64	
ctt ctg tcc gcc ttc cgg tgt cac gcg acc gcc tcc ccc tcc cac cct	240
Leu Leu Ser Ala Phe Arg Cys His Ala Thr Ala Ser Pro Ser His Pro	
65 70 75 80	
tct ctg tct acc tct ggg cgg gac tgc cgg gtg atg aga tac tcg gtc	288
Ser Leu Ser Thr Ser Gly Arg Asp Cys Arg Val Met Arg Tyr Ser Val	
81 86 91 96	
ggc gac ggt aga acg ggc gac ggc gac aac cgc aat cac atc cac gac	336
Gly Asp Gly Arg Thr Gly Asp Gly Asp Asn Arg Asn His Ile His Asp	
97 102 107 112	
ggg gat cat ggc aga ggt gag gag cct att gca ccg ccg ctg gcc ccc	384
Gly Asp His Gly Arg Gly Glu Glu Pro Ile Ala Pro Pro Leu Ala Pro	
113 118 123 128	
cgg acc cgg aag ccg cct ctg agg ccc ggg gac cga gcg ccc gtg tgc	432
Arg Thr Arg Lys Pro Pro Leu Arg Pro Gly Asp Arg Ala Pro Val Cys	
129 134 139 144	
agg tgg gct ggg ttg agg aat cac gcc cag aat aaa gcc aag ctc atc	480
Arg Trp Ala Gly Leu Arg Asn His Ala Gln Asn Lys Ala Lys Leu Ile	
145 150 155 160	
tct gag acc cgg agg agg ttc gaa gct gag tat gtg aca gat aag tca	528
Ser Glu Thr Arg Arg Arg Phe Glu Ala Glu Tyr Val Thr Asp Lys Ser	
161 166 171 176	
gat aaa tat gat gca cgt gat gtt gaa agg cta caa caa gat gat aac	576
Asp Lys Tyr Asp Ala Arg Asp Val Glu Arg Leu Gln Gln Asp Asp Asn	
177 182 187 192	
tgg gtt gaa agt tac tta tct tgg aga cat aat att gta gat gaa aca	624
Trp Val Glu Ser Tyr Leu Ser Trp Arg His Asn Ile Val Asp Glu Thr	
193 198 203 208	
ctg aag atg ctc gat gag agt ttt cag tgg agg aaa gaa att tct gtc	672
Leu Lys Met Leu Asp Glu Ser Phe Gln Trp Arg Lys Glu Ile Ser Val	
209 214 219 224	
aat gtc tgg atc agg gtg aag tat cat gta aaa gac cag aaa acc ata	720
Asn Val Trp Ile Arg Val Lys Tyr His Val Lys Asp Gln Lys Thr Ile	
225 230 235 240	
ttg gac aaa aag aag ctc ata gca ttc tgg ttg gaa cgt tat gct aag	768
Leu Asp Lys Lys Lys Leu Ile Ala Phe Trp Leu Glu Arg Tyr Ala Lys	
241 246 251 256	

agg gaa aat ggg aaa cct gta aca gtg atg ttt gac ctg tca gaa act	816
Arg Glu Asn Gly Lys Pro Val Thr Val Met Phe Asp Leu Ser Glu Thr	
257 262 267 272	
gga ata aat agc att gac atg gac ttt gta cgc ttt atc atc aac tgc	864
Gly Ile Asn Ser Ile Asp Met Asp Phe Val Arg Phe Ile Ile Asn Cys	
273 278 283 288	
ttt aag gtt tat tac cct aaa tac ctc tct gct ttc aaa att gtg aaa	912
Phe Lys Val Tyr Tyr Pro Lys Tyr Leu Ser Ala Phe Lys Ile Val Lys	
289 294 299 304	
acc tgg ctt ggt cca gaa gca gtg agc ttg ttg aag ttt aca agc aaa	960
Thr Trp Leu Gly Pro Glu Ala Val Ser Leu Leu Lys Phe Thr Ser Lys	
305 310 315 320	
aat gaa gtc cag gac tat gtc agt gta gaa tac ctg cct ccc cac atg	1008
Asn Glu Val Gln Asp Tyr Val Ser Val Glu Tyr Leu Pro Pro His Met	
321 326 331 336	
ggg gga act gat cct ttc aag tat agc tat cca cca cta gta gat gat	1056
Gly Gly Thr Asp Pro Phe Lys Tyr Ser Tyr Pro Pro Leu Val Asp Asp	
337 342 347 352	
gac ttc cag acc cca ctg tgt gag aat ggg cct att acc agt gag gat	1104
Asp Phe Gln Thr Pro Leu Cys Glu Asn Gly Pro Ile Thr Ser Glu Asp	
353 358 363 368	
gaa act tca agt aaa gaa gac ata gaa agt gat ggc aaa gaa aca ttg	1152
Glu Thr Ser Ser Lys Glu Asp Ile Glu Ser Asp Gly Lys Glu Thr Leu	
369 374 379 384	
gaa aca att tct aat gaa gaa caa aca cct ctt ctt aaa aag att aac	1200
Glu Thr Ile Ser Asn Glu Glu Gln Thr Pro Leu Leu Lys Lys Ile Asn	
385 390 395 400	
cca acc gaa tct act tcc aaa gca gaa gaa aat gaa aaa gtt gat tca	1248
Pro Thr Glu Ser Thr Ser Lys Ala Glu Glu Asn Glu Lys Val Asp Ser	
401 406 411 416	
aaa gtg aaa gct ttc aag aaa cca ttg agt gta ttt aaa ggc ccc tta	1296
Lys Val Lys Ala Phe Lys Lys Pro Leu Ser Val Phe Lys Gly Pro Leu	
417 422 427 432	
cta cac atc agc cca gca gaa gaa ctg tac ttt gga agt aca gaa tcc	1344
Leu His Ile Ser Pro Ala Glu Glu Leu Tyr Phe Gly Ser Thr Glu Ser	
433 438 443 448	
gga gag aag aaa acc tta ata gtg ttg aca aat gta act aaa aat ata	1392
Gly Glu Lys Lys Thr Leu Ile Val Leu Thr Asn Val Thr Lys Asn Ile	
449 454 459 464	
gtg gca ttt aag gtg aga aca aca gct cca gaa aaa tac aga gtc aag	1440
Val Ala Phe Lys Val Arg Thr Thr Ala Pro Glu Lys Tyr Arg Val Lys	
465 470 475 480	
cca agc aat agc agc tgt gac ccg ggt gca tca gtg gat ata gtt gtg	1488

Pro	Ser	Asn	Ser	Ser	Cys	Asp	Pro	Gly	Ala	Ser	Val	Asp	Ile	Val	Val	
481					486					491					496	
tct	ccc	cat	ggg	ggt	tta	aca	gtc	tct	gcc	caa	gac	cgt	ttt	ctg	ata	1536
Ser	Pro	His	Gly	Gly	Leu	Thr	Val	Ser	Ala	Gln	Asp	Arg	Phe	Leu	Ile	
497					502					507					512	
atg	gct	gca	gaa	atg	gaa	cag	tca	tct	ggc	aca	ggc	cca	gca	gaa	tta	1584
Met	Ala	Ala	Glu	Met	Glu	Gln	Ser	Ser	Gly	Thr	Gly	Pro	Ala	Glu	Leu	
513					518					523					528	
act	cag	ttt	tgg	aaa	gaa	gtt	ccc	aga	aac	aaa	gtg	atg	gaa	cat	agg	1632
Thr	Gln	Phe	Trp	Lys	Glu	Val	Pro	Arg	Asn	Lys	Val	Met	Glu	His	Arg	
529					534					539					544	
tta	aga	tgc	cat	act	gtt	gaa	agc	agt	aaa	cca	aac	act	ctt	acg	tta	1680
Leu	Arg	Cys	His	Thr	Val	Glu	Ser	Ser	Lys	Pro	Asn	Thr	Leu	Thr	Leu	
545					550					555					560	
aaa	gac	aat	gct	ttc	aat	atg	tca	gat	aaa	acc	agt	gaa	gat	ata	tgt	1728
Lys	Asp	Asn	Ala	Phe	Asn	Met	Ser	Asp	Lys	Thr	Ser	Glu	Asp	Ile	Cys	
561					566					571					576	
cta	caa	ctc	agt	cgt	tta	cta	gaa	agc	aat	agg	aag	ctt	gaa	gac	caa	1776
Leu	Gln	Leu	Ser	Arg	Leu	Leu	Glu	Ser	Asn	Arg	Lys	Leu	Glu	Asp	Gln	
577					582					587					592	
gtt	cag	cgt	tgt	atc	tgg	ttc	cag	cag	ctg	ctg	ctt	tcc	tta	aca	atg	1824
Val	Gln	Arg	Cys	Ile	Trp	Phe	Gln	Gln	Leu	Leu	Leu	Ser	Leu	Thr	Met	
593					598					603					608	
ctc	ttg	ctt	gct	ttt	gtc	acc	tct	ttc	ttc	tat	tta	ttg	tac	agt	taa	1872
Leu	Leu	Leu	Ala	Phe	Val	Thr	Ser	Phe	Phe	Tyr	Leu	Leu	Tyr	Ser	*	
609					614					619					624	
agaagtgggtg ccgggtagga accacggttc ctctcgccat tagttggaaa aagtaacaga															1932	
cctaaaactc taccaagcta ctaaaaacat tgcacatctg tgcttcctaa aaggaaatat															1992	
gcagcacgtg gaggggaaca catacatgtc ttgaaaataa actgctagaa taaagaaatg															2052	
ctggagaaat tgaaaaaaaa aaaaa															2077	

<210> 290
 <211> 601
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (89) .. (448)

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tccgagtaca cggagaagaa ctggaaac	atg caa aaa ctc caa aca cgg tcc	112
	Met Gln Lys Leu Gln Thr Arg Ser	
	1 5	
cct gcc atg tcc ctg tct gac cca ggc ctg ggg tac cac ccc acg tgc	160	
Pro Ala Met Ser Leu Ser Asp Pro Gly Leu Gly Tyr His Pro Thr Cys		
9 14 19 24		
tgg acc cta cgc tgg cca ccc ctg tgc tcc ctc cac gcc ctc cac gtg	208	
Trp Thr Leu Arg Trp Pro Pro Leu Cys Ser Leu His Ala Leu His Val		
25 30 35 40		
ttc cac tgc ctc ttc tct tct cgc ttg gga act cca gtc tca cct cgg	256	
Phe His Cys Leu Phe Ser Ser Arg Leu Gly Thr Pro Val Ser Pro Arg		
41 46 51 56		
ctt gca atg gac ccc aac tgc tcc tgc gag gct ggt ggc tcc tgc gcc	304	
Leu Ala Met Asp Pro Asn Cys Ser Cys Glu Ala Gly Gly Ser Cys Ala		
57 62 67 72		
tgc gcc ggc tcc tgc aag tgc aaa aag tgc aaa tgc acc tcc tgc aag	352	
Cys Ala Gly Ser Cys Lys Cys Lys Lys Cys Lys Cys Thr Ser Cys Lys		
73 78 83 88		
aag agc tgc tgc tcc tgt tgc ccc ctg ggc tgt gcc aag tgt gcc cag	400	
Lys Ser Cys Cys Ser Cys Cys Pro Leu Gly Cys Ala Lys Cys Ala Gln		
89 94 99 104		
ggc tgc atc tgc aaa ggg gcg tca gag aag tgc agc tgc tgt gcc tga	448	
Gly Cys Ile Cys Lys Gly Ala Ser Glu Lys Cys Ser Cys Cys Ala *		
105 110 115 120		
tgtcgggaca gccctgctgt cagatgaaaa cagaatgaca cgtaaaatcc aggatttttt	508	
tttttctaca actccgactc atttgctaca ttcttttttt ttctgtgaaa tatgtgaata	568	
ataattaaac acttagactt gaaaaaaaaaaa aaa	601	

<210> 291
 <211> 1856
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1061)..(1780)

<220>
 <221> misc_feature
 <222> (1)...(1856)
 <223> n = a,t,c or g

<400> 291

ccgcgcctttt tgcccgtgaa gcgcgcggtga cgcttgagat tggtttttggc atggggggcgt 60
 cgctgggtggc aatgggctaaa gatcgccctg agcaggactt cctcggcatt gaagtgcatt 120
 caccggggcgt tggtgcggtgc ctggcttctg cgcatagaaga aggtttaagc aacctgcgcg 180
 tgatgtgtca cgatgcgggtt gaagtgcgtgc ataaaatgat tcctgacaat tcattgcgca 240
 tgggtgcagct ctttttccct gaccgcgtggc acaaagcgcg ccataataaa cgccgtatcg 300
 ttcagggtgcc gtttgccgaa ctggtaaaaa gcaaaactgca gctgggggggc gtattccata 360
 tggcgaccga ctgggaacct tatgcggaac atatgcttga agtgatgtct tctattgacg 420
 gttataaaaa cctgtcagag agcaatgatt acgtaccgcg tccggcatca cgtccggtga 480
 cgaaatttga acaacgtggt catcgtcttg gtcacggagt atgggactta atgttcgaga 540
 gggtgaaata atggcaaaga accgtagccg tcgtctgcgt aaaaaaatgc acatcgacga 600
 attccaggaa ttaggatttt cgggtggcatg gcgattcccg gaaggtacat cggaagaaca 660
 gattgataaa accgttgatg attttattaa cgaggttatc gaaccgaaca aactggcctt 720
 tgacggcagc gggtatctgg cctgggaagg tctgatctgc atgcaggaaa tcggcaaagt 780
 caccgaagaa catcaggcga ttgtgcgtaa gtggctggaa gagcgcaaac tggatgaggt 840
 acgccccagc gaacttttcg acgtttggtg ggactaagaa agcatacggg cgatgacaaa 900
 tgcaaaactg cctgatgcgc tacgcttadc aggcctggaa agatgcacga tcgagtaggc 960
 gggataaggt gtttacgccg catccggcat ggaaaacgcg tactttgtta tcaatctggg 1020
 gccagcaaat gctggcctga ttttttcttg agggaagact atg atg cgc aaa atg 1075
 Met Met Arg Lys Met
 1
 ctg ctg gcg gca gca ctt tca gtg acg gca atg acc gct cac gcc gac 1123
 Leu Leu Ala Ala Ala Leu Ser Val Thr Ala Met Thr Ala His Ala Asp
 6 11 16 21
 tac cag tgc agc gtc acg ccg cgt gac gat gtg att gtc agc ccg caa 1171
 Tyr Gln Cys Ser Val Thr Pro Arg Asp Asp Val Ile Val Ser Pro Gln
 22 27 32 37
 acc gtg cag gtg aag ggc gaa aac ggc aat ctg gtg atc acg cca gac 1219
 Thr Val Gln Val Lys Gly Glu Asn Gly Asn Leu Val Ile Thr Pro Asp
 38 43 48 53
 ggc aac gtg atg tat aac ggt aag caa tat tcc ctg aat gcc gcc cag 1267
 Gly Asn Val Met Tyr Asn Gly Lys Gln Tyr Ser Leu Asn Ala Ala Gln
 54 59 64 69
 cgc gag cag gcg aag gat tat cag gct gaa cta cgc agc acg ctg ccg 1315
 Arg Glu Gln Ala Lys Asp Tyr Gln Ala Glu Leu Arg Ser Thr Leu Pro
 70 75 80 85

tgg att gat gaa ggc gcg aaa agc cgc gtc gag aaa gcc cgt att gct	1363
Trp Ile Asp Glu Gly Ala Lys Ser Arg Val Glu Lys Ala Arg Ile Ala	
86 91 96 101	
ctg gat aaa att atc gtt cag gag atg ggc gaa agc agc aaa atg cgc	1411
Leu Asp Lys Ile Ile Val Gln Glu Met Gly Glu Ser Ser Lys Met Arg	
102 107 112 117	
agc cgt ctg acc aaa ctt gat gcg cag ctg aaa gag cag atg aac cgc	1459
Ser Arg Leu Thr Lys Leu Asp Ala Gln Leu Lys Glu Gln Met Asn Arg	
118 123 128 133	
att att gaa acg cgc agc gat ggc ctg acg ttt cac tat aaa gcc att	1507
Ile Ile Glu Thr Arg Ser Asp Gly Leu Thr Phe His Tyr Lys Ala Ile	
134 139 144 149	
gat cag gtt cgc gcc gaa ggc cag caa tta gtg aat cag gca atg ggt	1555
Asp Gln Val Arg Ala Glu Gly Gln Gln Leu Val Asn Gln Ala Met Gly	
150 155 160 165	
gga att tta cag gac agc att aat gaa atg ggc gcg aaa gcg gtg ctg	1603
Gly Ile Leu Gln Asp Ser Ile Asn Glu Met Gly Ala Lys Ala Val Leu	
166 171 176 181	
aaa agc ggc ggt aac cca tta cag aat gtg ctg gga agc ctg ggg ggg	1651
Lys Ser Gly Gly Asn Pro Leu Gln Asn Val Leu Gly Ser Leu Gly Gly	
182 187 192 197	
ctg caa tcc tca atc caa acc gag tgg aaa aag cag gaa aaa gat ttc	1699
Leu Gln Ser Ser Ile Gln Thr Glu Trp Lys Lys Gln Glu Lys Asp Phe	
198 203 208 213	
cag cag ttt ggc aaa gat gtt tgt agc cgc gtt gtg act ctg gaa gat	1747
Gln Gln Phe Gly Lys Asp Val Cys Ser Arg Val Val Thr Leu Glu Asp	
214 219 224 229	
agc cgc aaa gcc ctg gtc ggg aat tta aaa taa tcctctat tttaagacgg	1798
Ser Arg Lys Ala Leu Val Gly Asn Leu Lys *	
230 235 240	
cataatactt ttttatgccg nttaattctt cgttttgtta cctgcctcta acctttgta	1856

<210> 292
 <211> 1450
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (30) .. (845)

<400> 292
 cggaagttgt ggactgcagt tgagtggaa atg ggc aac ggc ggg cgg agc ggc 53

Met Gly Asn Gly Gly Arg Ser Gly
1 5

ctg cag cag ggg aag ggg aac gtg gat ggg gtg gca gcg act cct act	101
Leu Gln Gln Gly Lys Gly Asn Val Asp Gly Val Ala Ala Thr Pro Thr	
9 14 19 24	
gct gcc tcg gcc tcc tgc cag tac agg tgc atc gaa tgc aac cag gag	149
Ala Ala Ser Ala Ser Cys Gln Tyr Arg Cys Ile Glu Cys Asn Gln Glu	
25 30 35 40	
gcc aaa gag ttg tac cga gac tat aac cac ggt gtg ctg aag ata acc	197
Ala Lys Glu Leu Tyr Arg Asp Tyr Asn His Gly Val Leu Lys Ile Thr	
41 46 51 56	
atc tgt aaa tcc tgc cag aaa cct gta gac aaa tat atc gag tat gat	245
Ile Cys Lys Ser Cys Gln Lys Pro Val Asp Lys Tyr Ile Glu Tyr Asp	
57 62 67 72	
cct gtt atc atc ttg att aat gct ata ttg tgc aaa gct cag gcc tac	293
Pro Val Ile Ile Leu Ile Asn Ala Ile Leu Cys Lys Ala Gln Ala Tyr	
73 78 83 88	
aga cat att ctt ttc aat act caa ata aat atc cat gga aaa ctc tgc	341
Arg His Ile Leu Phe Asn Thr Gln Ile Asn Ile His Gly Lys Leu Cys	
89 94 99 104	
ata ttt tgt ttg ctt tgt gaa gca tac ctg agg tgg tgg cag ctt caa	389
Ile Phe Cys Leu Leu Cys Glu Ala Tyr Leu Arg Trp Trp Gln Leu Gln	
105 110 115 120	
gat tcc aac cag aat act gcc cct gat gac ttg atc aga tat gct aag	437
Asp Ser Asn Gln Asn Thr Ala Pro Asp Asp Leu Ile Arg Tyr Ala Lys	
121 126 131 136	
gaa tgg gat ttc tat aga atg ttt gcg att gct gct tta gaa caa act	485
Glu Trp Asp Phe Tyr Arg Met Phe Ala Ile Ala Ala Leu Glu Gln Thr	
137 142 147 152	
gcc tat ttt att ggc att ttt acc ttc ctg tgg gta gaa cgg ccc atg	533
Ala Tyr Phe Ile Gly Ile Phe Thr Phe Leu Trp Val Glu Arg Pro Met	
153 158 163 168	
acg gca aaa aaa aag ccc aac ttc att ttg ctg ctg aaa gca tta tta	581
Thr Ala Lys Lys Lys Pro Asn Phe Ile Leu Leu Leu Lys Ala Leu Leu	
169 174 179 184	
tta tct agc tac gga aaa ctc ttg ctg att cca gct gtc att tgg gaa	629
Leu Ser Ser Tyr Gly Lys Leu Leu Leu Ile Pro Ala Val Ile Trp Glu	
185 190 195 200	
cat gac tac aca tct gtg tgc ctc aaa ctc att aaa gta ttt gtt ctt	677
His Asp Tyr Thr Ser Val Cys Leu Lys Leu Ile Lys Val Phe Val Leu	
201 206 211 216	
aca tca aat ttt cag gca att aga gtg acc cta aac atc aac cgt aag	725
Thr Ser Asn Phe Gln Ala Ile Arg Val Thr Leu Asn Ile Asn Arg Lys	

217	222	227	232	
ctc tcc ttc ttg gcc gtg ttg agt ggc tta ctg ctg gaa agc atc atg				773
Leu Ser Phe Leu Ala Val Leu Ser Gly Leu Leu Leu Glu Ser Ile Met				
233	238	243	248	
gtc tac ttc ttc cag agt atg gaa tgg gat gtt gga agt gat tat gcc				821
Val Tyr Phe Phe Gln Ser Met Glu Trp Asp Val Gly Ser Asp Tyr Ala				
249	254	259	264	
atc ttt aaa tct cag gac ttc tga agagttttat tcttcttcac tatctgtggc				875
Ile Phe Lys Ser Gln Asp Phe *				
265	270			
atgaccagct gtatctgaaa gagaaaagac atgaaatata aaccaacctc ctcatttctg				935
ttgagtaaaa tgaagcaaag attggaaaca ctttctgaaa aagaaagcaa tgataatagc				995
ggtggatacc cccccccaca aatgcaccca agagacaagc catttacata cagatattca				1055
cagtcacaca tagaaacacc cacatggaca caaggaatgt tgctgcagag actgaatgac				1115
atgcaacagg tgaaggttta tacgttatac acaaggccag gtaagcgctc ataattcaca				1175
cataataaaa catctagggtt tcattccttt gacatgttta tatcttttta atttaaattgt				1235
tgttactggc ttaaaatatt ttgtgttctt acaatagaaa cgcttttaaat aaagtctttc				1295
agaataaacc aagtttttgt aaattttcaa ttcaataatt aaggtaattct ttaaaattgg				1355
atgatccaaa aataagtgat aatgaaaacc actgagttat atactttgca agggtaaatt				1415
acatctgaat aaagctgtaa ttaaaaacaa aaaaa				1450

<210> 293
 <211> 2659
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (230) .. (2164)

<400> 293	
ggtccggaat tcccgggtcg acgatttcgt cgccggggag cagtccgcta cggagctcca	60
tccttctctt gagacgggga ccaggggatg gcagccatgc acctgacagc ctggccccag	120
gaacctattg tttcagaagt cggtgacctt tgaggacgtg gctgtgtact tcaccaggc	180
ggaatgggat ggccgtgtccc ctgcacagag gaccctgtac agggatgtg	235
	atg ctg
	Met Leu
	1

gag aat tat ggg aat gtg gca tcc ctg gga ttt cca ctt ctc aaa cct	283
Glu Asn Tyr Gly Asn Val Ala Ser Leu Gly Phe Pro Leu Leu Lys Pro	
3 8 13 18	
gct gtg atc tca caa ctg gag gga gga agt gag ctg ggg ggc tca tct	331
Ala Val Ile Ser Gln Leu Glu Gly Gly Ser Glu Leu Gly Gly Ser Ser	
19 24 29 34	
cca ctg gct gca gga aca ggc ctc cag ggc ctc cag act gta gat att	379
Pro Leu Ala Ala Gly Thr Gly Leu Gln Gly Leu Gln Thr Val Asp Ile	
35 40 45 50	
cag act gac aat gat ttg aca aag gaa atg tat gaa gga aaa gag aat	427
Gln Thr Asp Asn Asp Leu Thr Lys Glu Met Tyr Glu Gly Lys Glu Asn	
51 56 61 66	
gta tca ttt gaa ctt caa aga gac ttt tcc cag gaa aca gac ttt tca	475
Val Ser Phe Glu Leu Gln Arg Asp Phe Ser Gln Glu Thr Asp Phe Ser	
67 72 77 82	
gaa gcc tct ctt cta gag aaa caa cag gaa gtc cac tca gca gga aat	523
Glu Ala Ser Leu Leu Glu Lys Gln Gln Glu Val His Ser Ala Gly Asn	
83 88 93 98	
ata aag aag gag aag agc aac acc att gat gga aca gtg aaa gat gag	571
Ile Lys Lys Glu Lys Ser Asn Thr Ile Asp Gly Thr Val Lys Asp Glu	
99 104 109 114	
aca agc ccc gtg gag gag tgt ttt ttt agt caa agt tca aac tca tat	619
Thr Ser Pro Val Glu Glu Cys Phe Phe Ser Gln Ser Ser Asn Ser Tyr	
115 120 125 130	
cag tgt cat acc atc act gga gag cag ccc tct ggg tgt aca gga ttg	667
Gln Cys His Thr Ile Thr Gly Glu Gln Pro Ser Gly Cys Thr Gly Leu	
131 136 141 146	
ggg aaa tcc atc agc ttt gat aca aaa ctc gtg aag cat gaa ata att	715
Gly Lys Ser Ile Ser Phe Asp Thr Lys Leu Val Lys His Glu Ile Ile	
147 152 157 162	
aat tct gag gaa aga cct ttc aaa tgt gaa gaa tta gta gag ccc ttt	763
Asn Ser Glu Glu Arg Pro Phe Lys Cys Glu Glu Leu Val Glu Pro Phe	
163 168 173 178	
agg tgt gac tct caa ctt att caa cat caa gag aac aac act gag gaa	811
Arg Cys Asp Ser Gln Leu Ile Gln His Gln Glu Asn Asn Thr Glu Glu	
179 184 189 194	
aag cct tat cag tgt tcg gag tgt ggc aaa gct ttc agc att aat gag	859
Lys Pro Tyr Gln Cys Ser Glu Cys Gly Lys Ala Phe Ser Ile Asn Glu	
195 200 205 210	
aaa tta att tgg cat cag aga ctt cac agt ggg gag aaa ccc ttc aaa	907
Lys Leu Ile Trp His Gln Arg Leu His Ser Gly Glu Lys Pro Phe Lys	
211 216 221 226	
tgt gtg gag tgt ggg aaa agc ttc agc tac agt tcc cat tat atc aca	955

Cys Val Glu Cys Gly Lys Ser Phe Ser Tyr Ser Ser His Tyr Ile Thr	
227 232 237 242	
cat cag aca atc cac agt ggg gag aag ccc tat cag tgt aag atg tgt	1003
His Gln Thr Ile His Ser Gly Glu Lys Pro Tyr Gln Cys Lys Met Cys	
243 248 253 258	
ggg aag gcc ttc agt gtt aat gga agc cta agt agg cat cag aga atc	1051
Gly Lys Ala Phe Ser Val Asn Gly Ser Leu Ser Arg His Gln Arg Ile	
259 264 269 274	
cat acg gga gag aag ccc tat cag tgc aag gaa tgt gga aat ggc ttc	1099
His Thr Gly Glu Lys Pro Tyr Gln Cys Lys Glu Cys Gly Asn Gly Phe	
275 280 285 290	
agc tgt agt tct gca tat att aca cat cag aga gtc cac act gga gag	1147
Ser Cys Ser Ser Ala Tyr Ile Thr His Gln Arg Val His Thr Gly Glu	
291 296 301 306	
aaa cct tac gag tgt aat gac tgt ggg aaa gcg ttc aat gtt aat gca	1195
Lys Pro Tyr Glu Cys Asn Asp Cys Gly Lys Ala Phe Asn Val Asn Ala	
307 312 317 322	
aaa tta att caa cat cag aga atc cat act gga gag aaa cct tat gaa	1243
Lys Leu Ile Gln His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Glu	
323 328 333 338	
tgt aat gaa tgt gga aaa ggc ttc agg tgc agc tcc cag ctt agg cag	1291
Cys Asn Glu Cys Gly Lys Gly Phe Arg Cys Ser Ser Gln Leu Arg Gln	
339 344 349 354	
cat cag agc atc cac aca gga gaa aag ccc tat cag tgt aaa gag tgt	1339
His Gln Ser Ile His Thr Gly Glu Lys Pro Tyr Gln Cys Lys Glu Cys	
355 360 365 370	
gga aaa ggc ttc aat aat aat aca aaa ctc att cag cat cag aga atc	1387
Gly Lys Gly Phe Asn Asn Asn Thr Lys Leu Ile Gln His Gln Arg Ile	
371 376 381 386	
cac aca ggt gag aaa ccc tat gaa tgc act gaa tgt gga aaa gcc ttc	1435
His Thr Gly Glu Lys Pro Tyr Glu Cys Thr Glu Cys Gly Lys Ala Phe	
387 392 397 402	
agt gtc aaa ggg aag tta atc caa cac cag aga att cac aca ggc gag	1483
Ser Val Lys Gly Lys Leu Ile Gln His Gln Arg Ile His Thr Gly Glu	
403 408 413 418	
aaa ccc tat gag tgt aat gaa tgc ggg aaa gcc ttc aga tgt aac tcc	1531
Lys Pro Tyr Glu Cys Asn Glu Cys Gly Lys Ala Phe Arg Cys Asn Ser	
419 424 429 434	
caa ttt cgg cag cat ctg aga att cac act ggg gag aag ccc tat gag	1579
Gln Phe Arg Gln His Leu Arg Ile His Thr Gly Glu Lys Pro Tyr Glu	
435 440 445 450	
tgt aat gag tgt gga aag gcc ttc agc gtt aat ggg aaa cta atg cgg	1627
Cys Asn Glu Cys Gly Lys Ala Phe Ser Val Asn Gly Lys Leu Met Arg	

451	456	461	466	
cat cag aga att cac	act ggg gag aaa cct	ttt gaa tgt aat gag	tgt	1675
His Gln Arg Ile His	Thr Gly Glu Lys Pro	Phe Glu Cys Asn Glu	Cys	
467	472	477	482	
ggg aga tgc ttt act	tct aaa aga aac cta	ctt gat cat cac cga	atc	1723
Gly Arg Cys Phe Thr	Ser Lys Arg Asn Leu	Leu Asp His His Arg	Ile	
483	488	493	498	
cat act gga gaa aag	ccc tat caa tgt aag	gaa tgt ggg aaa gcc	ttc	1771
His Thr Gly Glu Lys	Pro Tyr Gln Cys Lys	Glu Cys Gly Lys Ala	Phe	
499	504	509	514	
agt atc aat gcc aaa	cta act agg cat cag	agg ata cat act ggg	gag	1819
Ser Ile Asn Ala Lys	Leu Thr Arg His Gln	Arg Ile His Thr Gly	Glu	
515	520	525	530	
aaa cct ttc aaa tgt	atg gaa tgt gag aaa	gca ttc agc tgt agt	tct	1867
Lys Pro Phe Lys Cys	Met Glu Cys Glu Lys	Ala Phe Ser Cys Ser	Ser	
531	536	541	546	
aac tat att gtg cac	cag aga atc cat aca	gga gag aaa ccc ttt	cag	1915
Asn Tyr Ile Val His	Gln Arg Ile His Thr	Gly Glu Lys Pro Phe	Gln	
547	552	557	562	
tgt aag gag tgt gga	aaa gcc ttc cat gtt	aat gcc cat tta att	cgg	1963
Cys Lys Glu Cys Gly	Lys Ala Phe His Val	Asn Ala His Leu Ile	Arg	
563	568	573	578	
cat cag aga agc cac	act ggg gag aaa ccc	ttc aga tgt gtg gaa	tgt	2011
His Gln Arg Ser His	Thr Gly Glu Lys Pro	Phe Arg Cys Val Glu	Cys	
579	584	589	594	
ggc aaa ggc ttc agc	ttt agt tct gac tac	att ata cat cag aca	gtc	2059
Gly Lys Gly Phe Ser	Phe Ser Ser Asp Tyr	Ile Ile His Gln Thr	Val	
595	600	605	610	
cac act tgg aag aaa	ccc tat atg tgt agt	gtg tgt ggg aaa gca	ttc	2107
His Thr Trp Lys Lys	Pro Tyr Met Cys Ser	Val Cys Gly Lys Ala	Phe	
611	616	621	626	
agg ttt agc ttc cag	ctc agt cag cat cag	agt gtc cat agt gaa	gga	2155
Arg Phe Ser Phe Gln	Leu Ser Gln His Gln	Ser Val His Ser Glu	Gly	
627	632	637	642	
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Lys Ser *				
643				
caagtatcat cagattcatc	cattgaaaaa cctccaagag	ggcatgaata tggcagagtc		2271
ttcatatgga aacagttttt	attctattca gtttaaata	ggaaaggatg accagttaaa		2331
gagaaacatc caaaaatagc	tttgttttgt accaacagga	attagaaaat ataataaaaa		2391
gatttcgttc ccagcagcat	caagaaaagt agattttcta	gaaataaaca gttatggagg		2451

acttgatatgg agaaatttaa gtcttcactg agggccactt tacaaaggaa atttgaataa 2511
atggagagag agagaagcct tggtgttgga taggaaaacc cgtactaaag atactctacc 2571
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His Ala Tyr Val Ser Leu Asp Pro Leu Glu Arg Pro Pro Thr Thr Thr
2 7 12 17

aaa ttc gcg gcc gcg tcc gac cgc cgc cgc gcc gcc atc atg gac acc 151
Lys Phe Ala Ala Ala Ser Asp Arg Arg Arg Ala Ala Ile Met Asp Thr
18 23 28 33

agc cgt gtg cag cct atc aag ctg gcc agg gtc acc aag gtc ctg ggc 199
Ser Arg Val Gln Pro Ile Lys Leu Ala Arg Val Thr Lys Val Leu Gly
34 39 44 49

agg acc ggt tct cag gga cag tgc acg cag gtg cgc gtg gaa ttc atg 247
Arg Thr Gly Ser Gln Gly Gln Cys Thr Gln Val Arg Val Glu Phe Met
50 55 60 65

gac gac acg agc cga tcc atc atc cgc aat gta aaa ggc ccc gtg cgc 295
Asp Asp Thr Ser Arg Ser Ile Ile Arg Asn Val Lys Gly Pro Val Arg
66 71 76 81

gag ggc gac gtg ctc acc ctt ttg gag tca gag cga gaa gcc cgg agg 343
Glu Gly Asp Val Leu Thr Leu Leu Glu Ser Glu Arg Glu Ala Arg Arg
82 87 92 97

ttg cgc tga gcttggc tgctcgtgg gtcttggatg tcgggttcga ccacttggcc 399
Leu Arg *
98

gatgggaatg gtctgtcaca atctgtcct tttttttgtc cgccacacgt aactgagatg 459
ctcctttaa taaagcgttt gtgtttcaag ttaactcaga aaaaaaaaaa a 510

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 caccaa atg gcg gat gac gcc ggt gca gcg ggg ggg ccc ggg ggc cct 108
 Met Ala Asp Asp Ala Gly Ala Ala Gly Gly Pro Gly Gly Pro
 1 5 10
 ggt ggc cct ggg atg ggg aac cgc ggt ggc ttc cgc gga ggt ttc ggc 156
 Gly Gly Pro Gly Met Gly Asn Arg Gly Gly Phe Arg Gly Gly Phe Gly
 15 20 25 30
 agt ggc atc cgg ggc cgg ggt cgc ggc cgt gga cgg ggc cgg ggc cga 204
 Ser Gly Ile Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg
 31 36 41 46
 ggc cgc gga gct cgc gga ggc aag gcc gag gat aag gag tgg atg ccc 252
 Gly Arg Gly Ala Arg Gly Gly Lys Ala Glu Asp Lys Glu Trp Met Pro
 47 52 57 62
 gtc acc aag ttg ggc cgc ttg gtc aag gac atg aag atc aag tcc ctg 300
 Val Thr Lys Leu Gly Arg Leu Val Lys Asp Met Lys Ile Lys Ser Leu
 63 68 73 78
 gag gag atc tat ctc ttc tcc ctg ccc att aag gaa tca gag atc att 348
 Glu Glu Ile Tyr Leu Phe Ser Leu Pro Ile Lys Glu Ser Glu Ile Ile
 79 84 89 94
 gat ttc ttc ctg ggg gcc tct ctc aag gat gag gtt ttg aag att atg 396
 Asp Phe Phe Leu Gly Ala Ser Leu Lys Asp Glu Val Leu Lys Ile Met
 95 100 105 110
 cca gtg cag aag cag acc cgt gcc ggc cag cgc acc agg ttc aag gca 444
 Pro Val Gln Lys Gln Thr Arg Ala Gly Gln Arg Thr Arg Phe Lys Ala
 111 116 121 126
 ttt gtt gct atc ggg gac tac aat ggc cac gtc ggt ctg ggt gtt aag 492
 Phe Val Ala Ile Gly Asp Tyr Asn Gly His Val Gly Leu Gly Val Lys
 127 132 137 142
 tgc tcc aag gag gtg gcc acc gcc atc cgt ggg gcc atc atc ctg gcc 540
 Cys Ser Lys Glu Val Ala Thr Ala Ile Arg Gly Ala Ile Ile Leu Ala
 143 148 153 158
 aag ctc tcc atc gtc ccc gtg cgc aga ggc tac tgg ggg aac aag atc 588

Lys	Leu	Ser	Ile	Val	Pro	Val	Arg	Arg	Gly	Tyr	Trp	Gly	Asn	Lys	Ile	
159					164					169					174	
ggc	aag	ccc	cac	act	gtc	cct	tgc	aag	gtg	aca	ggc	cgc	tgc	ggc	tct	636
Gly	Lys	Pro	His	Thr	Val	Pro	Cys	Lys	Val	Thr	Gly	Arg	Cys	Gly	Ser	
175					180					185					190	
gtg	ctg	gta	cgc	ctc	atc	cct	gca	ccc	agg	ggc	act	ggc	atc	gtc	tcc	684
Val	Leu	Val	Arg	Leu	Ile	Pro	Ala	Pro	Arg	Gly	Thr	Gly	Ile	Val	Ser	
191					196					201					206	
gca	cct	gtg	cct	aag	aag	ctg	ctc	atg	atg	gct	ggg	atc	gat	gac	tgc	732
Ala	Pro	Val	Pro	Lys	Lys	Leu	Leu	Met	Met	Ala	Gly	Ile	Asp	Asp	Cys	
207					212					217					222	
tac	acc	tca	gcc	cgg	ggc	tgc	act	gcc	acc	ctg	ggc	aac	ttc	gcc	aag	780
Tyr	Thr	Ser	Ala	Arg	Gly	Cys	Thr	Ala	Thr	Leu	Gly	Asn	Phe	Ala	Lys	
223					228					233					238	
gcc	acc	ttt	gat	gcc	att	tct	aag	acc	tac	agc	tac	ctg	acc	ccc	gac	828
Ala	Thr	Phe	Asp	Ala	Ile	Ser	Lys	Thr	Tyr	Ser	Tyr	Leu	Thr	Pro	Asp	
239					244					249					254	
ctc	tgg	aag	gag	act	gta	ttc	acc	aag	tct	ccc	tat	cag	gag	ttc	act	876
Leu	Trp	Lys	Glu	Thr	Val	Phe	Thr	Lys	Ser	Pro	Tyr	Gln	Glu	Phe	Thr	
255					260					265					270	
gac	cac	ctc	gtc	aag	acc	cac	acc	aga	gtc	tcc	gtg	cag	cgg	act	cag	924
Asp	His	Leu	Val	Lys	Thr	His	Thr	Arg	Val	Ser	Val	Gln	Arg	Thr	Gln	
271					276					281					286	
gct	cca	gct	gtg	gct	aca	aca	tag	gggtttttata	caagaaaaaat	aaagtgaatt						978
Ala	Pro	Ala	Val	Ala	Thr	Thr	*									
287					292											
aagcgtgaaa	aaaaaaaaa															997

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gcatgagacc gtgagacgag agacgggtcg gggccgccga c atg ttt ggc cgc	173
Met Phe Gly Arg	

tcg cgg agc tgg gtg ggc ggg ggc cat ggc aag act tcc cgc aac atc	221
Ser Arg Ser Trp Val Gly Gly Gly His Gly Lys Thr Ser Arg Asn Ile	
5 10 15 20	
cac tcc ttg gac cac ctc aag tat ctg tac cac gtt ttg acc aaa aac	269
His Ser Leu Asp His Leu Lys Tyr Leu Tyr His Val Leu Thr Lys Asn	
21 26 31 36	
acc aca gtc aca gaa cag aac cgg aac ctg cta gtg gag acc atc cgt	317
Thr Thr Val Thr Glu Gln Asn Arg Asn Leu Leu Val Glu Thr Ile Arg	
37 42 47 52	
tcc atc act gag atc ctg atc tgg gga gat caa aat gac agc tct gta	365
Ser Ile Thr Glu Ile Leu Ile Trp Gly Asp Gln Asn Asp Ser Ser Val	
53 58 63 68	
ttt gac ttc ttc ctg gag aag aat atg ttt gtt ttc ttc ttg aac atc	413
Phe Asp Phe Phe Leu Glu Lys Asn Met Phe Val Phe Phe Leu Asn Ile	
69 74 79 84	
ttg cgg caa aag tcg ggc cgt tac gtg tgc gtt cag ctg ctg cag acc	461
Leu Arg Gln Lys Ser Gly Arg Tyr Val Cys Val Gln Leu Leu Gln Thr	
85 90 95 100	
ttg aac atc ctc ttt gag aac atc agt cac gag acc tca ctt tat tat	509
Leu Asn Ile Leu Phe Glu Asn Ile Ser His Glu Thr Ser Leu Tyr Tyr	
101 106 111 116	
ttg ctc tca aat aac tac gta aat tct atc atc gtt cat aaa ttt gac	557
Leu Leu Ser Asn Asn Tyr Val Asn Ser Ile Ile Val His Lys Phe Asp	
117 122 127 132	
ttt tct gat gag gag att atg gcc tat tat ata tcg ttc ctg aaa aca	605
Phe Ser Asp Glu Glu Ile Met Ala Tyr Tyr Ile Ser Phe Leu Lys Thr	
133 138 143 148	
ctt tcg tta aaa ctc aac aac cac act gtc cat ttc ttt tat aat gag	653
Leu Ser Leu Lys Leu Asn Asn His Thr Val His Phe Phe Tyr Asn Glu	
149 154 159 164	
cac acc aat gac ttt gcc ctg tac aca gaa gcc atc aag ttt ttc aac	701
His Thr Asn Asp Phe Ala Leu Tyr Thr Glu Ala Ile Lys Phe Phe Asn	
165 170 175 180	
cac cct gaa agc atg gtt aga att gct gta aga acc ata act ttg aat	749
His Pro Glu Ser Met Val Arg Ile Ala Val Arg Thr Ile Thr Leu Asn	
181 186 191 196	
gtc tat aaa gtg tca ttg gat aac cag gcc atg ctg cac tac atc cga	797
Val Tyr Lys Val Ser Leu Asp Asn Gln Ala Met Leu His Tyr Ile Arg	
197 202 207 212	
gat aaa act gct gtt cct tac ttc tcc aat ttg gtc tgg ttc att ggg	845
Asp Lys Thr Ala Val Pro Tyr Phe Ser Asn Leu Val Trp Phe Ile Gly	
213 218 223 228	

agc cat gtg atc gaa ctc gat gac tgc gtg cag act gat gag gag cat	893
Ser His Val Ile Glu Leu Asp Asp Cys Val Gln Thr Asp Glu Glu His	
229 234 239 244	
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Arg Asn Arg Gly Lys Leu Ser Asp Leu Val Ala Glu His Leu Asp His	
245 250 255 260	
ctg cac tat ctc aat gac atc ctg atc atc aac tgt gag ttc ctc aac	989
Leu His Tyr Leu Asn Asp Ile Leu Ile Ile Asn Cys Glu Phe Leu Asn	
261 266 271 276	
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Asp Val Leu Thr Asp His Leu Leu Asn Arg Leu Phe Leu Pro Leu Tyr	
277 282 287 292	
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Val Tyr Ser Leu Glu Asn Gln Asp Lys Gly Gly Glu Arg Pro Lys Ile	
293 298 303 308	
agc ctg ccg gtg tct ctt tat ctt ctg tca cag gtc ttc tta att ata	1133
Ser Leu Pro Val Ser Leu Tyr Leu Leu Ser Gln Val Phe Leu Ile Ile	
309 314 319 324	
cat cat gca ccg ctg gtg aac tcg tta gct gaa gtc att ctg aat ggt	1181
His His Ala Pro Leu Val Asn Ser Leu Ala Glu Val Ile Leu Asn Gly	
325 330 335 340	
gat ctg tct gag atg tac gct aag act gaa cag gat att cag aga agt	1229
Asp Leu Ser Glu Met Tyr Ala Lys Thr Glu Gln Asp Ile Gln Arg Ser	
341 346 351 356	
tct gcc aag ccc agc att cgg tgc ttc att aaa ccc acc gag aca ctc	1277
Ser Ala Lys Pro Ser Ile Arg Cys Phe Ile Lys Pro Thr Glu Thr Leu	
357 362 367 372	
gag cgg tcc ctt gag atg aac aag cac aag ggc aag agg cgg gtg caa	1325
Glu Arg Ser Leu Glu Met Asn Lys His Lys Gly Lys Arg Arg Val Gln	
373 378 383 388	
aag aga ccc aac tac aaa aac gtt ggg gaa gaa gaa gat gag gag aaa	1373
Lys Arg Pro Asn Tyr Lys Asn Val Gly Glu Glu Glu Asp Glu Glu Lys	
389 394 399 404	
ggg ccc acc gag gat gcc caa gaa gac gcc gag aag gct aaa ggt aca	1421
Gly Pro Thr Glu Asp Ala Gln Glu Asp Ala Glu Lys Ala Lys Gly Thr	
405 410 415 420	
gag ggt ggt tca aaa ggc atc aag acg agt ggg gag agt gaa gag atc	1469
Glu Gly Gly Ser Lys Gly Ile Lys Thr Ser Gly Glu Ser Glu Glu Ile	
421 426 431 436	
gag atg gtg atc atg gag cgt agc aag ctc tca gag ctg gcc gcc agc	1517
Glu Met Val Ile Met Glu Arg Ser Lys Leu Ser Glu Leu Ala Ala Ser	
437 442 447 452	
acc tcc gtg cag gag cag aac acc acg gac gag gag aaa agc gcc gcc	1565

Thr	Ser	Val	Gln	Glu	Gln	Asn	Thr	Thr	Asp	Glu	Glu	Lys	Ser	Ala	Ala	
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Ala	Thr	Cys	Ser	Glu	Ser	Thr	Gln	Trp	Ser	Arg	Pro	Phe	Leu	Asp	Met	
469					474					479					484	
gtg	tac	cac	gcg	ctg	gac	agc	ccg	gat	gat	gat	tac	cat	gcc	ctg	ttc	1661
Val	Tyr	His	Ala	Leu	Asp	Ser	Pro	Asp	Asp	Asp	Tyr	His	Ala	Leu	Phe	
485					490					495					500	
gtg	ctc	tgc	ctc	ctc	tat	gcc	atg	tct	cat	aat	aaa	ggc	atg	gat	cct	1709
Val	Leu	Cys	Leu	Leu	Tyr	Ala	Met	Ser	His	Asn	Lys	Gly	Met	Asp	Pro	
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gaa	aaa	tta	gag	cga	atc	cag	ctc	ccc	gtg	cca	aat	gcg	gcc	gag	aag	1757
Glu	Lys	Leu	Glu	Arg	Ile	Gln	Leu	Pro	Val	Pro	Asn	Ala	Ala	Glu	Lys	
517					522					527					532	
acc	acc	tac	aac	cac	ccg	cta	gct	gaa	aga	ctc	atc	agg	atc	atg	aac	1805
Thr	Thr	Tyr	Asn	His	Pro	Leu	Ala	Glu	Arg	Leu	Ile	Arg	Ile	Met	Asn	
533					538					543					548	
aac	gct	gcc	cag	cca	gat	ggg	aag	atc	cgg	ctg	gcg	acg	ctg	gag	ctg	1853
Asn	Ala	Ala	Gln	Pro	Asp	Gly	Lys	Ile	Arg	Leu	Ala	Thr	Leu	Glu	Leu	
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Ser	Cys	Leu	Leu	Leu	Lys	Gln	Gln	Val	Leu	Met	Ser	Ala	Gly	Cys	Ile	
565					570					575					580	
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581					586					591					596	
gtt	cac	ctt	gta	cga	cat	ttt	tat	aag	gga	gaa	gac	att	ttt	ttg	gac	1997
Val	His	Leu	Val	Arg	His	Phe	Tyr	Lys	Gly	Glu	Asp	Ile	Phe	Leu	Asp	
597					602					607					612	
atg	ttt	gaa	gat	gag	tat	agg	agc	atg	aca	atg	aag	ccc	atg	aac	gtg	2045
Met	Phe	Glu	Asp	Glu	Tyr	Arg	Ser	Met	Thr	Met	Lys	Pro	Met	Asn	Val	
613					618					623					628	
gaa	tat	ctc	atg	atg	gac	gcc	tcc	atc	ctg	ctg	ccc	cca	aca	ggc	acg	2093
Glu	Tyr	Leu	Met	Met	Asp	Ala	Ser	Ile	Leu	Leu	Pro	Pro	Thr	Gly	Thr	
629					634					639					644	
cca	ctg	acg	ggc	att	gac	ttc	gtg	aag	cgg	ctg	ccg	tgt	ggc	gat	gtg	2141
Pro	Leu	Thr	Gly	Ile	Asp	Phe	Val	Lys	Arg	Leu	Pro	Cys	Gly	Asp	Val	
645					650					655					660	
gag	aag	acc	cgg	cgg	gcc	atc	cgg	gtg	ttc	ttc	atg	ctg	cgt	tcc	ctg	2189
Glu	Lys	Thr	Arg	Arg	Ala	Ile	Arg	Val	Phe	Phe	Met	Leu	Arg	Ser	Leu	
661					666					671					676	
tca	ctg	caa	ttg	cga	ggg	gag	cct	gag	aca	cag	ttg	ccg	ctg	act	cgg	2237
Ser	Leu	Gln	Leu	Arg	Gly	Glu	Pro	Glu	Thr	Gln	Leu	Pro	Leu	Thr	Arg	

677	682	687	692	
gag gag gac ctg atc	aag act gat gat gtc	ctg gat ctg aat aac agc	2285	
Glu Glu Asp Leu Ile	Lys Thr Asp Asp Val	Leu Asp Leu Asn Asn Ser		
693	698	703	708	
gac ttg att gca tgt	aca gtg atc acc aag	gat ggc ggc atg gtc cag	2333	
Asp Leu Ile Ala Cys	Thr Val Ile Thr Lys	Asp Gly Gly Met Val Gln		
709	714	719	724	
cga ttc ctg gct gtg	gat att tac cag atg	agt ttg gtg gag cct gat	2381	
Arg Phe Leu Ala Val	Asp Ile Tyr Gln Met	Ser Leu Val Glu Pro Asp		
725	730	735	740	
gtg tcc agg ctt ggc	tgg gga gtg gtc aag	ttt gca ggc cta ttg cag	2429	
Val Ser Arg Leu Gly	Trp Gly Val Val Lys	Phe Ala Gly Leu Leu Gln		
741	746	751	756	
gac atg cag gtg act	ggc gtg gag gac gac	agc cgt gcc ctg aac atc	2477	
Asp Met Gln Val Thr	Gly Val Glu Asp Asp	Ser Arg Ala Leu Asn Ile		
757	762	767	772	
acc atc cac aag cct	gcg tcc agc ccc cat	tcc aag ccc ttc ccc atc	2525	
Thr Ile His Lys Pro	Ala Ser Ser Pro His	Ser Lys Pro Phe Pro Ile		
773	778	783	788	
ctc cag gcc acc ttc	atc ttc tca gac cac	atc cgc tgc atc atc gcc	2573	
Leu Gln Ala Thr Phe	Ile Phe Ser Asp His	Ile Arg Cys Ile Ile Ala		
789	794	799	804	
aag cag cgc ctg gcc	aaa ggc cgc atc cag	gca agg cgc atg aag atg	2621	
Lys Gln Arg Leu Ala	Lys Gly Arg Ile Gln	Ala Arg Arg Met Lys Met		
805	810	815	820	
cag aga ata gct gcc	ctc ctg gac ctc cca	atc cag ccc acc act gaa	2669	
Gln Arg Ile Ala Ala	Leu Leu Asp Leu Pro	Ile Gln Pro Thr Thr Glu		
821	826	831	836	
gtc ctg ggg ttt gga	ctc ggc tcc tcc acc	tcc act cag cac ctg cct	2717	
Val Leu Gly Phe Gly	Leu Gly Ser Ser Thr	Ser Thr Gln His Leu Pro		
837	842	847	852	
ttc cgc ttc tac gac	cag ggg cgc cgg ggc	agc agc gac ccc aca gtg	2765	
Phe Arg Phe Tyr Asp	Gln Gly Arg Arg Gly	Ser Ser Asp Pro Thr Val		
853	858	863	868	
cag cgc tcc gtg ttt	gca tcg gtg gac aag	gtg cca ggc ttc gcc gtg	2813	
Gln Arg Ser Val Phe	Ala Ser Val Asp Lys	Val Pro Gly Phe Ala Val		
869	874	879	884	
gcc cag tgc ata aac	cag cac agc tcc ccg	tcc ctg tcc tca cag tcg	2861	
Ala Gln Cys Ile Asn	Gln His Ser Ser Pro	Ser Leu Ser Ser Gln Ser		
885	890	895	900	
cca ccc tcc gcc agc	ggg agc ccc agc ggc	agc ggg agc acc agc cac	2909	
Pro Pro Ser Ala Ser	Gly Ser Pro Ser Gly	Ser Gly Ser Thr Ser His		
901	906	911	916	

tgc gac tct gga ggc acc agc tcg tcc tcc acc ccc tcc aca gcc cag	2957
Cys Asp Ser Gly Gly Thr Ser Ser Ser Ser Thr Pro Ser Thr Ala Gln	
917 922 927 932	
agt cca gca gat gcc ccc atg agt cca gaa ctg cct aag cct cac ctt	3005
Ser Pro Ala Asp Ala Pro Met Ser Pro Glu Leu Pro Lys Pro His Leu	
933 938 943 948	
cct gac cag ttg gta atc gtc aac gaa acg gaa gca gac tct aag ccc	3053
Pro Asp Gln Leu Val Ile Val Asn Glu Thr Glu Ala Asp Ser Lys Pro	
949 954 959 964	
agc aag aac gtg gcc agg agc gca gcc gtg gag aca gcc agc ctg tcc	3101
Ser Lys Asn Val Ala Arg Ser Ala Ala Val Glu Thr Ala Ser Leu Ser	
965 970 975 980	
ccc agc ctc gtc cct gcc cgg cag ccc acc att tcc ctg ctc tgc gag	3149
Pro Ser Leu Val Pro Ala Arg Gln Pro Thr Ile Ser Leu Leu Cys Glu	
981 986 991 996	
gac acg gct gac acg ctg agc gtc gaa tcg ctg acc ctt gtc ccc cca	3197
Asp Thr Ala Asp Thr Leu Ser Val Glu Ser Leu Thr Leu Val Pro Pro	
997 1002 1007 1012	
gtt gac ccc cac agc ctc cgc agc ctc acc ggc atg ccc ccg ctg tcc	3245
Val Asp Pro His Ser Leu Arg Ser Leu Thr Gly Met Pro Pro Leu Ser	
1013 1018 1023 1028	
acg ccg gct gcc gcc tgc aca gag ccc gtg ggc gaa gag gct gca tgt	3293
Thr Pro Ala Ala Ala Cys Thr Glu Pro Val Gly Glu Glu Ala Ala Cys	
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Ala Glu Pro Val Gly Thr Ala Glu Asp *	
1045 1050	

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gccaaaaata ctgagtaact tcacattcag agggactgtt ttttctctct atatatagca	180

14	19	24	29	
gag ctg gac cag agg acg gaa gat aag aaa gca gag att gac atc ctg				385
Glu Leu Asp Gln Arg Thr Glu Asp Lys Lys Ala Glu Ile Asp Ile Leu				
30	35	40	45	
gct gca gag tac atc tcc acg gtg aag acg ctg tct cca gac cag cgc				433
Ala Ala Glu Tyr Ile Ser Thr Val Lys Thr Leu Ser Pro Asp Gln Arg				
46	51	56	61	
gtg gag cgc ctg cag aag atc cag aac gcc tac agc aag tgc aag gaa				481
Val Glu Arg Leu Gln Lys Ile Gln Asn Ala Tyr Ser Lys Cys Lys Glu				
62	67	72	77	
tac agt gac gac aaa gtg cag ctg gcc atg cag acc tac gag atg gtg				529
Tyr Ser Asp Asp Lys Val Gln Leu Ala Met Gln Thr Tyr Glu Met Val				
78	83	88	93	
gat aaa cac att cga agg ctt gat gca gac ctg gcg cgc ttt gaa gca				577
Asp Lys His Ile Arg Arg Leu Asp Ala Asp Leu Ala Arg Phe Glu Ala				
94	99	104	109	
gat ctg aag gac aag atg gag ggc agt gat ttt gaa agc tcc gga ggg				625
Asp Leu Lys Asp Lys Met Glu Gly Ser Asp Phe Glu Ser Ser Gly Gly				
110	115	120	125	
cga ggg tta aaa aaa ggc ctg cgt cag aaa gaa aaa aga ggg tcc cgg				673
Arg Gly Leu Lys Lys Gly Leu Arg Gln Lys Glu Lys Arg Gly Ser Arg				
126	131	136	141	
ggc cga ggc agg agg aca tca gag gaa gac aca cca aag aaa aag aag				721
Gly Arg Gly Arg Arg Thr Ser Glu Glu Asp Thr Pro Lys Lys Lys Lys				
142	147	152	157	
cac aaa gga ggg tct gag ttc act gac acc atc ctg tcc gtg cac ccc				769
His Lys Gly Gly Ser Glu Phe Thr Asp Thr Ile Leu Ser Val His Pro				
158	163	168	173	
tct gat gtg ctg gac atg ccc gtg gac cca aac gaa ccc acg tac tgc				817
Ser Asp Val Leu Asp Met Pro Val Asp Pro Asn Glu Pro Thr Tyr Cys				
174	179	184	189	
ctg tgc cac cag gtc tcc tat ggg gag atg att ggc tgt gac aat cca				865
Leu Cys His Gln Val Ser Tyr Gly Glu Met Ile Gly Cys Asp Asn Pro				
190	195	200	205	
gac tgt cca att gag tgg ttt cac ttt gcc tgc gtg gac ctt acc acg				913
Asp Cys Pro Ile Glu Trp Phe His Phe Ala Cys Val Asp Leu Thr Thr				
206	211	216	221	
aaa ccc aaa gga aaa tga tttcat ttaaataaaa acctgtagtc tgggcaacat				967
Lys Pro Lys Gly Lys *				
222	227			
cgggagaccc caactctaca aaaaatacaa aaattagtgct ctgtcctctt agccacagt				1027
tgtgctgccc cactagggac aggaggatgg tgagcaacgt gttgttgaca gaggccaatg				1087

tagaccactc ttttaagtagc tagattttctg tataatctgtc agttatttta tgtgtcaaca 1147
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ttaacttgaa gttttttgag atactttatt taaagcattc tcccactgac accctccctg 1267
ccaaaggtgt tgtataccct ccaaagagat cgtagcatta cctcagagga gtggcattta 1327
gagtaaagag aaaatgctca aatgccacgt agcctctctc cagatgatct ctgagaggga 1387
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Met Pro Ala Val Arg Val Trp Asp
1 5
gtg gca gag cac agc cag gtg gcc gag ctg cag gag cac aag tat ggt 159
Val Ala Glu His Ser Gln Val Ala Glu Leu Gln Glu His Lys Tyr Gly
9 14 19 24
gtg gct tgt gtg gcc ttc tct cct agc gcc aag tac att gtc tct gtg 207
Val Ala Cys Val Ala Phe Ser Pro Ser Ala Lys Tyr Ile Val Ser Val
25 30 35 40
ggc tac cag cat gac atg atc gtc aac gtg tgg gcc tgg aag aaa aac 255
Gly Tyr Gln His Asp Met Ile Val Asn Val Trp Ala Trp Lys Lys Asn
41 46 51 56
att gtg gtg gcc tcc aac aag gtg tcc agt cgg gtg aca gca gtg tcc 303
Ile Val Val Ala Ser Asn Lys Val Ser Ser Arg Val Thr Ala Val Ser
57 62 67 72
ttc tct gag gat tgc agc tac ttt gtc act gca ggc aac cga cac atc 351
Phe Ser Glu Asp Cys Ser Tyr Phe Val Thr Ala Gly Asn Arg His Ile
73 78 83 88
aaa ttc tgg tat ctc gat gac agc aag acc tca aag gtg aat gcc act 399
Lys Phe Trp Tyr Leu Asp Asp Ser Lys Thr Ser Lys Val Asn Ala Thr
89 94 99 104

gtg ccc ttg ctg ggc cgc tca ggg ctg ctg gga gag cta cgg aac aac	447
Val Pro Leu Leu Gly Arg Ser Gly Leu Leu Gly Glu Leu Arg Asn Asn	
105 110 115 120	
cta ttc act gat gtg gcc tgt ggc aga gga aaa aag gcg gac agt acc	495
Leu Phe Thr Asp Val Ala Cys Gly Arg Gly Lys Lys Ala Asp Ser Thr	
121 126 131 136	
ttc tgc atc acg tcc tca ggg ctg ctg tgc gag ttc agt gat cga agg	543
Phe Cys Ile Thr Ser Ser Gly Leu Leu Cys Glu Phe Ser Asp Arg Arg	
137 142 147 152	
ctt ttg gac aag tgg gtg gag ctg agg gtc tac ccc gag gtg aag gat	591
Leu Leu Asp Lys Trp Val Glu Leu Arg Val Tyr Pro Glu Val Lys Asp	
153 158 163 168	
agt aac cag gcc tgc ctg ccc ccc agt tcc ttt att acc tgc tcc tca	639
Ser Asn Gln Ala Cys Leu Pro Pro Ser Ser Phe Ile Thr Cys Ser Ser	
169 174 179 184	
gac aac acc atc cgc ctg tgg aac aca gag agc tcc ggg gtg cat ggc	687
Asp Asn Thr Ile Arg Leu Trp Asn Thr Glu Ser Ser Gly Val His Gly	
185 190 195 200	
tcc acc ctc cac cga aac atc ctc agc agt gac ctc att aaa atc atc	735
Ser Thr Leu His Arg Asn Ile Leu Ser Ser Asp Leu Ile Lys Ile Ile	
201 206 211 216	
tat gtg gat ggg aac acc cag gcc ctg ctg gac aca gag ctg cct gga	783
Tyr Val Asp Gly Asn Thr Gln Ala Leu Leu Asp Thr Glu Leu Pro Gly	
217 222 227 232	
gga gac aaa gct gat gca tcc ctg ttg gat ccc cgc gtg ggc atc cgc	831
Gly Asp Lys Ala Asp Ala Ser Leu Leu Asp Pro Arg Val Gly Ile Arg	
233 238 243 248	
tcg gtg tgt gtc agc ccc aat gga cag cat cta gca tca ggg gac cgt	879
Ser Val Cys Val Ser Pro Asn Gly Gln His Leu Ala Ser Gly Asp Arg	
249 254 259 264	
atg ggc aca ctt agg gtg cac gaa ctt cag tcc ctg agt gag atg ctg	927
Met Gly Thr Leu Arg Val His Glu Leu Gln Ser Leu Ser Glu Met Leu	
265 270 275 280	
aag gtg gag gcc cat gac tct gag att ctg tgc ctg gag tat tct aag	975
Lys Val Glu Ala His Asp Ser Glu Ile Leu Cys Leu Glu Tyr Ser Lys	
281 286 291 296	
cca gac aca ggt ctg aaa ctg cta gca tcg gcg agc cgg gac cgg ctg	1023
Pro Asp Thr Gly Leu Lys Leu Leu Ala Ser Ala Ser Arg Asp Arg Leu	
297 302 307 312	
atc cat gtg ctg gat gcc ggg cgg gag tac agc cta cag cag acg ctg	1071
Ile His Val Leu Asp Ala Gly Arg Glu Tyr Ser Leu Gln Gln Thr Leu	
313 318 323 328	

gac gaa cac tca tcc tcc atc act gct gtc aag ttt gca gcc agt gat	1119
Asp Glu His Ser Ser Ser Ile Thr Ala Val Lys Phe Ala Ala Ser Asp	
329 334 339 344	
ggg caa gtc cgc atg atc agc tgt gga gca gac aag agc atc tac ttc	1167
Gly Gln Val Arg Met Ile Ser Cys Gly Ala Asp Lys Ser Ile Tyr Phe	
345 350 355 360	
cgc act gcg cag aag tct gga gat gga gtg cag ttc aca cgg aca cac	1215
Arg Thr Ala Gln Lys Ser Gly Asp Gly Val Gln Phe Thr Arg Thr His	
361 366 371 376	
cac gtg gtg cgg aag acg acc ctc tat gac atg gat gtg gag ccc agc	1263
His Val Val Arg Lys Thr Thr Leu Tyr Asp Met Asp Val Glu Pro Ser	
377 382 387 392	
tgg aag tac acg gct atc ggc tgc cag gac cga aat att cgg ata ttt	1311
Trp Lys Tyr Thr Ala Ile Gly Cys Gln Asp Arg Asn Ile Arg Ile Phe	
393 398 403 408	
aac atc agc agt gga aag cag aag aag ctg ttt aaa ggg tca cag ggt	1359
Asn Ile Ser Ser Gly Lys Gln Lys Lys Leu Phe Lys Gly Ser Gln Gly	
409 414 419 424	
gag gac ggc aca ctc att aag gtg cag aca gac ccc tca ggg atc tac	1407
Glu Asp Gly Thr Leu Ile Lys Val Gln Thr Asp Pro Ser Gly Ile Tyr	
425 430 435 440	
att gcc acc agc tgt tct gac aag aat ctc tcc att ttt gac ttc tcc	1455
Ile Ala Thr Ser Cys Ser Asp Lys Asn Leu Ser Ile Phe Asp Phe Ser	
441 446 451 456	
tca ggc gag tgc gtg gcc acc atg ttt ggc cac tca gag att gtc act	1503
Ser Gly Glu Cys Val Ala Thr Met Phe Gly His Ser Glu Ile Val Thr	
457 462 467 472	
ggc atg aaa ttt agt aat gat tgt aaa cat ctc atc tct gtg tct ggg	1551
Gly Met Lys Phe Ser Asn Asp Cys Lys His Leu Ile Ser Val Ser Gly	
473 478 483 488	
gac agc tgc ata ttt gtg tgg cgc ctg agc tct gag atg acc atc agc	1599
Asp Ser Cys Ile Phe Val Trp Arg Leu Ser Ser Glu Met Thr Ile Ser	
489 494 499 504	
atg agg cag cgt ctg gcc gag ttg cgc cag cgt cag cgg ggc ggc aag	1647
Met Arg Gln Arg Leu Ala Glu Leu Arg Gln Arg Gln Arg Gly Gly Lys	
505 510 515 520	
cag caa gga cca tcc tct ccc caa agg gct tct gga ccc aac cgg cac	1695
Gln Gln Gly Pro Ser Ser Pro Gln Arg Ala Ser Gly Pro Asn Arg His	
521 526 531 536	
cag gcc cca tca atg ctg tct cct gga ccg gct ctc tca tca gac agt	1743
Gln Ala Pro Ser Met Leu Ser Pro Gly Pro Ala Leu Ser Ser Asp Ser	
537 542 547 552	
gac aag gag gga gaa gat gag ggg act gaa gaa gaa ctt cca gca ctg	1791

Asp Lys Glu Gly Glu	Asp Glu Gly Thr Glu	Glu Glu Leu Pro Ala Leu	553	558	563	568
ccc gtc ctt gcc aag	agt acc aag aag gca	ctg gcc tcg gtc ccc agc	1839			
Pro Val Leu Ala Lys	Ser Thr Lys Lys Ala	Leu Ala Ser Val Pro Ser	569	574	579	584
cca gct ttg ccc cga	agc ctg tcc cac tgg	gag atg agt cgg gca cag	1887			
Pro Ala Leu Pro Arg	Ser Leu Ser His Trp	Glu Met Ser Arg Ala Gln	585	590	595	600
gag tcc gtg ggg ttc	ctg gac cca gct cct	gca gcc aac cca gga ccc	1935			
Glu Ser Val Gly Phe	Leu Asp Pro Ala Pro	Ala Ala Asn Pro Gly Pro	601	606	611	616
aga aga aga ggg cgc	tgg gtt cag cca ggt	gtg gaa ctg agc gtt aga	1983			
Arg Arg Arg Gly Arg	Trp Val Gln Pro Gly	Val Glu Leu Ser Val Arg	617	622	627	632
tcc atg ctg gat ctg	cgg cag ctg gaa aca	ctg gcc cca agc ctg cag	2031			
Ser Met Leu Asp Leu	Arg Gln Leu Glu Thr	Leu Ala Pro Ser Leu Gln	633	638	643	648
gac cct agc cag gac	tcg ctg gcc atc atc	cca tct ggt ccc agg aag	2079			
Asp Pro Ser Gln Asp	Ser Leu Ala Ile Ile	Pro Ser Gly Pro Arg Lys	649	654	659	664
cat ggg cag gag gcc	ctt gag act tca ctc	act agc cag aat gaa aag	2127			
His Gly Gln Glu Ala	Leu Glu Thr Ser Leu	Thr Ser Gln Asn Glu Lys	665	670	675	680
ccc cct cgg cct cag	gct tcc caa cct tgt	tcc tat ccc cat att atc	2175			
Pro Pro Arg Pro Gln	Ala Ser Gln Pro Cys	Ser Tyr Pro His Ile Ile	681	686	691	696
cga tta ttg tca caa	gag gaa ggg gtc ttt	gcc caa gat ctg gaa cct	2223			
Arg Leu Leu Ser Gln	Glu Glu Gly Val Phe	Ala Gln Asp Leu Glu Pro	697	702	707	712
gca ccc att gaa gat	ggg att gtc tac ccg	gag ccg agt gac aac ccc	2271			
Ala Pro Ile Glu Asp	Gly Ile Val Tyr Pro	Glu Pro Ser Asp Asn Pro	713	718	723	728
acc atg gat acc agt	gag ttc caa gtg cag	gct cca gcc cgg gga act	2319			
Thr Met Asp Thr Ser	Glu Phe Gln Val Gln	Ala Pro Ala Arg Gly Thr	729	734	739	744
ctg gga aga gtg tac	cca ggc agc agg agc	tca gaa aag cac agc cct	2367			
Leu Gly Arg Val Tyr	Pro Gly Ser Arg Ser	Ser Glu Lys His Ser Pro	745	750	755	760
gac agt gcc tgc tct	gtg gat tac agc agc	agc tgc ctt tcc agc ccg	2415			
Asp Ser Ala Cys Ser	Val Asp Tyr Ser Ser	Ser Cys Leu Ser Ser Pro	761	766	771	776
gag cac ccc act gaa	gac tct gag agc acg	gag ccc ctc agt gtg gat	2463			
Glu His Pro Thr Glu	Asp Ser Glu Ser Thr	Glu Pro Leu Ser Val Asp				

777	782	787	792	
ggc atc tcc tca gac ctt gaa gag cca gct gag ggt gat gaa gaa gag				2511
Gly Ile Ser Ser Asp Leu Glu Glu Pro Ala Glu Gly Asp Glu Glu Glu				
793	798	803	808	
gaa gaa gag gag gga ggc atg ggc ccc tat ggg cta cag gag ggc agc				2559
Glu Glu Glu Glu Gly Gly Met Gly Pro Tyr Gly Leu Gln Glu Gly Ser				
809	814	819	824	
ccc cag act cca gac cag gag cag ttt cta aaa cag cac ttt gag act				2607
Pro Gln Thr Pro Asp Gln Glu Gln Phe Leu Lys Gln His Phe Glu Thr				
825	830	835	840	
ctg gcc agt gga gct gct cca ggg gcc cca gtg cag gtc cca gag agg				2655
Leu Ala Ser Gly Ala Ala Pro Gly Ala Pro Val Gln Val Pro Glu Arg				
841	846	851	856	
tca gag tct cgg agt atc tct tca cga ttc ctg ttg caa gta cag acc				2703
Ser Glu Ser Arg Ser Ile Ser Ser Arg Phe Leu Leu Gln Val Gln Thr				
857	862	867	872	
cgc cca ctc agg gaa cca tcc cca tcc tcc tca agc ctg gca ctg atg				2751
Arg Pro Leu Arg Glu Pro Ser Pro Ser Ser Ser Ser Leu Ala Leu Met				
873	878	883	888	
tcg aga cca gcc cag gtg cca cag gca tct ggt gag cag ccg aga ggc				2799
Ser Arg Pro Ala Gln Val Pro Gln Ala Ser Gly Glu Gln Pro Arg Gly				
889	894	899	904	
aat ggt gcc aat ccc cct gga gca ccc ccg gag gtg gaa ccg tcc tct				2847
Asn Gly Ala Asn Pro Pro Gly Ala Pro Pro Glu Val Glu Pro Ser Ser				
905	910	915	920	
ggc aac ccc agc ccc cag cag gca gcc tct gtg ctg ttg cca cga tgc				2895
Gly Asn Pro Ser Pro Gln Gln Ala Ala Ser Val Leu Leu Pro Arg Cys				
921	926	931	936	
cgt ctc aac cct gac agc agc tgg gct ccc aag aga gtg gcc aca gcc				2943
Arg Leu Asn Pro Asp Ser Ser Trp Ala Pro Lys Arg Val Ala Thr Ala				
937	942	947	952	
agc ccc ttt tct gga ctc cag aag gcc cag tct gtg cac agt ctg gtg				2991
Ser Pro Phe Ser Gly Leu Gln Lys Ala Gln Ser Val His Ser Leu Val				
953	958	963	968	
cca cag gaa aga cat gag gcc agt ctg cag gcc cct tca cca ggc gca				3039
Pro Gln Glu Arg His Glu Ala Ser Leu Gln Ala Pro Ser Pro Gly Ala				
969	974	979	984	
ctg ctg tct cgg gag atc gaa gct cag gat ggt ctg ggc tcc ctg ccc				3087
Leu Leu Ser Arg Glu Ile Glu Ala Gln Asp Gly Leu Gly Ser Leu Pro				
985	990	995	1000	
cca gct gat ggc cct ccg tct cgg cct cac tcc tat cag aac ccc acc				3135
Pro Ala Asp Gly Pro Pro Ser Arg Pro His Ser Tyr Gln Asn Pro Thr				
1001	1006	1011	1016	

acc agt tcc atg gcc aag ata tcc cgc agt atc tct gtt ggg gag aac	3183
Thr Ser Ser Met Ala Lys Ile Ser Arg Ser Ile Ser Val Gly Glu Asn	
1017 1022 1027 1032	
ctg ggc ctg gtg gct gaa cct caa gct cat gcc ccc atc cga gtc tca	3231
Leu Gly Leu Val Ala Glu Pro Gln Ala His Ala Pro Ile Arg Val Ser	
1033 1038 1043 1048	
cca ctc agc aag ctg gcc ctg ccc agc cgg gct cac ctg gtc ctg gac	3279
Pro Leu Ser Lys Leu Ala Leu Pro Ser Arg Ala His Leu Val Leu Asp	
1049 1054 1059 1064	
atc ccc aaa cca ctg cct gac cgt cct acc ctg gct gca ttc tct cct	3327
Ile Pro Lys Pro Leu Pro Asp Arg Pro Thr Leu Ala Ala Phe Ser Pro	
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Val Thr Lys Gly Arg Ala Pro Gly Glu Ala Glu Lys Pro Gly Phe Pro	
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Val Gly Leu Gly Lys Ala His Ser Thr Thr Glu Arg Trp Ala Cys Leu	
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Gly Glu Gly Thr Thr Pro Lys Pro Arg Thr Glu Cys Gln Ala His Pro	
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ggg ccc agc agc ccc tgt gcc cag caa ctg cca gtc agc agc ctc ttc	3519
Gly Pro Ser Ser Pro Cys Ala Gln Gln Leu Pro Val Ser Ser Leu Phe	
1129 1134 1139 1144	
caa ggc cct gaa aac ttg cag ccc cca ccc cct gag aag act ccc aac	3567
Gln Gly Pro Glu Asn Leu Gln Pro Pro Pro Pro Glu Lys Thr Pro Asn	
1145 1150 1155 1160	
ccc atg gaa tgc acc aag cca ggg gca gcc ctg agc cag gac tca gag	3615
Pro Met Glu Cys Thr Lys Pro Gly Ala Ala Leu Ser Gln Asp Ser Glu	
1161 1166 1171 1176	
cca gcg gtg agc ctg gag cag tgt gag cag ctg gtg gca gag ctc cgc	3663
Pro Ala Val Ser Leu Glu Gln Cys Glu Gln Leu Val Ala Glu Leu Arg	
1177 1182 1187 1192	
ggc agc gtg cgc cag gca gtg cgg ctc tac cac tcg gtg gct ggc tgc	3711
Gly Ser Val Arg Gln Ala Val Arg Leu Tyr His Ser Val Ala Gly Cys	
1193 1198 1203 1208	
aag atg ccc tca gca gag caa agt cgg att gcc cag ctc ctc aga gac	3759
Lys Met Pro Ser Ala Glu Gln Ser Arg Ile Ala Gln Leu Leu Arg Asp	
1209 1214 1219 1224	
acc ttc tct tca gtg cga cag gag ctg gaa gct gtg gct ggg gca gtg	3807
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Met Asp Pro
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Glu Glu Gln Glu Leu Asn Asp Tyr Arg Tyr Arg Ser Tyr Ser Ser
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Val Ile Glu Lys Ala Leu Arg Asn Phe Glu Ser Ser Ser Glu Trp Ala
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Asp Leu Ile Ser Ser Leu Gly Lys Leu Asn Lys Ala Leu Gln Ser Asn
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Leu Arg Tyr Ser Leu Leu Pro Arg Arg Leu Leu Ile Ser Lys Arg Leu
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Ala Gln Cys Leu His Pro Ala Leu Pro Ser Gly Val His Leu Lys Ala
68 73 78 83

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Leu Glu Thr Tyr Glu Ile Ile Phe Lys Ile Val Gly Thr Lys Trp Leu	
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Phe Glu Glu Cys Phe Arg Pro Val Lys Gln Arg Tyr Ser Val Arg Asn	
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Thr	Glu	Ser	Thr	Ser	Gly	Thr	Ser	Ser	Pro	Val	Lys	Gly	Glu	Asn	Gly	
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Lys	Ile	Ile	Leu	Glu	Thr	Lys	Ala	Val	Ile	Pro	Gly	Asp	Glu	Asp	Ala	
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Glu	Arg	Asp	Asp	Val	Trp	Lys	Lys	Gly	Gly	Ser	Met	Gln	Arg	Thr	Phe	
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Ala	Gly	Lys	Arg	Asp	Arg	Asp	Gly	Thr	Gln	Ser	Leu	Ala	Ala	Asn	Asp	
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Ser	Ser	Arg	Lys	Asn	Ser	Trp	Glu	Pro	Lys	Pro	Ile	Thr	Val	Pro	Gln	
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Phe	Lys	Gln	Met	Leu	Ser	Asp	Leu	Phe	Thr	Ala	Arg	Gly	Ser	Pro	Phe	
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Lys	Thr	Lys	Ser	Ser	Glu	Ser	Pro	Ser	Ser	Ser	Pro	Ser	Ser	Pro	Ala	
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Arg	Lys	Asn	Gly	Gly	Glu	Trp	Asp	Val	Glu	Lys	Val	Val	Ile	Asp	Leu	
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Gly	Gly	Ser	Arg	Glu	Glu	Arg	Arg	Glu	Ala	Phe	Ala	Ala	Ala	Cys	His	
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Ser Ser Phe Pro Ser Trp Leu Lys Ser Leu Met Thr Ile Cys Cys Cys				
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Val Thr Asp Cys Tyr Leu Gln Asn Val Ala Ile Ser Thr Leu Leu Glu				
804	809	814	819	
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Val Ile Asn His Ser Gln Ser Leu Ala Leu Val Ile Glu Asp Lys Met				
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Lys Arg Tyr Lys Ser Ser Gly His Asn Pro Phe Phe Gly Lys Leu Gln				
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Tyr Arg Leu His Cys Leu Ala Pro Thr Ala Asn Ile Cys Glu Asp Ile				
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Val Leu Asp Ser Leu Ala Cys Thr Asp Gly Ala Ile Gly Ala Ala Ala				
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Gln Gly Trp Leu Val Arg Ala Leu Ser Leu Gly Asp Val Ala Arg Ile				
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Asn Thr Ser Ser Phe Ser Ser Pro Ser His Asp Leu Gln Glu Leu Ser	
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Tyr	Glu	Ser	Glu	Ser	Val	Lys	Leu	Ser	Val	Ser	Thr	Thr	Ser	Lys	Arg		
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1588				1593				1598							1603		
acc	atg	gct	gca	ggg	gat	cct	gcc	aac	ttg	agg	aat	gcc	aga	aat	gcc	5022	
Thr	Met	Ala	Ala	Gly	Asp	Pro	Ala	Asn	Leu	Arg	Asn	Ala	Arg	Asn	Ala		
1604				1609				1614							1619		
att	ttg	gaa	gag	ctg	cct	cga	act	gtt	aac	acc	atg	gcc	ctt	ctc	tgg	5070	
Ile	Leu	Glu	Glu	Leu	Pro	Arg	Thr	Val	Asn	Thr	Met	Ala	Leu	Leu	Trp		
1620				1625				1630							1635		
aat	gtt	ctc	gga	aag	gag	gag	act	caa	aag	aga	cct	gtc	gat	ctc	cta	5118	
Asn	Val	Leu	Gly	Lys	Glu	Glu	Thr	Gln	Lys	Arg	Pro	Val	Asp	Leu	Leu		
1636				1641				1646							1651		
ggg	gcc	gag	aag	gga	tcc	tct	tcc	gtt	tac	ttt	aaa	acc	acc	aaa	acc	5166	
Gly	Ala	Ala	Lys	Gly	Ser	Ser	Ser	Val	Tyr	Phe	Lys	Thr	Thr	Lys	Thr		
1652				1657				1662							1667		
ata	aga	caa	aaa	att	tta	gac	ttc	tta	aac	ccc	ttg	acg	gcc	cat	ctt	5214	
Ile	Arg	Gln	Lys	Ile	Leu	Asp	Phe	Leu	Asn	Pro	Leu	Thr	Ala	His	Leu		

1668	1673	1678	1683	
ggg gtt cag ttg aca gcg gct gtt gcg gca gtg tgg agc aga aag aaa				5262
Gly Val Gln Leu Thr Ala Ala Val Ala Ala Val Trp Ser Arg Lys Lys				
1684	1689	1694	1699	
gcc cag cgt cac agt aag atg aag att atc cca acg gca agt gca tcc				5310
Ala Gln Arg His Ser Lys Met Lys Ile Ile Pro Thr Ala Ser Ala Ser				
1700	1705	1710	1715	
cag cta acc ctt gtc gac ttg gtg tgt gca ctc agc acc ctg cag act				5358
Gln Leu Thr Leu Val Asp Leu Val Cys Ala Leu Ser Thr Leu Gln Thr				
1716	1721	1726	1731	
gac acg ctg ctg cac ctg gtg aag gag gtg gtg aag agg cca ccc caa				5406
Asp Thr Leu Leu His Leu Val Lys Glu Val Val Lys Arg Pro Pro Gln				
1732	1737	1742	1747	
gtc aaa ggg ggt gat gag aaa tcg ccc cta gtg gac att cct gtg ttg				5454
Val Lys Gly Gly Asp Glu Lys Ser Pro Leu Val Asp Ile Pro Val Leu				
1748	1753	1758	1763	
cag ttt tgc tat gct ttt ctc caa agg ctc cca gta cca gcc ttg caa				5502
Gln Phe Cys Tyr Ala Phe Leu Gln Arg Leu Pro Val Pro Ala Leu Gln				
1764	1769	1774	1779	
gag aac ttt tct tca ctg ttg gga gta ttg aaa gag tct gta cag ttg				5550
Glu Asn Phe Ser Ser Leu Leu Gly Val Leu Lys Glu Ser Val Gln Leu				
1780	1785	1790	1795	
aat cta gcc cca cct ggg tat ttt ctg ctt ctc agc atg ctg aat gac				5598
Asn Leu Ala Pro Pro Gly Tyr Phe Leu Leu Leu Ser Met Leu Asn Asp				
1796	1801	1806	1811	
ttt gta aca aga act ccc aac ctg gaa aac aag aag gac caa aaa gac				5646
Phe Val Thr Arg Thr Pro Asn Leu Glu Asn Lys Lys Asp Gln Lys Asp				
1812	1817	1822	1827	
ctg cag gaa atc act cag aaa atc cta gaa gct gtg ggg aac att gcc				5694
Leu Gln Glu Ile Thr Gln Lys Ile Leu Glu Ala Val Gly Asn Ile Ala				
1828	1833	1838	1843	
ggc tct tcc ttg gag caa acc agc tgg cta agc aga aac ctg gaa gtg				5742
Gly Ser Ser Leu Glu Gln Thr Ser Trp Leu Ser Arg Asn Leu Glu Val				
1844	1849	1854	1859	
aag gcc caa cct cag gcc tct cta gaa gaa tct gat gct gag gag gac				5790
Lys Ala Gln Pro Gln Ala Ser Leu Glu Glu Ser Asp Ala Glu Glu Asp				
1860	1865	1870	1875	
ctg tat gat gct gct gca gct tca gca atg gtg tct tca tcc gcc ccg				5838
Leu Tyr Asp Ala Ala Ala Ala Ser Ala Met Val Ser Ser Ser Ala Pro				
1876	1881	1886	1891	
tcg gtg tac agc gtg caa gcc ctc tct ctc ctg gca gag gta ctg gct				5886
Ser Val Tyr Ser Val Gln Ala Leu Ser Leu Leu Ala Glu Val Leu Ala				
1892	1897	1902	1907	

tcc ctc ctg gac atg gtt tat cga agt gat gag aag gag aaa gct gtg	5934
Ser Leu Leu Asp Met Val Tyr Arg Ser Asp Glu Lys Glu Lys Ala Val	
1908 1913 1918 1923	
ccg tta atc tcc cgt ctg ctt tac tat gtt ttt cca tac tta cgc aac	5982
Pro Leu Ile Ser Arg Leu Leu Tyr Tyr Val Phe Pro Tyr Leu Arg Asn	
1924 1929 1934 1939	
cac agt gcc tac aat gct ccc agc ttc cgg gct ggc gct cag ctg ctg	6030
His Ser Ala Tyr Asn Ala Pro Ser Phe Arg Ala Gly Ala Gln Leu Leu	
1940 1945 1950 1955	
agc tcc ctg agt ggc tat gcc tac aca aag cga gcc tgg agg aag gag	6078
Ser Ser Leu Ser Gly Tyr Ala Tyr Thr Lys Arg Ala Trp Arg Lys Glu	
1956 1961 1966 1971	
gtc ctg gag ctg ttt ctc gac ccc gct ttc ttt cag atg gat act tcc	6126
Val Leu Glu Leu Phe Leu Asp Pro Ala Phe Phe Gln Met Asp Thr Ser	
1972 1977 1982 1987	
tgt gtt cat tgg aag tcc att att gac cat ctt ttg act cat gag aaa	6174
Cys Val His Trp Lys Ser Ile Ile Asp His Leu Leu Thr His Glu Lys	
1988 1993 1998 2003	
aca atg ttt aag gat tta atg aac atg cag agc agt tct ttg aaa cta	6222
Thr Met Phe Lys Asp Leu Met Asn Met Gln Ser Ser Ser Leu Lys Leu	
2004 2009 2014 2019	
ttc tca agt ttt gaa cag aaa gcc atg ctg tta aag cgc cag gct ttt	6270
Phe Ser Ser Phe Glu Gln Lys Ala Met Leu Leu Lys Arg Gln Ala Phe	
2020 2025 2030 2035	
gct gtc ttc agt gga gaa ctt gat caa tac cac ctt tac ctt cca ctg	6318
Ala Val Phe Ser Gly Glu Leu Asp Gln Tyr His Leu Tyr Leu Pro Leu	
2036 2041 2046 2051	
ata caa gaa cgc ctg aca gac aat ctc aga gtt gga cag aca tcc ata	6366
Ile Gln Glu Arg Leu Thr Asp Asn Leu Arg Val Gly Gln Thr Ser Ile	
2052 2057 2062 2067	
gtt gct gct cag atg ttt ctt ttt ttc aga gtt ttg ctg cta aga ata	6414
Val Ala Ala Gln Met Phe Leu Phe Phe Arg Val Leu Leu Leu Arg Ile	
2068 2073 2078 2083	
tct cct caa cat ttg act tca ttg tgg cca ata atg gtc tct gaa ttg	6462
Ser Pro Gln His Leu Thr Ser Leu Trp Pro Ile Met Val Ser Glu Leu	
2084 2089 2094 2099	
att cag aca ttc aca cag ctt gaa gaa gat cta aaa gat gaa gat gag	6510
Ile Gln Thr Phe Thr Gln Leu Glu Glu Asp Leu Lys Asp Glu Asp Glu	
2100 2105 2110 2115	
tca ttg aga agc acc aac aaa gta aac aga acg aaa gtt tca gtc ccg	6558
Ser Leu Arg Ser Thr Asn Lys Val Asn Arg Thr Lys Val Ser Val Pro	
2116 2121 2126 2131	

gat gca aat gga ccc tca gtg ggg gag ata ccc cag agt gaa ctc atc Asp Ala Asn Gly Pro Ser Val Gly Glu Ile Pro Gln Ser Glu Leu Ile 2132 2137 2142 2147	6606
ttg tat tta tca gct tgc aaa ttc ttg gac aca gcg ctt tct ttt cca Leu Tyr Leu Ser Ala Cys Lys Phe Leu Asp Thr Ala Leu Ser Phe Pro 2148 2153 2158 2163	6654
cct gac aag atg cca tta ttt caa att tat agg tgg gca ttt att cca Pro Asp Lys Met Pro Leu Phe Gln Ile Tyr Arg Trp Ala Phe Ile Pro 2164 2169 2174 2179	6702
gaa gtg gac aca gag ggc cct gcc ttc ctg tgc gat gta gag gag aat Glu Val Asp Thr Glu Gly Pro Ala Phe Leu Ser Asp Val Glu Glu Asn 2180 2185 2190 2195	6750
cac caa gaa tgc aaa ccc cac act gtc agg att cta gaa ctt cta aaa His Gln Glu Cys Lys Pro His Thr Val Arg Ile Leu Glu Leu Leu Lys 2196 2201 2206 2211	6798
tta aag ttt ggg gaa atc agt agc tct gat gag atc acc atg aag agt Leu Lys Phe Gly Glu Ile Ser Ser Ser Asp Glu Ile Thr Met Lys Ser 2212 2217 2222 2227	6846
gaa ttc ccg ctt ctg cgc caa cat tct gtt tcc agc atc agg cag ttg Glu Phe Pro Leu Leu Arg Gln His Ser Val Ser Ser Ile Arg Gln Leu 2228 2233 2238 2243	6894
atg cca ttc ttc atg act cta aat ggt gca ttt aag acc cag aga cag Met Pro Phe Phe Met Thr Leu Asn Gly Ala Phe Lys Thr Gln Arg Gln 2244 2249 2254 2259	6942
ctg cct gct gat agc cca gga act cca ttc ttg gac ttt cct gtc aca Leu Pro Ala Asp Ser Pro Gly Thr Pro Phe Leu Asp Phe Pro Val Thr 2260 2265 2270 2275	6990
gat agc cca agg atc tta aaa caa ctg gaa gaa tgc atc gaa tat gat Asp Ser Pro Arg Ile Leu Lys Gln Leu Glu Glu Cys Ile Glu Tyr Asp 2276 2281 2286 2291	7038
ttt ctg gaa cat cca gaa tgt taa ccatgtgaga gagaatatgt ttaatccatg Phe Leu Glu His Pro Glu Cys * 2292 2297	7092
tattggtact ttactgaaaa ccagggtata ttctaaagaa gaaagaaggc aggatagtgc	7152
ttttgaacaa gcctatattcc attttgaaag tagatttcag gctaggtgcg gtggctcaca	7212
cctgtaatct cagcactttg ggaggccaag gcaggcagat cacttgaggt caggagttcg	7272
agaccagcct gaccaacatg gtgagaccct gtctctacta aaaatacaaaa aattagctgg	7332
gtgtggtggc ggcgcctgta atcccageta cttgggaggc taaggcatga gaattgcttg	7392
aaccaggag gtggaggctg cagtgagccg agatcacgac actgcactcc agctgtgtga	7452
cagaatgaga ccatctccaa aaaaaaaaaa aagtagattt cagataattt actgttcagc	7512

aacaggacac acctccctaa atgccttgta atatatttga atctgattct gcatttcttc 7572
 ctcaatttat gtaatgaaaa taaaattaat atatcatcta acagtagcac aaaatttgta 7632
 atatgaagta aagtatgaag ataatgaaga agttgttttc tttgttgaag cagttatatg 7692
 ggtctttctc agtatatttc tcttttctct aaaagtttaa acttattaaa agaattgtat 7752
 ttttaacctt tcaaaaaaaaa aa 7774

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 tcaccaaga tcctctcacc tcccatgaag ggaacggctc tctaa atg cag ttt 174
 Met Gln Phe
 1
 tcc ttc cag cag ggt gga tgg gga gca tcg ctg gct gac agg ctg gtc 222
 Ser Phe Gln Gln Gly Gly Trp Gly Ala Ser Leu Ala Asp Arg Leu Val
 4 9 14 19
 aga aaa tgt gat gtt ctg aat cgt gga ttt tca ggt tac aat acc agg 270
 Arg Lys Cys Asp Val Leu Asn Arg Gly Phe Ser Gly Tyr Asn Thr Arg
 20 25 30 35
 tgg gcc aaa att atc ctt cca aga tta atc agg aaa gga aac agt ttg 318
 Trp Ala Lys Ile Ile Leu Pro Arg Leu Ile Arg Lys Gly Asn Ser Leu
 36 41 46 51
 gac atc cca gta gca gtt aca att ttc ttt ggg gcc aat gac agt gca 366
 Asp Ile Pro Val Ala Val Thr Ile Phe Phe Gly Ala Asn Asp Ser Ala
 52 57 62 67
 cta aaa gat gag aat ccc aag cag cac att ccc ctg gag gag tac gct 414
 Leu Lys Asp Glu Asn Pro Lys Gln His Ile Pro Leu Glu Glu Tyr Ala
 68 73 78 83

gcg aac cta aag agc atg gtg cag tac ctg aag tcc gtg gac atc cct	462
Ala Asn Leu Lys Ser Met Val Gln Tyr Leu Lys Ser Val Asp Ile Pro	
84 89 94 99	
gag aat cga gtc att ctc atc acg ccg acc cca ctt tgt gaa aca gcc	510
Glu Asn Arg Val Ile Leu Ile Thr Pro Thr Leu Cys Glu Thr Ala	
100 105 110 115	
tgg gaa gaa cag tgc atc ata caa ggt tgc aaa cta aat cgc ctg aac	558
Trp Glu Glu Gln Cys Ile Ile Gln Gly Cys Lys Leu Asn Arg Leu Asn	
116 121 126 131	
tct gtt gtt ggt gaa tat gcc aat gcg tgt tta caa gtg gcc caa gac	606
Ser Val Val Gly Glu Tyr Ala Asn Ala Cys Leu Gln Val Ala Gln Asp	
132 137 142 147	
tgt ggg act gac gta ctt gac ctg tgg acc ctg atg cag gac agc cag	654
Cys Gly Thr Asp Val Leu Asp Leu Trp Thr Leu Met Gln Asp Ser Gln	
148 153 158 163	
gac ttc tca tct tat tta tca gat gga cta cat ttg tct cca aag ggg	702
Asp Phe Ser Ser Tyr Leu Ser Asp Gly Leu His Leu Ser Pro Lys Gly	
164 169 174 179	
aat gaa ttt ttg ttc tcg cat ctc tgg cct ttg ata gag aaa aag gtc	750
Asn Glu Phe Leu Phe Ser His Leu Trp Pro Leu Ile Glu Lys Lys Val	
180 185 190 195	
tct tct cta cct ttg ctg ctt cct tac tgg cgg gat gta gca gaa gca	798
Ser Ser Leu Pro Leu Leu Leu Pro Tyr Trp Arg Asp Val Ala Glu Ala	
196 201 206 211	
aaa cct gaa tta agt ctg ctg gga gat gga gac cat tag ccaatcacag	847
Lys Pro Glu Leu Ser Leu Leu Gly Asp Gly Asp His *	
212 217 222	
gagacccaaa tctgcttggt atctacagaa ctcaaagttg tcaatacgta gaggtacgct 907	
tttttctca ggcttaaacc ttgccactg atattaataa taaaagtatt agatgatttt 967	
tcagggaagt ttatactta ggtccattgt gtttcgacag tatttattaa tgcagatata 1027	
agtgtctacag ctataaaata taccctgagc agcttggttaa ttctataaat gacaaagact 1087	
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actaaaggta taaggattat catgactagg ttaaaaggat aggcaaatac cataagggt 1267	
caagttccaa ggtattaggt ataacaagg atctggggta accaaatgtc cttgggaatg 1327	
gggggggtgg nggggtatat ggtaggtcc ccgggttggg ttaactgccc ntcaaattta 1387	
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<210> 302
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 <212> DNA
 <213> Homo sapiens

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<220>
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 <223> n = a,t,c or g

<400> 302

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agctgaaggt aagtacatTT tccactaatt cctcagcttg ctaagtgctt ttggacc      117
atg aat aga gca gct agg aac aaa tct gag aag agg tac tat tca gaa      165
Met Asn Arg Ala Ala Arg Asn Lys Ser Glu Lys Arg Tyr Tyr Ser Glu
   1             5             10             15

ttc ctc caa ata gct cat ctt ttt aat tat ggg ctt tca tcc ttc cta      213
Phe Leu Gln Ile Ala His Leu Phe Asn Tyr Gly Leu Ser Ser Phe Leu
   17             22             27             32

agg gag ttt att att ttt cta att aaa cta cta caa tga aggctattac      262
Arg Glu Phe Ile Ile Phe Leu Ile Lys Leu Leu Gln *
   33             38             43

ctttttgtct agctaaaaca atcttttcta ttaatgaatt tattggcttc tctagtactc      322

ttcaaattgt cattgagctc tattcaagga ctacagccag ttttttcta atagaattag      382

gggtgaaaca aatcatgctt ctattatcac ttctggagtt agcccttcac ctgatcagct      442

tgtctagggt taagagtgcg ggggttttag cgccacaaag acgtgggcat gcggcagctt      502

cctgaacctc aggcattggt gtctaagcaa ctccaccatc cacacgtgtg acgttacagt      562

tctgggagat gcacgcacac tntctgtgcc tttctcaacc actagcttaa tcagcctcca      622

ccttcctagg cagcaacacg ggggtgcagga taaacaataa ctaaaagcat actgattatc      682

acatactcct gcaaagtgtt tgcaccaga aagcatgcag tcaactgcat catgaggggc      742

tcacaccttt ctttggtggt ctctgtcggg gggcacatgt tacctataaa agaggcccaa      802

gcattcgatt aaacagctct tctttataat tcagtttggc taagctgcct tcaaaaaact      862

tgtccccaat tcttcactta cccccccca cttttacaca cgcataacc caacttacc      922

gggcccactt ggaaacacta catacatagc atgcttgcca aaagttcaca tagggattag      982

gattgcgaaa ggggtaccac aggtgggcca cagcgtcctg cgtctggacg taacacagtg     1042
  
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aggacgggct gtcattgcttc tgtgatcctc gtcacgccac gcctacgacg cgagtgccgt 1102
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gccagcctct cgtgtcgcgc c 1183

<210> 303
<211> 1885
<212> DNA
<213> Homo sapiens

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<222> (1115) .. (1744)

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gatgactggc tgctctacct tctttttgga cttcatcttt ttctttgcgg aggccttagg 180
gtcatcactt atggggatgt attccggagc ctcaactttg actggcttct ttttacttcc 240
tttcttaggg ctgctctcca tggacctgga gggcttggag tggcctggga gggcatctcc 300
ctcctgggtg attttttttt tcttcttcac cttccattg tgttctctgg ggctcttccg 360
cttccgtttc tgccccaagg ctgcctgttc ctcatccttc tccccactg agcaagtgtc 420
cccaacatcc ctggcctccc tggcctcaca gaaccaaggg tcctggaccg agaaggctgt 480
ggggtcctgg gccccctttt tttccttctt gtgttttttg agcttcttgc caactctggt 540
ttcctcctca ccctgtctag ggtctgggga ggttttcacc ccagaggcat gggacatggc 600
tagaggtgac ttcttatttt tcttttcccc actgaggaac tccaagtggc caaacacctg 660
cttctgagg ctgggtgact tctctgtccg tctagcaggc agcgtggtct caggttctac 720
atgctcctcg caaaggggtgc tgacaccctt ctttttcttc ttctttttct tctactagagg 780
catctcaggt gcctgccccat gggccacact cttagagggg gatgtagctc ttaaaggaga 840
aacatcagca aagtaatcat cattgtttta aactgagtat cgagtctctg gttctttgac 900
cactttcttc ttctttttct tctctgggag cccaaggctt actttgtgtg tcttgggtgat 960
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agtccacttc gagtcgccgg cccacctct cgggttcggg cttcttcggg gtcgcgccct 1080
tccggcgaac gcggttaccg tggaaaccgc ggcc atg gcg gca ccg cg caa 1132

Met Ala Ala Pro Arg Gln
1

atc ccc agc cac ata gtg cgc ctc aag ccc agc tgc tct aca gac tcg Ile Pro Ser His Ile Val Arg Leu Lys Pro Ser Cys Ser Thr Asp Ser 7 12 17 22	1180
tcg ttc acc cgg acg ccg gtg ccc acc gtg tct ctc gcg tcc cgc gag Ser Phe Thr Arg Thr Pro Val Pro Thr Val Ser Leu Ala Ser Arg Glu 23 28 33 38	1228
ctg cct gtc tcg tcg tgg cag gtc acc gag ccg tca agc aag aat ctg Leu Pro Val Ser Ser Trp Gln Val Thr Glu Pro Ser Ser Lys Asn Leu 39 44 49 54	1276
tgg gag cag atc tgc aag gag tat gaa gct gag cag cct ccc ttt cca Trp Glu Gln Ile Cys Lys Glu Tyr Glu Ala Glu Gln Pro Pro Phe Pro 55 60 65 70	1324
gaa gga tat aaa gtc aaa cag gag cct gtg att acg gtt gcg cca gta Glu Gly Tyr Lys Val Lys Gln Glu Pro Val Ile Thr Val Ala Pro Val 71 76 81 86	1372
gag gaa atg ctt ttt cat ggc ttc agt gca gag cac tat ttt ccg gtt Glu Glu Met Leu Phe His Gly Phe Ser Ala Glu His Tyr Phe Pro Val 87 92 97 102	1420
tcc cat ttc acc atg atc tca cgt aca ccc tgt cct caa gat aaa tcg Ser His Phe Thr Met Ile Ser Arg Thr Pro Cys Pro Gln Asp Lys Ser 103 108 113 118	1468
gaa aca atc aac cca aaa aca tgt tct ccc aaa gaa tat ttg gaa act Glu Thr Ile Asn Pro Lys Thr Cys Ser Pro Lys Glu Tyr Leu Glu Thr 119 124 129 134	1516
ttc atc ttt cct gtt ctg ctt ccc gga atg gct agc ctg ctt cac caa Phe Ile Phe Pro Val Leu Leu Pro Gly Met Ala Ser Leu Leu His Gln 135 140 145 150	1564
gcg aag aaa gaa aaa tgt ttt gag gtt cgc tgt gat cct gag att caa Ala Lys Lys Glu Lys Cys Phe Glu Val Arg Cys Asp Pro Glu Ile Gln 151 156 161 166	1612
gaa ctg cgt cag tgg cag aag aaa ctt cgc gag gcc aag cac att cac Glu Leu Arg Gln Trp Gln Lys Lys Leu Arg Glu Ala Lys His Ile His 167 172 177 182	1660
cag caa gtc aaa att ttc tgg gcc aag caa gaa caa aaa gtg aaa tgc Gln Gln Val Lys Ile Phe Trp Ala Lys Gln Glu Gln Lys Val Lys Cys 183 188 193 198	1708
aaa atg gag gac gat cag tac ctg cag cca aga tga aaat tccatcatct Lys Met Glu Asp Asp Gln Tyr Leu Gln Pro Arg * 199 204 209	1758
taaccatagc taagacgtat ctttgcccat tcgacacaag ttaccttggtg caaggaaaat	1818

gtccaaatga tgctctctct cttgtgattt ctttaacaag acttgaaca tgtgcaaaaa 1878
 aaaaaaa 1885

<210> 304
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 <212> DNA
 <213> Homo sapiens

<220>
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<400> 304
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 Met
 1
 gat tcc ttt ggg caa ccc aga cca gaa gat aat cag tca gta gtc aga 165
 Asp Ser Phe Gly Gln Pro Arg Pro Glu Asp Asn Gln Ser Val Val Arg
 2 7 12 17
 aga atg caa aag aaa tac tgg aaa act aaa cag gtc ttt atc aaa gca 213
 Arg Met Gln Lys Lys Tyr Trp Lys Thr Lys Gln Val Phe Ile Lys Ala
 18 23 28 33
 aca gga aaa aaa gag gat gag cac ttg gtg gcg tct gat gct gaa ctg 261
 Thr Gly Lys Lys Glu Asp Glu His Leu Val Ala Ser Asp Ala Glu Leu
 34 39 44 49
 gat gct aaa ctt gag gtt ttt cac tct gtt caa gag aca tgc act gaa 309
 Asp Ala Lys Leu Glu Val Phe His Ser Val Gln Glu Thr Cys Thr Glu
 50 55 60 65
 ctt ctg aag ata atc gag aaa tac cag cta aga ctc aat ggt atg aaa 357
 Leu Leu Lys Ile Ile Glu Lys Tyr Gln Leu Arg Leu Asn Gly Met Lys
 66 71 76 81
 tca tag ttatctatct gataattccc atttaaaata aatattagca ttttttaaaa 413
 Ser *
 82
 tgaaagattt aatgtaaaaa caattttgtg aatagcttct tatggcaaaa tatgaatatt 473
 tacagctacc tggtctcaaa ggccccagta ttctctcttc tttcctcagt taatcaaadc 533
 ctctgaccca gatttatattt ttgctgatat tttttttctt tgagacaggg tctttctctg 593
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tctgggacat ccagcacagt gagcggcccc tgggcaccac cagaaaacat ttgtgggtga      180
acgtggagtg atgaccatgt ggacactgtc ttccagggtt ttcttgagc ctctgcagag      240
tctggggggc aggtttctta gtggaaactg caggatcttc cttctgacct ctgcttgctt      300
cgccccagca gctccggttg agtccacaga tgccagctca gcttccagct tggggaagag      360
tggggttgct agcaggagag cctgaggggt gaggcccagc gtgaac   atg gca gct      415
                                   Met Ala Ala
                                   1

aat ggg gac tct ccc cca tgg tcc ccg gcc ctg gct gca gag gga cgt      463
Asn Gly Asp Ser Pro Pro Trp Ser Pro Ala Leu Ala Ala Glu Gly Arg
   4                               9                               14                               19

ggc agc tca tgt gag gct tca gtg tca ttt gag gac gtg act gtg gac      511
Gly Ser Ser Cys Glu Ala Ser Val Ser Phe Glu Asp Val Thr Val Asp
  20                               25                               30                               35

ttc agc aag gag gag tgg cag cac ttg gac cct gcc cag aga cgc ctg      559
Phe Ser Lys Glu Glu Trp Gln His Leu Asp Pro Ala Gln Arg Arg Leu
  36                               41                               46                               51

tac tgg gat gtg aca cta gag aac tac agc cac ctg ctc tca gtg ggg      607
Tyr Trp Asp Val Thr Leu Glu Asn Tyr Ser His Leu Leu Ser Val Gly
  52                               57                               62                               67

tac caa att ccc aag tca gag gct gcc ttc aag ttg gag caa gga gag      655
Tyr Gln Ile Pro Lys Ser Glu Ala Ala Phe Lys Leu Glu Gln Gly Glu
  68                               73                               78                               83

ggg cca tgg atg ctg gag ggg gaa gcc cca cat cag agc tgt tca ggt      703
Gly Pro Trp Met Leu Glu Gly Glu Ala Pro His Gln Ser Cys Ser Gly
  84                               89                               94                               99

gag gct att ggg aaa atg cag caa cag gga att cct gga gga att ttc      751
Glu Ala Ile Gly Lys Met Gln Gln Gln Gly Ile Pro Gly Gly Ile Phe
 100                               105                               110                               115

ttc cac tgt gag aga ttt gat caa ccc ata gga gaa gat tca tta tgt      799
Phe His Cys Glu Arg Phe Asp Gln Pro Ile Gly Glu Asp Ser Leu Cys

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116	121	126	131	
tct att tta gaa gaa ctg tgg caa gat aat gac cag cta gag caa cgt				847
Ser Ile Leu Glu Glu Leu Trp Gln Asp Asn Asp Gln Leu Glu Gln Arg				
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cag gaa aac cag aat aac ctt tta agt cat gtg aaa gta ttg att aag				895
Gln Glu Asn Gln Asn Asn Leu Leu Ser His Val Lys Val Leu Ile Lys				
148	153	158	163	
gag agg ggc tat gaa cat aaa aac att gaa aaa ata att cat gtg act				943
Glu Arg Gly Tyr Glu His Lys Asn Ile Glu Lys Ile Ile His Val Thr				
164	169	174	179	
acc aag ctt gtt cct tca att aaa aga ctc cat aac tgt gac aca att				991
Thr Lys Leu Val Pro Ser Ile Lys Arg Leu His Asn Cys Asp Thr Ile				
180	185	190	195	
ttg aag cat act tta aac tca cat aat cat aat aga aac agt gca aca				1039
Leu Lys His Thr Leu Asn Ser His Asn His Asn Arg Asn Ser Ala Thr				
196	201	206	211	
aag aac ctt ggc aag att ttt gga aat ggt aac aat ttc ccc cat agc				1087
Lys Asn Leu Gly Lys Ile Phe Gly Asn Gly Asn Asn Phe Pro His Ser				
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cct tcc tct act aag aat gag aat gct aaa aca gga gca aat tcc tgt				1135
Pro Ser Ser Thr Lys Asn Glu Asn Ala Lys Thr Gly Ala Asn Ser Cys				
228	233	238	243	
gaa cat gac cac tat gaa aaa cat ctc agc cac aaa caa gct ccc acc				1183
Glu His Asp His Tyr Glu Lys His Leu Ser His Lys Gln Ala Pro Thr				
244	249	254	259	
cac cat cag aaa att cat cct gag gag aag ctt tat gtg tgt act gaa				1231
His His Gln Lys Ile His Pro Glu Glu Lys Leu Tyr Val Cys Thr Glu				
260	265	270	275	
tgt gta atg ggc ttc act cag aag tca cat ctg ttt gag cat cag aga				1279
Cys Val Met Gly Phe Thr Gln Lys Ser His Leu Phe Glu His Gln Arg				
276	281	286	291	
att cat gct gga gaa aag tcc cgt gaa tgt gac aaa agc aac aaa gtc				1327
Ile His Ala Gly Glu Lys Ser Arg Glu Cys Asp Lys Ser Asn Lys Val				
292	297	302	307	
ttc ccc cag aaa ccc cag gtt gat gta cat cca agt gtt tat aca gga				1375
Phe Pro Gln Lys Pro Gln Val Asp Val His Pro Ser Val Tyr Thr Gly				
308	313	318	323	
gaa aaa ccc tat ctg tgt act caa tgt ggg aaa gtc ttt acc ctc aaa				1423
Glu Lys Pro Tyr Leu Cys Thr Gln Cys Gly Lys Val Phe Thr Leu Lys				
324	329	334	339	
tca aac ctc att aca cat caa aaa att cat acc ggg cag aaa ccc tac				1471
Ser Asn Leu Ile Thr His Gln Lys Ile His Thr Gly Gln Lys Pro Tyr				
340	345	350	355	

aaa tgc agt gaa tgt gga aaa gcc ttt ttc cag aga tca gac ctc ttt	1519
Lys Cys Ser Glu Cys Gly Lys Ala Phe Phe Gln Arg Ser Asp Leu Phe	
356 361 366 371	
aga cat ctg aga att cat aca gga gaa aaa cct tat gaa tgc agt gaa	1567
Arg His Leu Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Ser Glu	
372 377 382 387	
tgt gga aaa ggc ttc tcc cag aac tca gac ctc agt ata cat cag aaa	1615
Cys Gly Lys Gly Phe Ser Gln Asn Ser Asp Leu Ser Ile His Gln Lys	
388 393 398 403	
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Thr His Thr Gly Glu Lys His Tyr Glu Cys Asn Glu Cys Gly Lys Ala	
404 409 414 419	
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Phe Thr Arg Lys Ser Ala Leu Arg Met His Gln Arg Ile His Thr Gly	
420 425 430 435	
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Glu Lys Pro Tyr Val Cys Ala Asp Cys Gly Lys Ala Phe Ile Gln Lys	
436 441 446 451	
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Ser His Phe Asn Thr His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr	
452 457 462 467	
gaa tgc agt gac tgt ggg aaa tcc ttc act aag aag tca caa ctc cat	1855
Glu Cys Ser Asp Cys Gly Lys Ser Phe Thr Lys Lys Ser Gln Leu His	
468 473 478 483	
gtg cat caa aga att cac acc gga gag aaa ccc tat ata tgt aca gaa	1903
Val His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Ile Cys Thr Glu	
484 489 494 499	
tgt gga aag gtc ttc act cac agg aca aac ctc acc aca cat cag aaa	1951
Cys Gly Lys Val Phe Thr His Arg Thr Asn Leu Thr Thr His Gln Lys	
500 505 510 515	
act cat act ggg gaa aaa ccc tat atg tgt gct gaa tgt gga aag gct	1999
Thr His Thr Gly Glu Lys Pro Tyr Met Cys Ala Glu Cys Gly Lys Ala	
516 521 526 531	
ttt act gac cag tca aat ctc att aaa cac cag aaa act cac act gga	2047
Phe Thr Asp Gln Ser Asn Leu Ile Lys His Gln Lys Thr His Thr Gly	
532 537 542 547	
gag aaa ccc tat aag tgc aat ggc tgt gga aaa gcc ttc ata tgg aag	2095
Glu Lys Pro Tyr Lys Cys Asn Gly Cys Gly Lys Ala Phe Ile Trp Lys	
548 553 558 563	
tcg cgc ctc aaa ata cat cag aaa tct cat att gga gag aga cac tat	2143
Ser Arg Leu Lys Ile His Gln Lys Ser His Ile Gly Glu Arg His Tyr	
564 569 574 579	

gaa tgc aag gac tgc ggg aaa gcc ttc atc cag aaa tca aca cta agc	2191
Glu Cys Lys Asp Cys Gly Lys Ala Phe Ile Gln Lys Ser Thr Leu Ser	
580 585 590 595	
gtg cat cag aga atc cat aca gga gag aaa ccg tac gtt tgt cct gaa	2239
Val His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Val Cys Pro Glu	
596 601 606 611	
tgc ggg aag gcc ttt atc cag aaa tcg cac ttc att gcg cat cat aga	2287
Cys Gly Lys Ala Phe Ile Gln Lys Ser His Phe Ile Ala His His Arg	
612 617 622 627	
atc cat act gga gag aag cct tat gaa tgc agc gac tgt ggg aaa tgc	2335
Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Ser Asp Cys Gly Lys Cys	
628 633 638 643	
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Phe Thr Lys Lys Ser Gln Leu Arg Val His Gln Lys Ile His Thr Gly	
644 649 654 659	
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Glu Lys Pro Asn Ile Cys Ala Glu Cys Gly Lys Ala Phe Thr Asp Arg	
660 665 670 675	
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Ser Asn Leu Ile Thr His Gln Lys Ile His Thr Arg Glu Lys Pro Tyr	
676 681 686 691	
gaa tgt ggt gac tgc ggg aaa acc ttc acc tgg aag tca cgc ctc aat	2527
Glu Cys Gly Asp Cys Gly Lys Thr Phe Thr Trp Lys Ser Arg Leu Asn	
692 697 702 707	
ata cat cag aag tct cat act gga gaa aga cac tat gaa tgt agt aaa	2575
Ile His Gln Lys Ser His Thr Gly Glu Arg His Tyr Glu Cys Ser Lys	
708 713 718 723	
tgt ggg aaa gct ttc atc cag aaa gcc aca cta agt atg cat cag ata	2623
Cys Gly Lys Ala Phe Ile Gln Lys Ala Thr Leu Ser Met His Gln Ile	
724 729 734 739	
att cat aca gga aag aaa cct tat gct tgt aca gaa tgt cag aag gcc	2671
Ile His Thr Gly Lys Lys Pro Tyr Ala Cys Thr Glu Cys Gln Lys Ala	
740 745 750 755	
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Phe Thr Asp Arg Ser Asn Leu Ile Lys His Gln Lys Met His Ser Gly	
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Glu Lys Arg Tyr Lys Ala Ser Asp *	
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                                   Met Ser Gly Arg Gly Lys Gly Gly
                                   1                               5

aag ggg ctg ggt aag gga ggc gcc aag cgc cac cgg aag gtg ctg cgg      219
Lys Gly Leu Gly Lys Gly Gly Ala Lys Arg His Arg Lys Val Leu Arg
  9                               14                               19                               24

gac aat atc caa ggc att aca aag ccg gcg att cgc cgt ctc gcc cga      267
Asp Asn Ile Gln Gly Ile Thr Lys Pro Ala Ile Arg Arg Leu Ala Arg
 25                               30                               35                               40

cgt ggg ggc gtc aag cgc att tct ggt ctc atc tac gag gag acc cgg      315
Arg Gly Gly Val Lys Arg Ile Ser Gly Leu Ile Tyr Glu Glu Thr Arg
 41                               46                               51                               56

gga gtc ctc aaa gtc ttc ctg gag aac gtg atc cgt gac gcg gtg act      363
Gly Val Leu Lys Val Phe Leu Glu Asn Val Ile Arg Asp Ala Val Thr
 57                               62                               67                               72

tac acg gag cac gcc aag cgc aag acc gtc acg gcc atg gat gtg gtg      411
Tyr Thr Glu His Ala Lys Arg Lys Thr Val Thr Ala Met Asp Val Val
 73                               78                               83                               88

tac gcg ctg aaa cgc cag ggt cgc acc ctt tat ggt ttc ggc ggt tga      459
Tyr Ala Leu Lys Arg Gln Gly Arg Thr Leu Tyr Gly Phe Gly Gly *
 89                               94                               99                               104

gctgtcccca cagcttctct acagactcca aaaggccctt ttcagggccc ccaaactgtc      519
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Glu Ala Lys Leu Met Gly Phe Thr Gln Gly Cys Val Thr Phe Glu Asp	
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gtg gcc att tac ttc tcc cag gaa gaa tgg ggg ctc ctt gat gag gct	144
Val Ala Ile Tyr Phe Ser Gln Glu Glu Trp Gly Leu Leu Asp Glu Ala	
33 38 43 48	
cag agg ctc ctg tac cgc gat gtg atg ctg gag aac ttt gca ctt ata	192
Gln Arg Leu Leu Tyr Arg Asp Val Met Leu Glu Asn Phe Ala Leu Ile	
49 54 59 64	
act gcg ctg gtt tgt tgg cat ggg atg gag gat gaa gag aca cct gag	240
Thr Ala Leu Val Cys Trp His Gly Met Glu Asp Glu Glu Thr Pro Glu	
65 70 75 80	
caa agt gtt tct gta gaa gga gta cct cag gtc agg act cca gag gcc	288
Gln Ser Val Ser Val Glu Gly Val Pro Gln Val Arg Thr Pro Glu Ala	
81 86 91 96	
agt cca tcc acc cag aag att caa tcc tgt gac atg tgt gtc cca ttc	336
Ser Pro Ser Thr Gln Lys Ile Gln Ser Cys Asp Met Cys Val Pro Phe	
97 102 107 112	
ctg acc gac att ttg cac ctg acc gat ttg cct ggg cag gaa cta tac	384
Leu Thr Asp Ile Leu His Leu Thr Asp Leu Pro Gly Gln Glu Leu Tyr	
113 118 123 128	
ttg act ggg gca tgt gcg gtc ttt cac cag gac cag aag cat cat agt	432
Leu Thr Gly Ala Cys Ala Val Phe His Gln Asp Gln Lys His His Ser	
129 134 139 144	
gca gag aaa ccc ttg gaa agt gac atg gac aag gcc tca ttt gtg cag	480
Ala Glu Lys Pro Leu Glu Ser Asp Met Asp Lys Ala Ser Phe Val Glu	
145 150 155 160	
tgc tgc ctg ttc cat gag tca gga atg cct ttc acc agc agt gag gtt	528
Cys Cys Leu Phe His Glu Ser Gly Met Pro Phe Thr Ser Ser Glu Val	
161 166 171 176	
ggg aag gac ttc cta gcc cca ttg ggc att ctt cag ccg caa gct att	576

Gly	Lys	Asp	Phe	Leu	Ala	Pro	Leu	Gly	Ile	Leu	Gln	Pro	Gln	Ala	Ile	
177					182					187					192	
gct	aac	tat	gag	aag	cca	aac	aaa	atc	agc	aaa	tgt	gag	gag	gcc	ttt	624
Ala	Asn	Tyr	Glu	Lys	Pro	Asn	Lys	Ile	Ser	Lys	Cys	Glu	Glu	Ala	Phe	
193					198					203					208	
cat	gtt	gga	ata	agt	cat	tac	aag	tgg	agt	caa	tgc	agg	aga	gag	tcc	672
His	Val	Gly	Ile	Ser	His	Tyr	Lys	Trp	Ser	Gln	Cys	Arg	Arg	Glu	Ser	
209					214					219					224	
agc	cac	aaa	cac	act	ttt	ttt	cac	cct	aga	gtc	tgc	act	gga	aaa	agg	720
Ser	His	Lys	His	Thr	Phe	Phe	His	Pro	Arg	Val	Cys	Thr	Gly	Lys	Arg	
225					230					235					240	
ctt	tat	gaa	tct	agc	aaa	tgt	ggg	aaa	gcc	tgc	tgc	tgt	gag	tgc	tcc	768
Leu	Tyr	Glu	Ser	Ser	Lys	Cys	Gly	Lys	Ala	Cys	Cys	Cys	Glu	Cys	Ser	
241					246					251					256	
ctt	gtt	cag	ctg	caa	aga	gtc	cac	cct	gga	gaa	agg	cct	tat	gag	tgc	816
Leu	Val	Gln	Leu	Gln	Arg	Val	His	Pro	Gly	Glu	Arg	Pro	Tyr	Glu	Cys	
257					262					267					272	
agt	gaa	tgt	ggg	aaa	tct	ttt	agc	caa	acc	tct	cat	ctg	aat	gat	cat	864
Ser	Glu	Cys	Gly	Lys	Ser	Phe	Ser	Gln	Thr	Ser	His	Leu	Asn	Asp	His	
273					278					283					288	
cgg	aga	atc	cac	act	gga	gaa	agg	cct	tat	gtg	tgt	ggg	cag	tgt	ggg	912
Arg	Arg	Ile	His	Thr	Gly	Glu	Arg	Pro	Tyr	Val	Cys	Gly	Gln	Cys	Gly	
289					294					299					304	
aaa	tca	ttt	agc	caa	aga	gcc	acc	ctc	att	aaa	cat	cac	aga	gtt	cac	960
Lys	Ser	Phe	Ser	Gln	Arg	Ala	Thr	Leu	Ile	Lys	His	His	Arg	Val	His	
305					310					315					320	
act	gga	gaa	agg	cct	tac	gag	tgt	ggg	gaa	tgt	ggg	aaa	tct	ttt	agc	1008
Thr	Gly	Glu	Arg	Pro	Tyr	Glu	Cys	Gly	Glu	Cys	Gly	Lys	Ser	Phe	Ser	
321					326					331					336	
caa	agt	tcc	aac	ctt	att	gaa	cat	tgc	aga	att	cac	act	gga	gaa	agg	1056
Gln	Ser	Ser	Asn	Leu	Ile	Glu	His	Cys	Arg	Ile	His	Thr	Gly	Glu	Arg	
337					342					347					352	
cct	tat	gag	tgt	gat	gaa	tgt	gga	aaa	gcc	ttt	ggg	tcc	aaa	tcc	act	1104
Pro	Tyr	Glu	Cys	Asp	Glu	Cys	Gly	Lys	Ala	Phe	Gly	Ser	Lys	Ser	Thr	
353					358					363					368	
ctt	gtt	cga	cac	cag	aga	act	cac	aca	gga	gaa	aag	cca	tat	gag	tgt	1152
Leu	Val	Arg	His	Gln	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	
369					374					379					384	
ggg	gaa	tgt	ggg	aaa	tta	ttc	aga	caa	agc	ttc	agc	ctt	gtt	gta	cac	1200
Gly	Glu	Cys	Gly	Lys	Leu	Phe	Arg	Gln	Ser	Phe	Ser	Leu	Val	Val	His	
385					390					395					400	
cag	aga	att	cac	act	aca	gca	agg	cct	tat	gag	tgt	ggc	cag	tgt	ggg	1248
Gln	Arg	Ile	His	Thr	Thr	Ala	Arg	Pro	Tyr	Glu	Cys	Gly	Gln	Cys	Gly	

401	406	411	416	
aaa tca ttt agc cta aag tgt ggc ctc att cag cac cag tta att cac				1296
Lys Ser Phe Ser Leu Lys Cys Gly Leu Ile Gln His Gln Leu Ile His				
417	422	427	432	
agt gga gct agg ccc ttt gag tgt gat gag tgc gga aaa tcc ttt agc				1344
Ser Gly Ala Arg Pro Phe Glu Cys Asp Glu Cys Gly Lys Ser Phe Ser				
433	438	443	448	
caa aga acc acc ctc aat aaa cac cac aaa gtt cac act gca gaa agg				1392
Gln Arg Thr Thr Leu Asn Lys His His Lys Val His Thr Ala Glu Arg				
449	454	459	464	
cct tat gta tgt ggg gaa tgt ggg aaa gct ttt atg ttc aaa tct aaa				1440
Pro Tyr Val Cys Gly Glu Cys Gly Lys Ala Phe Met Phe Lys Ser Lys				
465	470	475	480	
ctt gtt agg cac cag aga act cac act gga gaa agg cct ttt gag tgc				1488
Leu Val Arg His Gln Arg Thr His Thr Gly Glu Arg Pro Phe Glu Cys				
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agt gaa tgt ggg aaa ttt ttt aga caa agc tat acc ctc gtt gaa cac				1536
Ser Glu Cys Gly Lys Phe Phe Arg Gln Ser Tyr Thr Leu Val Glu His				
497	502	507	512	
cag aaa att cac act gga tta agg cct tac gac tgt gga cag tgc ggg				1584
Gln Lys Ile His Thr Gly Leu Arg Pro Tyr Asp Cys Gly Gln Cys Gly				
513	518	523	528	
aaa tcc ttt atc caa aag tct agc ctc att caa cac caa gtg gtt cac				1632
Lys Ser Phe Ile Gln Lys Ser Ser Leu Ile Gln His Gln Val Val His				
529	534	539	544	
aca gga gaa agg cca tat gag tgt ggc aaa tgt ggg aag tcc ttt aca				1680
Thr Gly Glu Arg Pro Tyr Glu Cys Gly Lys Cys Gly Lys Ser Phe Thr				
545	550	555	560	
caa cac tct ggc ctc att ctc cac cga aaa tct cac act gtg gag agg				1728
Gln His Ser Gly Leu Ile Leu His Arg Lys Ser His Thr Val Glu Arg				
561	566	571	576	
cct cgt gac agc agc aaa tgt gga aaa ccc tac agc cca aga tct aac				1776
Pro Arg Asp Ser Ser Lys Cys Gly Lys Pro Tyr Ser Pro Arg Ser Asn				
577	582	587	592	
att gtt taa ctcttga aactccaaac ctgagaaaag ccttagacct gcaggggaatg				1832
Ile Val *				
593				
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 cgatac atg cac aca act gct tca aat ggt agg atg ctc ttc atg aag 948
 Met His Thr Thr Ala Ser Asn Gly Arg Met Leu Phe Met Lys
 1 5 10
 gtc acg atg tac atg agg cgg gga gtg cag atc atg ggc tgg tca gtg 996
 Val Thr Met Tyr Met Arg Arg Gly Val Gln Ile Met Gly Trp Ser Val
 15 20 25 30
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 Arg Met Ala Phe Met Ala Cys Phe Thr Gln *
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 <222> (375)..(1127)

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 gcgttcccc ccatgtccta gctgccctcc ctgtggcgtg agccttcggc ctggtgcgcc 180
 ccgtgccct tcctggctgt gactctggtg gggttccgaa ggccccctta tgcccggcag 240
 acccctaccg acggcggcat tacattctgg ggccacgagg aggcactcat cgtttcgttc 300

caaccgcccgc caacggccct ggcctctcgcg agctctggaa ctacagaggt cgcacgcccg 360
 ggcagtgagt gtgg atg gct tgg cag gtg agc ctg ctg gag ctg gag gac 410
 Met Ala Trp Gln Val Ser Leu Leu Glu Leu Glu Asp
 1 5 10
 cgg ctt cag tgt ccc atc tgc ctg gag gtc ttc aag gag tcc cta atg 458
 Arg Leu Gln Cys Pro Ile Cys Leu Glu Val Phe Lys Glu Ser Leu Met
 13 18 23 28
 cta cag tgc ggc cac tcc tac tgc aag ggc tgc ctg gtt tcc ctg tcc 506
 Leu Gln Cys Gly His Ser Tyr Cys Lys Gly Cys Leu Val Ser Leu Ser
 29 34 39 44
 tac cac ctg gac acc aag gtg cgc tgc ccc atg tgc tgg cag gtg gtg 554
 Tyr His Leu Asp Thr Lys Val Arg Cys Pro Met Cys Trp Gln Val Val
 45 50 55 60
 gac ggc agc agc tcc ttg ccc aac gtc tcc ctg gcc tgg gtg atc gaa 602
 Asp Gly Ser Ser Ser Leu Pro Asn Val Ser Leu Ala Trp Val Ile Glu
 61 66 71 76
 gcc ctg agg ctc cct ggg gac ccg gag ccc aag gtc tgc gtg cac cac 650
 Ala Leu Arg Leu Pro Gly Asp Pro Glu Pro Lys Val Cys Val His His
 77 82 87 92
 cgg aac ccg ctc agc ctt ttc tgc gag aag gac cag gag ctc atc tgt 698
 Arg Asn Pro Leu Ser Leu Phe Cys Glu Lys Asp Gln Glu Leu Ile Cys
 93 98 103 108
 ggc ctc tgc ggt ctg ctg ggc tcc cac caa cac cac ccg gtc acg ccc 746
 Gly Leu Cys Gly Leu Leu Gly Ser His Gln His His Pro Val Thr Pro
 109 114 119 124
 gtc tcc acc gtc tgc agc cgc atg aag gag gag ctc gca gcc ctc ttc 794
 Val Ser Thr Val Cys Ser Arg Met Lys Glu Glu Leu Ala Ala Leu Phe
 125 130 135 140
 tct gag ctg aag cag gag cag aag aag gtg gat gag ctc atc gcc aaa 842
 Ser Glu Leu Lys Gln Glu Gln Lys Lys Val Asp Glu Leu Ile Ala Lys
 141 146 151 156
 ctg gtg aaa aac cgg acc cga atc gtc aat gag tgc gat gtc ttc agc 890
 Leu Val Lys Asn Arg Thr Arg Ile Val Asn Glu Ser Asp Val Phe Ser
 157 162 167 172
 tgg gtg atc cgc cgc gag ttc cag gag ctg cgc cac ccg gtg gac gag 938
 Trp Val Ile Arg Arg Glu Phe Gln Glu Leu Arg His Pro Val Asp Glu
 173 178 183 188
 gag cag gcc cgc tgc ctg gag ggg ata ggg ggt cac acc cgt ggc ctg 986
 Glu Gln Ala Arg Cys Leu Glu Gly Ile Gly Gly His Thr Arg Gly Leu
 189 194 199 204
 gtg gcc tcc ctg gac atg cag ctg gag cag gcc cag gga acc cgg gag 1034
 Val Ala Ser Leu Asp Met Gln Leu Glu Gln Ala Gln Gly Thr Arg Glu

205	210	215	220	
cgg ctg gcc caa gcc gag tgt gtg ctg gaa cag ttc ggc aat gag gac				1082
Arg Leu Ala Gln Ala Glu Cys Val Leu Glu Gln Phe Gly Asn Glu Asp				
221	226	231	236	
cac cat gag ttc atc tgg aag ttc cac tcc atg gcc tcc agg taa taa				1130
His His Glu Phe Ile Trp Lys Phe His Ser Met Ala Ser Arg *				
237	242	247		
ccttgagag agctcagcca ggggtctggtg gctgcgggca cgggcatctc agtccactg				1190
gttcctccat tcagcttaac cagcgctcc caagcagctg cctatagctg gctctataac				1250
tgagcctggg gaagatagag gaaagtcacg tccctgcctt caagggcttc gcagacaggt				1310
ggggaggcag atggtgaact gtgggtacct agaacagcag aagttcactc aagctacaga				1370
aatactagag gaggggtggct catgcctgca atcccagtac tttgggaggc caaggcagga				1430
gtattgctgg aggccgggag ttcgagacca gcctggccaa tgtagtaaca cccccgtctc				1490
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Met Ala Pro Leu Asp Leu Asp Lys Tyr Val Glu Ile Ala				
1 5 10				
cgg ctg tgc aag tac ctg cca gag aac gac ctg aag cgg cta tgt gac				157
Arg Leu Cys Lys Tyr Leu Pro Glu Asn Asp Leu Lys Arg Leu Cys Asp				
14 19 24 29				
tac gtt tgt gac ctc ctc tta gaa gag tca aat gtt cag cca gta tca				205
Tyr Val Cys Asp Leu Leu Leu Glu Glu Ser Asn Val Gln Pro Val Ser				
30 35 40 45				
aca cca gta aca gtg tgt gga gat atc cat gga cag ttt tat gac ctt				253
Thr Pro Val Thr Val Cys Gly Asp Ile His Gly Gln Phe Tyr Asp Leu				
46 51 56 61				
tgt gaa ctg ttc aga act gga ggt cag gtt cct gac aca aac tac ata				301
Cys Glu Leu Phe Arg Thr Gly Gly Gln Val Pro Asp Thr Asn Tyr Ile				

62	67	72	77	
ttt atg ggt gat ttt gta gac aga ggt tac tat agt ttg gag acc ttc				349
Phe Met Gly Asp Phe Val Asp Arg Gly Tyr Tyr Ser Leu Glu Thr Phe				
78	83	88	93	
act tac ctt ctt gca tta aag gct aaa tgg cct gat cgt att aca ctt				397
Thr Tyr Leu Leu Ala Leu Lys Ala Lys Trp Pro Asp Arg Ile Thr Leu				
94	99	104	109	
ttg cga gga aat cat gag agt aga cag ata aca cag gtc tat gga ttt				445
Leu Arg Gly Asn His Glu Ser Arg Gln Ile Thr Gln Val Tyr Gly Phe				
110	115	120	125	
tat gat gag tgc caa acc aaa tat gga aat gct aat gcc tgg aga tac				493
Tyr Asp Glu Cys Gln Thr Lys Tyr Gly Asn Ala Asn Ala Trp Arg Tyr				
126	131	136	141	
tgt acc aaa gtt ttt gac atg ctc aca gta gca gct tta ata gat gag				541
Cys Thr Lys Val Phe Asp Met Leu Thr Val Ala Ala Leu Ile Asp Glu				
142	147	152	157	
cag att ttg tgt gtc cat ggt ggt tta tct cct gat atc aaa aca ctg				589
Gln Ile Leu Cys Val His Gly Gly Leu Ser Pro Asp Ile Lys Thr Leu				
158	163	168	173	
gat caa att cga acc atc gaa cgg aat cag gaa att cct cat aaa gga				637
Asp Gln Ile Arg Thr Ile Glu Arg Asn Gln Glu Ile Pro His Lys Gly				
174	179	184	189	
gca ttt tgt gat ctg gtt tgg tca gat cct gaa gat gtg gat acc tgg				685
Ala Phe Cys Asp Leu Val Trp Ser Asp Pro Glu Asp Val Asp Thr Trp				
190	195	200	205	
gct atc agt ccc cga gga gca ggt tgg ctt ttt gga gca aag gtc aca				733
Ala Ile Ser Pro Arg Gly Ala Gly Trp Leu Phe Gly Ala Lys Val Thr				
206	211	216	221	
aat gag ttt gtt cat atc aac aac tta aaa ctc atc tgc aga gca cat				781
Asn Glu Phe Val His Ile Asn Asn Leu Lys Leu Ile Cys Arg Ala His				
222	227	232	237	
caa cta gtg cac gaa ggc tat aaa ttt atg ttt gat gag aag ctg gtg				829
Gln Leu Val His Glu Gly Tyr Lys Phe Met Phe Asp Glu Lys Leu Val				
238	243	248	253	
aca gta tgg tct gct cct aat tac tgc tat cgt tgt gga aat att gct				877
Thr Val Trp Ser Ala Pro Asn Tyr Cys Tyr Arg Cys Gly Asn Ile Ala				
254	259	264	269	
tcg atc atg gtc ttc aaa gat gta aat aca aga gaa cca aag tta ttc				925
Ser Ile Met Val Phe Lys Asp Val Asn Thr Arg Glu Pro Lys Leu Phe				
270	275	280	285	
cgg gca gtt cca gat tca gaa cgt gtt att cct ccc aga acg aca acg				973
Arg Ala Val Pro Asp Ser Glu Arg Val Ile Pro Pro Arg Thr Thr Thr				
286	291	296	301	

cca tat ttc ctt tga ggccctcgcc catcctgctg acccattttt ctgccctctt	1028
Pro Tyr Phe Leu *	
302	
cttacccecaa ttttcttgta ttaccctcta caatatactt tttattgagc actttgctgc	1088
tgaaatgctg cctcttgcc tttttttttt aaatttttaa ttatctaaat ttattgtttg	1148
ttgtgggtgc tatagcaaag tttttctatc aattttcccc catcccatcc ccaccctgga	1208
ctcatttgag aagacttgag aaatgtctta atactcacac tgctgcatgt agctcttgct	1268
tatttactgg tctgggaaac aggatgtgtt tccttttttt aaaagccaat tgacagatta	1328
cacctaaata ctccctcttt tgtatcattc agccttttgt tttagtttgg taagttttaa	1388
gaaatttcag cagcaaagtt gttattcagt gggcacgatg gactccaaat gcctcaagtt	1448
atgtatacct gtcccagatg taaacttcat tgccttttgt tggatgatat tttaaatgga	1508
tataaaataa attggtctaa agggctgccc tccttggtgt gtttttaaatt tttagttaaa	1568
aactgctaca gcttatgact ttgtacttta agataattgt attgatcttt tttcagattc	1628
cttgtatttt ttaataaagt aatcttaaatt aaaactcaga taggttaagt gttagaaatt	1688
ttaaacagct tacattgtta gcgtaaagtt atcttttctt ttttctaat cagagttctt	1748
gaccctttgg ttattgagtt taaaacttca attgaaattc aatagtattt attttttaaa	1808
aaaatcacta aactgtgcct aaagaacata actgccatat taatgttttg gtttatatcc	1868
tctatagtaa tagaaaaaca ttttaatactt gtaatgctga tgtgttaatt tgataccagt	1928
tgagtagaat gtgatcaatc cagttttaca totatcatga gtattattaa ctaaaatcta	1988
tgtgcttttc aataggaatc attcttctct tgctgtaaca cttgacctta acttttagaa	2048
agtgttcatt tttaaactgc aactggaaag gttgaaaagt taggactctt gtatttgtga	2108
actgtaatct gaagcagatt atttaaagtg tagaaaaaga aacaagttct tttttgcaa	2168
ggtctgtgat accatatttc agctttgtgt aagtaatttg aatata	2214

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<400> 312

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tgcgcacagc agtactcatc ttggccctgg gaagaaactc aagaagaagc ttttgaaaca 120

taaagcttgg atgggggttg acctctgcag ggcagcgccc agctatagga gttcccctgc 180

tgagcagaga ag atg act gca gaa ttg aga gaa gcc atg gcc cta gcc 228
Met Thr Ala Glu Leu Arg Glu Ala Met Ala Leu Ala
1 5 10

cca tgg ggc cca gtg aag gtg aaa aag gag gag gaa gaa gaa gaa aac 276
Pro Trp Gly Pro Val Lys Val Lys Lys Glu Glu Glu Glu Glu Glu Asn
13 18 23 28

ttc cca ggt cag gca tcc agc caa caa gtg cac tcc gag aac atc aaa 324
Phe Pro Gly Gln Ala Ser Ser Gln Gln Val His Ser Glu Asn Ile Lys
29 34 39 44

gtc tgg gcc cca gtg cag ggt ctt cag aca ggc ctt gat gga tca gaa 372
Val Trp Ala Pro Val Gln Gly Leu Gln Thr Gly Leu Asp Gly Ser Glu
45 50 55 60

gag gaa gaa aag ggt cag aac ata tcc tgg gat atg gcg gta gtc ctg 420
Glu Glu Glu Lys Gly Gln Asn Ile Ser Trp Asp Met Ala Val Val Leu
61 66 71 76

aaa gca act cag gag gca cct gct gct tca acc ctt ggc agc tac tca 468
Lys Ala Thr Gln Glu Ala Pro Ala Ala Ser Thr Leu Gly Ser Tyr Ser
77 82 87 92

tta cca ggg act ctg gcc aag agt gag ata ctg gag act cat ggg acc 516
Leu Pro Gly Thr Leu Ala Lys Ser Glu Ile Leu Glu Thr His Gly Thr
93 98 103 108

atg aac ttt cta ggt gct gaa acc aag aac cta cag tta ctg gtt cca 564
Met Asn Phe Leu Gly Ala Glu Thr Lys Asn Leu Gln Leu Leu Val Pro
109 114 119 124

aaa act gag ata tgt gag gaa gct gaa aaa ccc ctc atc ata tca gaa 612
Lys Thr Glu Ile Cys Glu Glu Ala Glu Lys Pro Leu Ile Ile Ser Glu
125 130 135 140

aga atc cag aaa gct gat cct caa gga cct gag tta gga gaa gct tgt 660
Arg Ile Gln Lys Ala Asp Pro Gln Gly Pro Glu Leu Gly Glu Ala Cys
141 146 151 156

gaa aag gga aac atg tta aag agg cag aga ata aag aga gaa aag aaa 708
Glu Lys Gly Asn Met Leu Lys Arg Gln Arg Ile Lys Arg Glu Lys Lys
157 162 167 172

gat ttc aga caa gtg ata gtg aat gac tgt cac tta cct gaa agc ttc 756
Asp Phe Arg Gln Val Ile Val Asn Asp Cys His Leu Pro Glu Ser Phe
173 178 183 188

aaa gaa gag gaa aac cag aaa tgt aag aaa tct gga gga aaa tat agc 804
Lys Glu Glu Glu Asn Gln Lys Cys Lys Lys Ser Gly Gly Lys Tyr Ser

189	194	199	204	
ctt aat tct ggc gct gtt aaa aat cca aaa acc cag ctt gga caa aag				852
Leu Asn Ser Gly Ala Val Lys Asn Pro Lys Thr Gln Leu Gly Gln Lys				
205	210	215	220	
cct ttt acg tgt agc gtg tgt ggg aaa gga ttt agt cag agt gca aac				900
Pro Phe Thr Cys Ser Val Cys Gly Lys Gly Phe Ser Gln Ser Ala Asn				
221	226	231	236	
ctc gtt gtg cat cag cga atc cac act gga gag aaa ccc ttt gaa tgt				948
Leu Val Val His Gln Arg Ile His Thr Gly Glu Lys Pro Phe Glu Cys				
237	242	247	252	
cat gag tgt ggg aag gcc ttc att cag agt gca aac ctc gtt gtg cat				996
His Glu Cys Gly Lys Ala Phe Ile Gln Ser Ala Asn Leu Val Val His				
253	258	263	268	
cag aga atc cac act gga cag aaa cct tat gtt tgc tca aaa tgt ggg				1044
Gln Arg Ile His Thr Gly Gln Lys Pro Tyr Val Cys Ser Lys Cys Gly				
269	274	279	284	
aaa gcc ttc act cag agt tca aat ctg act gta cat caa aaa atc cac				1092
Lys Ala Phe Thr Gln Ser Ser Asn Leu Thr Val His Gln Lys Ile His				
285	290	295	300	
tcc tta gaa aaa act ttt aag tgc aat gaa tgt gag aaa gcc ttt agt				1140
Ser Leu Glu Lys Thr Phe Lys Cys Asn Glu Cys Glu Lys Ala Phe Ser				
301	306	311	316	
tac agc tca caa ctt gct cgg cac cag aaa gtc cac att acg gaa aaa				1188
Tyr Ser Ser Gln Leu Ala Arg His Gln Lys Val His Ile Thr Glu Lys				
317	322	327	332	
tgc tat gaa tgt aat gaa tgt ggg aaa aca ttt act agg agc tca aac				1236
Cys Tyr Glu Cys Asn Glu Cys Gly Lys Thr Phe Thr Arg Ser Ser Asn				
333	338	343	348	
ctc att gtc cac cag agg atc cac act ggg gag aag ccc ttt gcc tgt				1284
Leu Ile Val His Gln Arg Ile His Thr Gly Glu Lys Pro Phe Ala Cys				
349	354	359	364	
aac gac tgt ggc aaa gcc ttt acc cag agt gca aat ctt att gta cat				1332
Asn Asp Cys Gly Lys Ala Phe Thr Gln Ser Ala Asn Leu Ile Val His				
365	370	375	380	
cag cga agc cat act ggt gag aag cca tat gag tgt aaa gag tgt ggg				1380
Gln Arg Ser His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys Gly				
381	386	391	396	
aaa gcc ttt agt tgt ttt tca cac ctt att gtg cac cag aga att cac				1428
Lys Ala Phe Ser Cys Phe Ser His Leu Ile Val His Gln Arg Ile His				
397	402	407	412	
act gca gag aaa cct tac gac tgc agc gaa tgt ggg aaa gcc ttc agt				1476
Thr Ala Glu Lys Pro Tyr Asp Cys Ser Glu Cys Gly Lys Ala Phe Ser				
413	418	423	428	

cag ctc tct tgc ctt att gtc cac cag aga att cac agt gga gat ctt	1524
Gln Leu Ser Cys Leu Ile Val His Gln Arg Ile His Ser Gly Asp Leu	
429 434 439 444	
cct tac gtg tgt aat gaa tgt ggg aag gcc ttc aca tgt agc tca tac	1572
Pro Tyr Val Cys Asn Glu Cys Gly Lys Ala Phe Thr Cys Ser Ser Tyr	
445 450 455 460	
cta ctt att cat cag aga att cat aat gga gaa aaa cct tac aca tgt	1620
Leu Leu Ile His Gln Arg Ile His Asn Gly Glu Lys Pro Tyr Thr Cys	
461 466 471 476	
aat gag tgt ggg aag gcc ttc aga cag agg tcg agc ctc acc gtg cac	1668
Asn Glu Cys Gly Lys Ala Phe Arg Gln Arg Ser Ser Leu Thr Val His	
477 482 487 492	
cag aga acc cac act ggg gag aag ccc tat gaa tgt gag aag tgt ggt	1716
Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Glu Lys Cys Gly	
493 498 503 508	
gca gct ttc att tcc aac tca cac ctc atg cga cac cat aga acc cat	1764
Ala Ala Phe Ile Ser Asn Ser His Leu Met Arg His His Arg Thr His	
509 514 519 524	
ctt gtt gaa taa caa gtaaggaaga ggaagacctc cagcattggt cataaccttc	1819
Leu Val Glu *	
525	
tgccctcccta atgagacacc tctttgctgt tttcttcctc ctctataaaa gtgagggctg	1879
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ctatacctcc tgaaccttgg tattgtaaag atctggggac ctctgggtct gttctgacca	2419
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cgctgggtcc gggccaggta actggagccg gaaaccgggtg gaggtggtgt ccgcccgcag	180
aggagcttgc ctggtctcgg tctgagcgtc gccacgcgat ttgccaccgc acgcacgccg	240
gatcccgggc tttaccgccc gcctttccag gccccgcccc gcctaaagtc cc atg	295
	Met
	1
gcc gag gca gcg cta gtg aat acg ccg cag att ccc atg gta aca gaa	343
Ala Glu Ala Ala Leu Val Asn Thr Pro Gln Ile Pro Met Val Thr Glu	
2 7 12 17	
gag ttt gtg aaa cca tca cag ggc cat gtg acc ttt gag gat att gct	391
Glu Phe Val Lys Pro Ser Gln Gly His Val Thr Phe Glu Asp Ile Ala	
18 23 28 33	
gtg tac ttc tcc cag gag gag tgg ggc ctc ctt gat gaa gct caa agg	439
Val Tyr Phe Ser Gln Glu Glu Trp Gly Leu Leu Asp Glu Ala Gln Arg	
34 39 44 49	
tgc ctg tat cat gat gtg atg ctg gag aac ttt tcg ctt atg gcc tca	487
Cys Leu Tyr His Asp Val Met Leu Glu Asn Phe Ser Leu Met Ala Ser	
50 55 60 65	
gta ggt tgt ttg cat gga ata gag gct gag gag gcc cct tct gag cag	535
Val Gly Cys Leu His Gly Ile Glu Ala Glu Glu Ala Pro Ser Glu Gln	
66 71 76 81	
act ctt tct gcg caa gga gtg tca cag gcc agg act cca aag cta ggt	583
Thr Leu Ser Ala Gln Gly Val Ser Gln Ala Arg Thr Pro Lys Leu Gly	
82 87 92 97	
cct tcc atc cca aat gct cat tct tgt gag atg tgt atc ctg gtc atg	631
Pro Ser Ile Pro Asn Ala His Ser Cys Glu Met Cys Ile Leu Val Met	
98 103 108 113	
aaa gac att ttg tac ctc agt gag cat cag ggg aca ctt ccc tgg cag	679
Lys Asp Ile Leu Tyr Leu Ser Glu His Gln Gly Thr Leu Pro Trp Gln	
114 119 124 129	

aaa cct tat acg tct gtg gcc agt ggg aaa tgg ttt tca ttt ggt tct	727
Lys Pro Tyr Thr Ser Val Ala Ser Gly Lys Trp Phe Ser Phe Gly Ser	
130 135 140 145	
aac ctg caa cag cac cag aac cag gac agt gga gag aaa cac atc aga	775
Asn Leu Gln Gln His Gln Asn Gln Asp Ser Gly Glu Lys His Ile Arg	
146 151 156 161	
aag gag gag agc agt gcc ttg ctt ctg aat agc tgc aaa att cct ctg	823
Lys Glu Glu Ser Ser Ala Leu Leu Leu Asn Ser Cys Lys Ile Pro Leu	
162 167 172 177	
tca gac aat ctt ttc cca tgc aaa gat gtt gag aag gat ttt cca acc	871
Ser Asp Asn Leu Phe Pro Cys Lys Asp Val Glu Lys Asp Phe Pro Thr	
178 183 188 193	
atc ctg ggc ctt ctc caa cac cag acc acc cac agc aga caa gag tat	919
Ile Leu Gly Leu Leu Gln His Gln Thr Thr His Ser Arg Gln Glu Tyr	
194 199 204 209	
gca cat aga agc agg gag acc ttt caa caa aga cgt tac aaa tgt gag	967
Ala His Arg Ser Arg Glu Thr Phe Gln Gln Arg Arg Tyr Lys Cys Glu	
210 215 220 225	
caa gtt ttc aat gag aaa gtt cat gtt act gag cat cag aga gtc cac	1015
Gln Val Phe Asn Glu Lys Val His Val Thr Glu His Gln Arg Val His	
226 231 236 241	
act gga gaa aaa gct tat aag cgt agg gaa tat ggg aaa tcc ttg aac	1063
Thr Gly Glu Lys Ala Tyr Lys Arg Arg Glu Tyr Gly Lys Ser Leu Asn	
242 247 252 257	
tct aaa tac tta ttt gtt gaa cac cag aga acc cat aat gca gaa aag	1111
Ser Lys Tyr Leu Phe Val Glu His Gln Arg Thr His Asn Ala Glu Lys	
258 263 268 273	
cct tat gtg tgc aat ata tgt ggg aaa tca ttc ctc cat aaa caa aca	1159
Pro Tyr Val Cys Asn Ile Cys Gly Lys Ser Phe Leu His Lys Gln Thr	
274 279 284 289	
ctc gtt ggg cac cag cag aga att cac act aga gaa agg tct tat gtg	1207
Leu Val Gly His Gln Gln Arg Ile His Thr Arg Glu Arg Ser Tyr Val	
290 295 300 305	
tgc atc gaa tgt ggg aaa tcc ttg agc tcc aaa tac tca ctt gtg gaa	1255
Cys Ile Glu Cys Gly Lys Ser Leu Ser Ser Lys Tyr Ser Leu Val Glu	
306 311 316 321	
cac cag aga acc cat aat gga gaa aag cct tat gtg tgc aat gta tgt	1303
His Gln Arg Thr His Asn Gly Glu Lys Pro Tyr Val Cys Asn Val Cys	
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Gln	Ser	Leu	Leu	Asp	His	His	Arg	Ile	His	Thr	Gly	Glu	Arg	Pro	Tyr	
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gag tgg gag ttc gag gtg aca gcc ttc tac cgg ggc cgc caa gtc ttc Glu Trp Glu Phe Glu Val Thr Ala Phe Tyr Arg Gly Arg Gln Val Phe 201 206 211 216	855
cag cag acc atc tcc tgc ccg gag ggc ctg cgg ctg gtg ggg tcc gaa Gln Gln Thr Ile Ser Cys Pro Glu Gly Leu Arg Leu Val Gly Ser Glu 217 222 227 232	903
gtg gga gac agg acg ctg cct gga tgg cca gtc aca ctg cca gac cct Val Gly Asp Arg Thr Leu Pro Gly Trp Pro Val Thr Leu Pro Asp Pro 233 238 243 248	951
ggc atg tcc ctg aca gac agg gga gtg atg agc tac gtg agg cat gtg Gly Met Ser Leu Thr Asp Arg Gly Val Met Ser Tyr Val Arg His Val 249 254 259 264	999
ctg agc tgc ctg ggt ggg gga ctg gct ctc tgg cgg gcc ggg cag tgg Leu Ser Cys Leu Gly Gly Gly Leu Ala Leu Trp Arg Ala Gly Gln Trp 265 270 275 280	1047
ctc tgg gcc cag cgg ctg ggg cac tgc cac aca tac tgg gca gtg agc Leu Trp Ala Gln Arg Leu Gly His Cys His Thr Tyr Trp Ala Val Ser 281 286 291 296	1095
gag gag ctg ctc ccc aac agc ggg cat ggg cct gat ggc gag gtc ccc Glu Glu Leu Leu Pro Asn Ser Gly His Gly Pro Asp Gly Glu Val Pro 297 302 307 312	1143
aag gac aag gaa gga ggc gtg ttt gac ctg ggg ccc ttc att gta gat Lys Asp Lys Glu Gly Gly Val Phe Asp Leu Gly Pro Phe Ile Val Asp 313 318 323 328	1191
ctg att acc ttc acg gaa gga agc gga cgc tca cca cgc tat gcc ctc Leu Ile Thr Phe Thr Glu Gly Ser Gly Arg Ser Pro Arg Tyr Ala Leu 329 334 339 344	1239
tgg ttc tgt gtg ggg gag tca tgg ccc cag gac cag ccg tgg acc aag Trp Phe Cys Val Gly Glu Ser Trp Pro Gln Asp Gln Pro Trp Thr Lys 345 350 355 360	1287

agg ctc gtg atg gtc aag gtt gtg ccc acg tgc ctc agg gcc ttg gta	1335
Arg Leu Val Met Val Lys Val Val Pro Thr Cys Leu Arg Ala Leu Val	
361 366 371 376	
 gaa atg gcc cgg gta ggg ggt gcc tcc tcc ctg gag aat act gtg gac	1383
Glu Met Ala Arg Val Gly Gly Ala Ser Ser Leu Glu Asn Thr Val Asp	
377 382 387 392	
 ctg cac att tcc aac agc cac cca ctc tcc ctc acc tcc gac cag tac	1431
Leu His Ile Ser Asn Ser His Pro Leu Ser Leu Thr Ser Asp Gln Tyr	
393 398 403 408	
 aag gcc tac ctg cag gac ttg gtg gag ggc atg gat ttc cag ggc cct	1479
Lys Ala Tyr Leu Gln Asp Leu Val Glu Gly Met Asp Phe Gln Gly Pro	
409 414 419 424	
 ggg gag agc tga gcc ctcgctcctc atggtgtgcc tccaaccccc ctgttcccca	1534
Gly Glu Ser *	
425	
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	Met Ala Arg Val Leu
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 aag gct gca gcc gcg aat gcc gta ggg ctt ttt tcc aga ctt caa gct	101
Lys Ala Ala Ala Ala Asn Ala Val Gly Leu Phe Ser Arg Leu Gln Ala	
6 11 16 21	
 ccc att cca aca gta aga gct tct tcc aca tca cag ccc ttg gat caa	149
Pro Ile Pro Thr Val Arg Ala Ser Ser Thr Ser Gln Pro Leu Asp Gln	
22 27 32 37	
 gtg aca ggt tct gtg tgg aac ctg ggt cga ctc aac cat gta gcc ata	197
Val Thr Gly Ser Val Trp Asn Leu Gly Arg Leu Asn His Val Ala Ile	
38 43 48 53	
 gca gtg cca gat ttg gaa aag gct gca gca ttt tat aag aat att ctg	245
Ala Val Pro Asp Leu Glu Lys Ala Ala Ala Phe Tyr Lys Asn Ile Leu	
54 59 64 69	
 ggg gcc cag gta agt gaa gcg gtc cct ctt cct gaa cat gga gta tct	293
Gly Ala Gln Val Ser Glu Ala Val Pro Leu Pro Glu His Gly Val Ser	

70	75	80	85	
gtt gtt ttt gtc aac ctg gga aat acc aag atg gaa ctg ctt cat cca				341
Val Val Phe Val Asn Leu Gly Asn Thr Lys Met Glu Leu Leu His Pro				
86	91	96	101	
ttg gga cgt gac agt cca att gca ggt ttt ctg cag aaa aac aag gct				389
Leu Gly Arg Asp Ser Pro Ile Ala Gly Phe Leu Gln Lys Asn Lys Ala				
102	107	112	117	
gga gga atg cat cac atc tgc atc gag gtg gat aat att aat gca gct				437
Gly Gly Met His His Ile Cys Ile Glu Val Asp Asn Ile Asn Ala Ala				
118	123	128	133	
gtg atg gat ttg aaa aaa aag aag atc cgc agt cta agt gaa gag gtc				485
Val Met Asp Leu Lys Lys Lys Lys Ile Arg Ser Leu Ser Glu Glu Val				
134	139	144	149	
aaa ata gga gca cat gga aaa cca gtg att ttt ctc cat cct aaa gac				533
Lys Ile Gly Ala His Gly Lys Pro Val Ile Phe Leu His Pro Lys Asp				
150	155	160	165	
tgt ggt gga gtc ctt gtg gaa ctg gag caa gct tga ttta tatttgcaag				583
Cys Gly Gly Val Leu Val Glu Leu Glu Gln Ala *				
166	171	176		
caactaaatt aattgacctg aaaaagccta tcaaatacta tcaaaatgta ctatgacatt				643
gagtccttca ctgcttccat catgtaaaag ttcacagtta aagactgaat tacagaaaga				703
ttaaaatata tacatatata aatacataaa tatgtatatt atttagatta acaaacatat				763
ttgttaattt gaatttgaag aaaatcttga ttactaatta cttagggaac attattaaaa				823
tcatatagaa ataaattatt cctctttctac aatgggggtaa aaaaaaaaaa				873

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tcg aat ctt gtg ctc caa gct gac cgt tct ctc att gac cgg acc cgc	96
Ser Asn Leu Val Leu Gln Ala Asp Arg Ser Leu Ile Asp Arg Thr Arg	
17	22
27	32

cgg gat gaa ccc aca gga gag gtg ctg tcc ctt gtt ggg aag ctg gag	144
Arg Asp Glu Pro Thr Gly Glu Val Leu Ser Leu Val Gly Lys Leu Glu	
33 38 43 48	
ggc acc cgt atg gga gac aag gct caa cgg acc aaa ccg cag atg cag	192
Gly Thr Arg Met Gly Asp Lys Ala Gln Arg Thr Lys Pro Gln Met Gln	
49 54 59 64	
gag gaa aga aga gcc aag cga aga aag cgt gat gag gac cgg cat gac	240
Glu Glu Arg Arg Ala Lys Arg Arg Lys Arg Asp Glu Asp Arg His Asp	
65 70 75 80	
atc aac aag atg aag ggt tat act ctg ctg tcg gag ggc att gat gag	288
Ile Asn Lys Met Lys Gly Tyr Thr Leu Leu Ser Glu Gly Ile Asp Glu	
81 86 91 96	
atg gtg ggc atc atc tac aag ccc aaa act aaa gag act cgg gag acc	336
Met Val Gly Ile Ile Tyr Lys Pro Lys Thr Lys Glu Thr Arg Glu Thr	
97 102 107 112	
tat gag gtg cta ctc agc ttc atc cag gct gct ctt ggg gac cag cca	384
Tyr Glu Val Leu Leu Ser Phe Ile Gln Ala Ala Leu Gly Asp Gln Pro	
113 118 123 128	
cgt gat atc ctt tgt ggg gca gct gat gaa gtt cta gct gtt cta aag	432
Arg Asp Ile Leu Cys Gly Ala Ala Asp Glu Val Leu Ala Val Leu Lys	
129 134 139 144	
aat gaa aag ctg cgg gac aag gaa agg cga aag gag att gac ctg ctg	480
Asn Glu Lys Leu Arg Asp Lys Glu Arg Arg Lys Glu Ile Asp Leu Leu	
145 150 155 160	
ctg ggt caa aca gat gat acc aga tac cat gtg cta gtg aac ctg ggc	528
Leu Gly Gln Thr Asp Asp Thr Arg Tyr His Val Leu Val Asn Leu Gly	
161 166 171 176	
aaa aag atc aca gac tat ggt gga gat aag gaa atc caa aat atg gat	576
Lys Lys Ile Thr Asp Tyr Gly Gly Asp Lys Glu Ile Gln Asn Met Asp	
177 182 187 192	
gac aac att gat gag aca tac ggt gtg aat gtg cag ttt gag tct gat	624
Asp Asn Ile Asp Glu Thr Tyr Gly Val Asn Val Gln Phe Glu Ser Asp	
193 198 203 208	
gag gag gaa ggt gat gaa gac gta tac ggg gag gtt cga gaa gag gca	672
Glu Glu Glu Gly Asp Glu Asp Val Tyr Gly Glu Val Arg Glu Glu Ala	
209 214 219 224	
tct gat gat gac atg gaa ggg gac gag gct gtc gtg cgc tgc acc ctc	720
Ser Asp Asp Asp Met Glu Gly Asp Glu Ala Val Val Arg Cys Thr Leu	
225 230 235 240	
tcg gct aat atg tat gtt gat gaa atc tta gtc tgg tgt gct tct gaa	768
Ser Ala Asn Met Tyr Val Asp Glu Ile Leu Val Trp Cys Ala Ser Glu	
241 246 251 256	
ctc aat att cca gag ttt ttt cct ctg gaa agt cct cac aag aag gtg	816

Leu Asn Ile Pro Glu Phe Phe Pro Leu Glu Ser Pro His Lys Lys Val	
257 262 267 272	
ggc tat gga ttg tca agt aga act tgg ttg cag ggt ggt ggc aaa gtg	864
Gly Tyr Gly Leu Ser Ser Arg Thr Trp Leu Gln Gly Gly Gly Lys Val	
273 278 283 288	
atc gag gct ggc aga gac ctg ctc gta gcc tca ggt gaa ctg atg agt	912
Ile Glu Ala Gly Arg Asp Leu Leu Val Ala Ser Gly Glu Leu Met Ser	
289 294 299 304	
tcc aag aag aag gat ttg cac cct cgg gat att gat gca ttt tgg ctg	960
Ser Lys Lys Lys Asp Leu His Pro Arg Asp Ile Asp Ala Phe Trp Leu	
305 310 315 320	
cag cgg cag ctc agt cgt ttc tat gat gat gcc atc gtg tcg cag aag	1008
Gln Arg Gln Leu Ser Arg Phe Tyr Asp Asp Ala Ile Val Ser Gln Lys	
321 326 331 336	
aag gca gat gaa gta ttg gag att ttg aag acg gcc agt gat gat cgg	1056
Lys Ala Asp Glu Val Leu Glu Ile Leu Lys Thr Ala Ser Asp Asp Arg	
337 342 347 352	
gaa tgt gaa aat cag ctg gtt ctg ctg ctt ggt ttc aac acc ttt gat	1104
Glu Cys Glu Asn Gln Leu Val Leu Leu Leu Gly Phe Asn Thr Phe Asp	
353 358 363 368	
ttc att aaa gtg ttg cgg cag cac agg atg atg att tta tac tgt acc	1152
Phe Ile Lys Val Leu Arg Gln His Arg Met Met Ile Leu Tyr Cys Thr	
369 374 379 384	
ttg ctg gcc agt gca caa agt gaa gct gaa aag gaa agg att atg gga	1200
Leu Leu Ala Ser Ala Gln Ser Glu Ala Glu Lys Glu Arg Ile Met Gly	
385 390 395 400	
aag atg gaa gct gac cca gag cta tcc aag ttc ctc tac cag ctt cat	1248
Lys Met Glu Ala Asp Pro Glu Leu Ser Lys Phe Leu Tyr Gln Leu His	
401 406 411 416	
gaa acc gag aag gag gat ctg atc cga gag gaa agg tcc cgg aga gag	1296
Glu Thr Glu Lys Glu Asp Leu Ile Arg Glu Glu Arg Ser Arg Arg Glu	
417 422 427 432	
cga gtg cgt cag tct cga atg gac aca gat ctg gaa acc atg gat ctc	1344
Arg Val Arg Gln Ser Arg Met Asp Thr Asp Leu Glu Thr Met Asp Leu	
433 438 443 448	
gac cag ggt gga gag gca ctg gct cca cgg cag gtt ctg gac ttg gag	1392
Asp Gln Gly Gly Glu Ala Leu Ala Pro Arg Gln Val Leu Asp Leu Glu	
449 454 459 464	
gac ctg gtt ttt acc caa ggg agc cac ttt atg gcc aat aaa cgc tgt	1440
Asp Leu Val Phe Thr Gln Gly Ser His Phe Met Ala Asn Lys Arg Cys	
465 470 475 480	
cag ctt cct gat gga tcc ttc cgt cgc cag cgt aag ggc tat gaa gag	1488
Gln Leu Pro Asp Gly Ser Phe Arg Arg Gln Arg Lys Gly Tyr Glu Glu	

481	486	491	496	
gtg cat gtg cct gct ctg aag ccc aag ccc ttt ggc tca gaa gaa caa				1536
Val His Val Pro Ala Leu Lys Pro Lys Pro Phe Gly Ser Glu Glu Gln				
497	502	507	512	
ctg ctt cca gtg gaa aag ctg cca aag tat gcc cag gct ggg ttt gag				1584
Leu Leu Pro Val Glu Lys Leu Pro Lys Tyr Ala Gln Ala Gly Phe Glu				
513	518	523	528	
ggc ttc aaa aca ctg aat cgg atc cag agt aag ctc tac cgt gct gcc				1632
Gly Phe Lys Thr Leu Asn Arg Ile Gln Ser Lys Leu Tyr Arg Ala Ala				
529	534	539	544	
ctt gag acg gat gag aat ctg ctg ctg tgt gct cct act ggt gct ggg				1680
Leu Glu Thr Asp Glu Asn Leu Leu Leu Cys Ala Pro Thr Gly Ala Gly				
545	550	555	560	
aag acc aac gtg gcc ctg atg tgc atg ctc cga gag att ggg aaa cac				1728
Lys Thr Asn Val Ala Leu Met Cys Met Leu Arg Glu Ile Gly Lys His				
561	566	571	576	
ata aac atg gac ggc acc atc aat gtg gat gac ttc aag att atc tac				1776
Ile Asn Met Asp Gly Thr Ile Asn Val Asp Asp Phe Lys Ile Ile Tyr				
577	582	587	592	
att gcc ccc atg cgc tcc ttg gtg cag gag atg gtg ggc agc ttt gga				1824
Ile Ala Pro Met Arg Ser Leu Val Gln Glu Met Val Gly Ser Phe Gly				
593	598	603	608	
aag cgc ctg gcc act tat ggc atc act gtt gct gaa ctg act ggg gac				1872
Lys Arg Leu Ala Thr Tyr Gly Ile Thr Val Ala Glu Leu Thr Gly Asp				
609	614	619	624	
cac cag ctg tgc aaa gaa gag atc agt gcc act cag atc atc gtc tgc				1920
His Gln Leu Cys Lys Glu Glu Ile Ser Ala Thr Gln Ile Ile Val Cys				
625	630	635	640	
acc ccc gag aag tgg gac atc atc acc cgc aag ggt ggt gag cgc acc				1968
Thr Pro Glu Lys Trp Asp Ile Ile Thr Arg Lys Gly Gly Glu Arg Thr				
641	646	651	656	
tac acc cag ctg gtg cgg ctc atc att ctg gat gag att cat ctt ctc				2016
Tyr Thr Gln Leu Val Arg Leu Ile Ile Leu Asp Glu Ile His Leu Leu				
657	662	667	672	
cac gat gac aga ggt cct gtc tta gaa gct tta gtg gcc agg gcc atc				2064
His Asp Asp Arg Gly Pro Val Leu Glu Ala Leu Val Ala Arg Ala Ile				
673	678	683	688	
cga aac att gag atg acc caa gag gat gtc cga ctc att ggt ctc agt				2112
Arg Asn Ile Glu Met Thr Gln Glu Asp Val Arg Leu Ile Gly Leu Ser				
689	694	699	704	
gcc acc cta ccc aac tat gaa gat gta gcc acc ttt cta cgt gtt gac				2160
Ala Thr Leu Pro Asn Tyr Glu Asp Val Ala Thr Phe Leu Arg Val Asp				
705	710	715	720	

cct gcc aag ggt ctc ttt tac ttt gac aac agc ttc cgt cca gtg cct	2208
Pro Ala Lys Gly Leu Phe Tyr Phe Asp Asn Ser Phe Arg Pro Val Pro	
721 726 731 736	
ctg gaa cag aca tat gtg ggt atc aca gag aaa aaa gct atc aag cgt	2256
Leu Glu Gln Thr Tyr Val Gly Ile Thr Glu Lys Lys Ala Ile Lys Arg	
737 742 747 752	
ttc cag atc atg aat gaa ata gtc tat gaa aaa atc atg gaa cat gct	2304
Phe Gln Ile Met Asn Glu Ile Val Tyr Glu Lys Ile Met Glu His Ala	
753 758 763 768	
gga aaa aat cag gtg ctc gtg ttt gtc cat tct cgc aaa gaa act ggg	2352
Gly Lys Asn Gln Val Leu Val Phe Val His Ser Arg Lys Glu Thr Gly	
769 774 779 784	
aag aca gca agg gca atc cgt gac atg tgt ctg gag aag gac act ttg	2400
Lys Thr Ala Arg Ala Ile Arg Asp Met Cys Leu Glu Lys Asp Thr Leu	
785 790 795 800	
ggc ctg ttt ctt cgc gag ggt tct gcc tcc act gaa gtc ctt cgt aca	2448
Gly Leu Phe Leu Arg Glu Gly Ser Ala Ser Thr Glu Val Leu Arg Thr	
801 806 811 816	
gaa gca gag cag tgc aag aac ttg gag ctg aag gat ctt ttg ccc tat	2496
Glu Ala Glu Gln Cys Lys Asn Leu Glu Leu Lys Asp Leu Leu Pro Tyr	
817 822 827 832	
ggc ttt gct att cat cat gca ggc atg act aga gtt gac cga aca ctt	2544
Gly Phe Ala Ile His His Ala Gly Met Thr Arg Val Asp Arg Thr Leu	
833 838 843 848	
gta gaa gat ctt ttt ggt gac aag cat att cag gtt tta gtt tcc acc	2592
Val Glu Asp Leu Phe Gly Asp Lys His Ile Gln Val Leu Val Ser Thr	
849 854 859 864	
gca act ctg gcg tgg ggt gta aat ctt cct gca cat aca gtc atc att	2640
Ala Thr Leu Ala Trp Gly Val Asn Leu Pro Ala His Thr Val Ile Ile	
865 870 875 880	
aaa ggt acc caa gtg tac agt cca gag aag ggg cgt tgg aca gag ctg	2688
Lys Gly Thr Gln Val Tyr Ser Pro Glu Lys Gly Arg Trp Thr Glu Leu	
881 886 891 896	
gga gca ctg gat atc ctg cag atg ctg ggc cgt gct gga cgg ccg cag	2736
Gly Ala Leu Asp Ile Leu Gln Met Leu Gly Arg Ala Gly Arg Pro Gln	
897 902 907 912	
tat gac acc aag ggt gaa ggc atc ctc atc aca tcc cat ggg gag ctc	2784
Tyr Asp Thr Lys Gly Glu Gly Ile Leu Ile Thr Ser His Gly Glu Leu	
913 918 923 928	
cag tac tac ctc tcc ctc ctc aac cag cag ctg cct atc gag agc cag	2832
Gln Tyr Tyr Leu Ser Leu Leu Asn Gln Gln Leu Pro Ile Glu Ser Gln	
929 934 939 944	

atg gtc tcc aag ctg cct gac atg ctc aat gcg gaa att gtt ctg ggc	2880
Met Val Ser Lys Leu Pro Asp Met Leu Asn Ala Glu Ile Val Leu Gly	
945 950 955 960	
aat gtc cag aat gca aag gat gca gtg aac tgg ctg ggc tat gcc tac	2928
Asn Val Gln Asn Ala Lys Asp Ala Val Asn Trp Leu Gly Tyr Ala Tyr	
961 966 971 976	
cta tac atc cga atg ctc cgg tcc cct acc ctc tat ggc att tct cat	2976
Leu Tyr Ile Arg Met Leu Arg Ser Pro Thr Leu Tyr Gly Ile Ser His	
977 982 987 992	
gat gac ctc aag gga gat ccc ttg ctg gac cag cgc cga ctc gat ctt	3024
Asp Asp Leu Lys Gly Asp Pro Leu Leu Asp Gln Arg Arg Leu Asp Leu	
993 998 1003 1008	
gtt cac act gct gcc ttg atg ctg gac aag aac aat ctg gtc aag tac	3072
Val His Thr Ala Ala Leu Met Leu Asp Lys Asn Asn Leu Val Lys Tyr	
1009 1014 1019 1024	
gac aag aag aca ggc aac ttc cag gtg aca gaa ctt ggc cgg ata gca	3120
Asp Lys Lys Thr Gly Asn Phe Gln Val Thr Glu Leu Gly Arg Ile Ala	
1025 1030 1035 1040	
agt cac tac tat atc acc aat gat act gtg cag acc tac aac cag ctg	3168
Ser His Tyr Tyr Ile Thr Asn Asp Thr Val Gln Thr Tyr Asn Gln Leu	
1041 1046 1051 1056	
ctg aag cct act ctg agt gag att gag ctt ttc cga gtg ttc tcc ttg	3216
Leu Lys Pro Thr Leu Ser Glu Ile Glu Leu Phe Arg Val Phe Ser Leu	
1057 1062 1067 1072	
tcc tca gag ttc aag aac atc act gta aga gag gag gag aag ctg gag	3264
Ser Ser Glu Phe Lys Asn Ile Thr Val Arg Glu Glu Glu Lys Leu Glu	
1073 1078 1083 1088	
ctg cag aag ttg ctg gag aga gtg ccc atc cct gta aag gag agc att	3312
Leu Gln Lys Leu Leu Glu Arg Val Pro Ile Pro Val Lys Glu Ser Ile	
1089 1094 1099 1104	
gag gaa ccc agc gct aag atc aac gtg ctt ctc caa gcc ttc atc tca	3360
Glu Glu Pro Ser Ala Lys Ile Asn Val Leu Leu Gln Ala Phe Ile Ser	
1105 1110 1115 1120	
cag ctg aaa ctc gaa ggc ttt gcg ctg atg gct gac atg gtg tat gtg	3408
Gln Leu Lys Leu Glu Gly Phe Ala Leu Met Ala Asp Met Val Tyr Val	
1121 1126 1131 1136	
acc cag tcg gct ggc cgg ttg atg cgt gca atc ttc gaa att gtc ctg	3456
Thr Gln Ser Ala Gly Arg Leu Met Arg Ala Ile Phe Glu Ile Val Leu	
1137 1142 1147 1152	
aac cga ggt tgg gca cag ctt aca gat aag acc ctg aat ctc tgc aag	3504
Asn Arg Gly Trp Ala Gln Leu Thr Asp Lys Thr Leu Asn Leu Cys Lys	
1153 1158 1163 1168	
atg att gac aag cgc atg tgg cag tcc atg tgt cct ctt cgc cag ttc	3552

Met Ile Asp Lys Arg Met Trp Gln Ser Met Cys Pro Leu Arg Gln Phe	
1169 1174 1179 1184	
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Arg Lys Leu Pro Glu Glu Val Val Lys Lys Ile Glu Lys Lys Asn Phe	
1185 1190 1195 1200	
ccc ttt gag cgg ctg tat gac ttg aat cat aat gag ata ggt gaa ctt	3648
Pro Phe Glu Arg Leu Tyr Asp Leu Asn His Asn Glu Ile Gly Glu Leu	
1201 1206 1211 1216	
att cga atg ccg aag atg ggg aag acc atc cac aag tat gtc cat ctt	3696
Ile Arg Met Pro Lys Met Gly Lys Thr Ile His Lys Tyr Val His Leu	
1217 1222 1227 1232	
ttc ccc aag ttg gag ttg tca gtg cac ctg cag cct att aca cgc tct	3744
Phe Pro Lys Leu Glu Leu Ser Val His Leu Gln Pro Ile Thr Arg Ser	
1233 1238 1243 1248	
acg ctg aaa gta gag ctg act atc aca cca gat ttc cag tgg gat gaa	3792
Thr Leu Lys Val Glu Leu Thr Ile Thr Pro Asp Phe Gln Trp Asp Glu	
1249 1254 1259 1264	
aag gtc cat ggt tgc tca gag gca ttt tgg att ctg gtg gag gat gtg	3840
Lys Val His Gly Ser Ser Glu Ala Phe Trp Ile Leu Val Glu Asp Val	
1265 1270 1275 1280	
gac agc gag gtg att ctg cac cat gaa tat ttt ctg ctg aag gcc aag	3888
Asp Ser Glu Val Ile Leu His His Glu Tyr Phe Leu Leu Lys Ala Lys	
1281 1286 1291 1296	
tat gcc cag gat gag cac ctc atc aca ttc ttt gtt cca gtc ttt gaa	3936
Tyr Ala Gln Asp Glu His Leu Ile Thr Phe Phe Val Pro Val Phe Glu	
1297 1302 1307 1312	
cca cta cct cct cag tac ttc att cga gta gtg tct gat cgc tgg ctc	3984
Pro Leu Pro Pro Gln Tyr Phe Ile Arg Val Val Ser Asp Arg Trp Leu	
1313 1318 1323 1328	
tct tgt gag acg cag cta cct gtc tcc ttc cgg cat ctg atc cta cca	4032
Ser Cys Glu Thr Gln Leu Pro Val Ser Phe Arg His Leu Ile Leu Pro	
1329 1334 1339 1344	
gag aag tac cca cct cca act gaa ctg ttg gac ctg cag cca ttg cct	4080
Glu Lys Tyr Pro Pro Pro Thr Glu Leu Leu Asp Leu Gln Pro Leu Pro	
1345 1350 1355 1360	
gtg tct gct ctg aga aac agt gct ttt gag agc ctt tac caa gat aaa	4128
Val Ser Ala Leu Arg Asn Ser Ala Phe Glu Ser Leu Tyr Gln Asp Lys	
1361 1366 1371 1376	
ttt cct ttc ttc aat ccc atc cag act caa gta ttt aat acc gtg tac	4176
Phe Pro Phe Phe Asn Pro Ile Gln Thr Gln Val Phe Asn Thr Val Tyr	
1377 1382 1387 1392	
aac agt gat gat aac gtg ttt gtg ggg gcc ccc acg ggc agc ggg aag	4224
Asn Ser Asp Asp Asn Val Phe Val Gly Ala Pro Thr Gly Ser Gly Lys	

1393	1398	1403	1408	
act atc tgc gcg gag ttt gcc atc ctt cgg atg ctg ctg cag aat tct				4272
Thr Ile Cys Ala Glu Phe Ala Ile Leu Arg Met Leu Leu Gln Asn Ser				
1409	1414	1419	1424	
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Glu Gly Arg Cys Val Tyr Ile Thr Pro Met Arg Leu Trp Gln Glu Gln				
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1115

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Met Val Gly Ile Ile Tyr Lys Pro Lys Thr Lys Glu Thr Arg Glu Thr	
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Tyr Glu Val Leu Leu Ser Phe Ile Gln Ala Ala Leu Gly Asp Gln Pro	
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Trp Leu Ser Cys Glu Thr Gln Leu Pro Val Ser Phe Arg His Leu Ile	
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Leu Pro Glu Lys Tyr Pro Pro Pro Thr Glu Leu Leu Asp Leu Gln Pro	
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Leu Pro Val Ser Ala Leu Arg Asn Ser Ala Phe Glu Ser Leu Tyr Gln	
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Asp Lys Phe Pro Phe Phe Asn Pro Ile Gln Thr Gln Val Phe Asn Thr	
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Val Tyr Asn Ser Asp Asp Asn Val Phe Val Gly Ala Pro Thr Gly Ser	
1377 1382 1387 1392	
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Gly Lys Thr Ile Cys Ala Glu Phe Ala Ile Leu Arg Met Leu Leu Gln	
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Ser Ser Glu Gly Arg Cys Val Tyr Ile Thr Pro Met Glu Ala Leu Ala	
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Glu Gln Val Tyr Met Asp Trp Tyr Glu Lys Phe Gln Asp Arg Leu Asn	

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Lys Lys Val Val Leu Leu	Thr Gly Glu Thr Ser	Thr Asp Leu Lys Leu		
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Leu Gly Lys Gly Asn Ile	Ile Ile Ser Thr Pro	Glu Lys Trp Asp Ile		
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Leu Ser Arg Arg Trp Lys	Gln Arg Lys Asn Val	Gln Asn Ile Asn Leu		
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Phe Val Val Asp Glu Val	His Leu Ile Gly Gly	Glu Asn Gly Pro Val		
1489	1494	1499	1504	
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Leu Glu Val Ile Cys Ser	Arg Met Arg Tyr Ile	Ser Ser Gln Ile Glu		
1505	1510	1515	1520	
cgg ccc att cgc att gtg	gca ctc agc tct tgc	ctc tcc aat gcc aag		4608
Arg Pro Ile Arg Ile Val	Ala Leu Ser Ser Ser	Leu Ser Asn Ala Lys		
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gat gtg gcc cac tgg ctg	ggc tgc agt gcc acc	tcc acc ttc aac ttc		4656
Asp Val Ala His Trp Leu	Gly Cys Ser Ala Thr	Ser Thr Phe Asn Phe		
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cat ccc aat gtg cgt ccc	gtc ccc ttg gag ctg	cac atc cag ggc ttc		4704
His Pro Asn Val Arg Pro	Val Pro Leu Glu Leu	His Ile Gln Gly Phe		
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Asn Ile Ser His Thr Gln	Thr Arg Leu Leu Ser	Met Ala Lys Pro Val		
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Tyr His Ala Ile Thr Lys	His Ser Pro Lys Lys	Pro Val Ile Val Phe		
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Val Pro Ser Arg Lys Gln	Thr Arg Leu Thr Ala	Ile Asp Ile Leu Thr		
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Thr Cys Ala Ala Asp Ile	Gln Arg Gln Arg Phe	Leu His Cys Thr Glu		
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Lys Asp Leu Ile Pro Tyr	Leu Glu Lys Leu Ser	Asp Ser Thr Leu Lys		
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gaa acg ctg cta aat ggg	gtg ggc tac ctg cat	gag ggg ctc agc ccc		4992
Glu Thr Leu Leu Asn Gly	Val Gly Tyr Leu His	Glu Gly Leu Ser Pro		
1649	1654	1659	1664	

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Met Glu Arg Arg Leu Val Glu Gln Leu Phe Ser Ser Gly Ala Ile Gln	
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Val Val Val Ala Ser Arg Ser Leu Cys Trp Gly Met Asn Val Ala Ala	
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His Leu Val Ile Ile Met Asp Thr Gln Tyr Tyr Asn Gly Lys Ile His	
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gcc tat gtg gat tac ccc atc tat gac gtg ctt cag atg gtg ggc cac	5184
Ala Tyr Val Asp Tyr Pro Ile Tyr Asp Val Leu Gln Met Val Gly His	
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Ala Asn Arg Pro Leu Gln Asp Asp Glu Gly Arg Cys Val Ile Met Cys	
1729 1734 1739 1744	
cag ggc tcc aag aag gat ttc ttc aag aag ttc tta tat gag cca ttg	5280
Gln Gly Ser Lys Lys Asp Phe Phe Lys Lys Phe Leu Tyr Glu Pro Leu	
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cca gta gaa tct cac ctg gac cac tgt atg cat gac cac ttc aat gct	5328
Pro Val Glu Ser His Leu Asp His Cys Met His Asp His Phe Asn Ala	
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Glu Ile Val Thr Lys Thr Ile Glu Asn Lys Gln Asp Ala Val Asp Tyr	
1777 1782 1787 1792	
ctc acc tgg acc ttt ctg tac cgc cgc atg aca cag aac ccc aat tac	5424
Leu Thr Trp Thr Phe Leu Tyr Arg Arg Met Thr Gln Asn Pro Asn Tyr	
1793 1798 1803 1808	
tac aac ctg cag ggc atc tcc cat cgt cac ttg tcg gac cac ttg tca	5472
Tyr Asn Leu Gln Gly Ile Ser His Arg His Leu Ser Asp His Leu Ser	
1809 1814 1819 1824	
gag ctg gtg gag cag acc ctg agt gac ctg gag cag tcc aag tgc atc	5520
Glu Leu Val Glu Gln Thr Leu Ser Asp Leu Glu Gln Ser Lys Cys Ile	
1825 1830 1835 1840	
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Ser Ile Glu Asp Glu Met Asp Val Ala Pro Leu Asn Leu Gly Met Ile	
1841 1846 1851 1856	
gcc gcc tac tat tac atc aac tac acc acc att gag ctc ttc agc atg	5616
Ala Ala Tyr Tyr Tyr Ile Asn Tyr Thr Thr Ile Glu Leu Phe Ser Met	
1857 1862 1867 1872	
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Ser Leu Asn Ala Lys Thr Lys Val Arg Gly Leu Ile Glu Ile Ile Ser	
1873 1878 1883 1888	

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ctc ctg agg cag ttg gct cag aag gtc ccc cac aag ctg aat aac cct Leu Leu Arg Gln Leu Ala Gln Lys Val Pro His Lys Leu Asn Asn Pro 1905 1910 1915 1920	5760
aag ttc aat gat ccg cac gtc aag acc aac ctg ctc ctg cag gct cac Lys Phe Asn Asp Pro His Val Lys Thr Asn Leu Leu Leu Gln Ala His 1921 1926 1931 1936	5808
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cga gag gag gaa gtc aca ggc cct gtc att gcg cct ctc ttc ccg cag Arg Glu Glu Glu Val Thr Gly Pro Val Ile Ala Pro Leu Phe Pro Gln 2081 2086 2091 2096	6288
aaa cgt gaa gag ggc tgg tgg gtg gtg att gga gat gcc aag tcc aat Lys Arg Glu Glu Gly Trp Trp Val Val Ile Gly Asp Ala Lys Ser Asn 2097 2102 2107 2112	6336
agc ctc atc tcc atc aag agg ctg acc ttg cag cag aag gcc aag gtg	6384

Ser	Leu	Ile	Ser	Ile	Lys	Arg	Leu	Thr	Leu	Gln	Gln	Lys	Ala	Lys	Val	
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Lys	Leu	Asp	Phe	Val	Ala	Pro	Ala	Thr	Gly	Ala	His	Asn	Tyr	Thr	Leu	
2129					2134					2139					2144	
tac	ttc	atg	agt	gac	gct	tac	atg	gga	tgt	gac	cag	gag	tac	aaa	ttc	6480
Tyr	Phe	Met	Ser	Asp	Ala	Tyr	Met	Gly	Cys	Asp	Gln	Glu	Tyr	Lys	Phe	
2145					2150					2155					2160	
agc	gtg	gat	gtg	aaa	gaa	gct	gag	aca	gac	agt	gat	tca	gat	tga		6525
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gctacctgcc	cagggctccc	ggtggccagt	gtcagcagc	ccgggactcc	ccgcagcctt											240
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		Met	Ile	Val	Leu	Gly	Phe	Ser	Asn	Pro	Ile	Asn	Trp			
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Val Arg Thr Arg Ile Lys Ala Phe Leu Ile Trp Ala Tyr Phe Asp Lys																
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Glu Phe Ser Ile Thr Glu Phe Ser Glu Gly Ala Lys Gln Ala Phe Ala																
29					34						39				44	
cat gta tcc aag ttg ctg tca cag tgt aaa ttt gat ctg ttg gaa gaa																493
His Val Ser Lys Leu Leu Ser Gln Cys Lys Phe Asp Leu Leu Glu Glu																
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Leu Val Ala Lys Glu Val Leu His Ala Leu Lys Glu Lys Val Thr Ser																

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cta cct gac aac cat	aaa aat gcc ctt gct	gct aac ata gat gaa att		589
Leu Pro Asp Asn His	Lys Asn Ala Leu Ala	Ala Asn Ile Asp Glu Ile		
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gta ttt aca tca aca	gga gac atc tcc att	tac tat gat gag aaa gga		637
Val Phe Thr Ser Thr	Gly Asp Ile Ser Ile	Tyr Tyr Asp Glu Lys Gly		
93	98	103	108	
agg aag ttt gtt aac	atc ctg atg tgc ttt	tgg tat cta acc agt gcc		685
Arg Lys Phe Val Asn	Ile Leu Met Cys Phe	Trp Tyr Leu Thr Ser Ala		
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aac atc ccc agt gaa	act tta aga gga gcc	agt gta ttc cag gtt aag		733
Asn Ile Pro Ser Glu	Thr Leu Arg Gly Ala	Ser Val Phe Gln Val Lys		
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Leu Gly Asn Gln Asn	Val Glu Thr Lys Gln	Leu Leu Ser Ala Ser Tyr		
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Glu Phe Gln Arg Glu	Phe Thr Gln Gly Val	Lys Pro Asp Trp Thr Ile		
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Ala Arg Ile Glu His	Ser Lys Leu Leu Glu	*		
173	178	183		
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Lys Lys Asp Gly Ser Gly Gly Ala Ser Gly Thr Leu Gln Pro Ser Ser	
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Gly Gly Gly Ser Ser Asn Ser Arg Glu Arg His Arg Leu Val Ser Lys	
26 31 36 41	
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His Lys Arg His Lys Ser Lys His Ser Lys Asp Met Gly Leu Val Thr	
42 47 52 57	
ccc gaa gca gca tcc ctg ggc aca gtt atc aaa cct ttg gtg gag tat	362
Pro Glu Ala Ala Ser Leu Gly Thr Val Ile Lys Pro Leu Val Glu Tyr	
58 63 68 73	
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Asp Asp Ile Ser Ser Asp Ser Asp Thr Phe Ser Asp Asp Met Ala Phe	
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Lys Leu Asp Arg Arg Glu Asn Asp Glu Arg Arg Gly Ser Asp Arg Ser	
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Asp Arg Leu His Lys His Arg His His Gln His Arg Arg Ser Arg Asp	
106 111 116 121	
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Leu Leu Lys Ala Lys Gln Thr Glu Lys Glu Lys Ser Gln Glu Val Ser	
122 127 132 137	
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Ser Lys Ser Gly Ser Met Lys Asp Arg Ile Ser Gly Ser Ser Lys Arg	
138 143 148 153	
tcg aat gag gag act gat gac tat ggg aag gcg cag gta gcc aaa agc	650
Ser Asn Glu Glu Thr Asp Asp Tyr Gly Lys Ala Gln Val Ala Lys Ser	
154 159 164 169	
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Ser Ser Lys Glu Ser Arg Ser Ser Lys Leu His Lys Glu Lys Thr Arg	
170 175 180 185	
aaa gaa cgg gag ctg aag tct ggg cac aaa gac cgg agt aaa agt cat	746
Lys Glu Arg Glu Leu Lys Ser Gly His Lys Asp Arg Ser Lys Ser His	
186 191 196 201	
cga aaa agg gaa aca ccc aaa agt tac aaa aca gtg gac agc cca aaa	794
Arg Lys Arg Glu Thr Pro Lys Ser Tyr Lys Thr Val Asp Ser Pro Lys	
202 207 212 217	

cg	aga	tcc	agg	agc	ccc	cac	agg	aag	tgg	tct	gac	agc	tcc	aaa	caa	842
Arg	Arg	Ser	Arg	Ser	Pro	His	Arg	Lys	Trp	Ser	Asp	Ser	Ser	Lys	Gln	
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Asp	Asp	Ser	Pro	Ser	Gly	Ala	Ser	Tyr	Gly	Gln	Asp	Tyr	Asp	Leu	Ser	
234					239					244					249	
ccc	tca	cga	tct	cat	acc	tcg	agc	aat	tat	gac	tcc	tac	aag	aaa	agt	938
Pro	Ser	Arg	Ser	His	Thr	Ser	Ser	Asn	Tyr	Asp	Ser	Tyr	Lys	Lys	Ser	
250					255					260					265	
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Pro	Gly	Ser	Thr	Ser	Arg	Arg	Gln	Ser	Val	Ser	Pro	Pro	Tyr	Lys	Glu	
266					271					276					281	
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Pro	Ser	Ala	Tyr	Gln	Ser	Ser	Thr	Arg	Ser	Pro	Ser	Pro	Tyr	Ser	Arg	
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Arg	Arg	Ser	Ser	Ser	Pro	Phe	Leu	Ser	Lys	Arg	Ser	Leu	Ser	Arg	Ser	
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Pro	Leu	Pro	Ser	Arg	Lys	Ser	Met	Lys	Ser	Arg	Ser	Arg	Ser	Pro	Ala	
346					351					356					361	
tat	tca	aga	cat	tca	tct	tct	cat	agt	aaa	aag	aag	aga	tcc	agt	tca	1274
Tyr	Ser	Arg	His	Ser	Ser	Ser	His	Ser	Lys	Lys	Lys	Arg	Ser	Ser	Ser	
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cgc	agt	cgt	cat	tcc	agt	atc	tca	cct	gtc	agg	ctt	cca	ctt	aat	tcc	1322
Arg	Ser	Arg	His	Ser	Ser	Ile	Ser	Pro	Val	Arg	Leu	Pro	Leu	Asn	Ser	
378					383					388					393	
agt	ctg	gga	gct	gaa	ctc	agt	aaa	aaa	aaa	aag	aaa	aaa	gca	gct	gct	1370
Ser	Leu	Gly	Ala	Glu	Leu	Ser	Lys	Lys	Lys	Lys	Lys	Lys	Ala	Ala	Ala	
394					399					404					409	
gct	gct	gca	gca	aag	atg	gat	gga	aag	gag	tcc	aag	ggg	tca	cct	gta	1418
Ala	Ala	Ala	Ala	Lys	Met	Asp	Gly	Lys	Glu	Ser	Lys	Gly	Ser	Pro	Val	
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Phe	Leu	Pro	Arg	Lys	Glu	Asn	Ser	Ser	Val	Glu	Ala	Lys	Asp	Ser	Gly	
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Pro Asp Thr Glu Leu Val Asn Val Thr His Leu Asn Thr Glu Val Lys	
458 463 468 473	
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Asn Ser Ser Asp Thr Gly Lys Val Lys Leu Asp Glu Asn Ser Glu Lys	
474 479 484 489	
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His Leu Val Lys Asp Leu Lys Ala Gln Gly Thr Arg Asp Ser Lys Pro	
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Ile Ala Leu Lys Glu Glu Ile Val Thr Pro Lys Glu Thr Glu Thr Ser	
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Glu Lys Glu Thr Pro Pro Pro Leu Pro Thr Ile Ala Ser Pro Pro Pro	
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Pro Leu Pro Thr Thr Thr Pro Pro Pro Gln Thr Pro Pro Leu Pro Pro	
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Leu Pro Pro Ile Pro Ala Leu Pro Gln Gln Pro Pro Leu Pro Pro Ser	
554 559 564 569	
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Gln Pro Ala Phe Ser Gln Val Pro Ala Ser Ser Thr Ser Thr Leu Pro	
570 575 580 585	
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Pro Ser Thr His Ser Lys Thr Ser Ala Val Ser Ser Gln Ala Asn Ser	
586 591 596 601	
cag ccc cct gta cag gtt tct gtg aag act caa gta tct gta aca gct	1994
Gln Pro Pro Val Gln Val Ser Val Lys Thr Gln Val Ser Val Thr Ala	
602 607 612 617	
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Ala Ile Pro His Leu Lys Thr Ser Thr Leu Pro Pro Leu Pro Leu Pro	
618 623 628 633	
ccc tta tta cct gga ggt gat gac atg gat agt cca aaa gaa act ctt	2090
Pro Leu Leu Pro Gly Gly Asp Asp Met Asp Ser Pro Lys Glu Thr Leu	
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cct tca aaa cct gtg aag aaa gag aag gaa cag agg aca cgt cac tta	2138
Pro Ser Lys Pro Val Lys Lys Glu Lys Glu Gln Arg Thr Arg His Leu	
650 655 660 665	
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Leu Thr Asp Leu Pro Leu Pro Pro Glu Leu Pro Gly Gly Asp Leu Ser	
666 671 676 681	
ccc cca gac tct cca gaa cca aag gca atc aca cca cct cag caa cca	2234
Pro Pro Asp Ser Pro Glu Pro Lys Ala Ile Thr Pro Pro Gln Gln Pro	
682 687 692 697	
tat aaa aag aga cca aaa att tgt tgt cct cgt tat gga gaa aga aga	2282
Tyr Lys Lys Arg Pro Lys Ile Cys Cys Pro Arg Tyr Gly Glu Arg Arg	
698 703 708 713	
caa aca gaa agc gac tgg ggg aaa cgc tgt gtg gac aag ttt gac att	2330
Gln Thr Glu Ser Asp Trp Gly Lys Arg Cys Val Asp Lys Phe Asp Ile	
714 719 724 729	
att ggg att att gga gaa gga acc tat ggc caa gta tat aaa gcc agg	2378
Ile Gly Ile Ile Gly Glu Gly Thr Tyr Gly Gln Val Tyr Lys Ala Arg	
730 735 740 745	
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Asp Lys Asp Thr Gly Glu Leu Val Ala Leu Lys Lys Val Arg Leu Asp	
746 751 756 761	
aat gag aaa gag ggc ttc cca atc aca gcc att cgt gaa atc aaa atc	2474
Asn Glu Lys Glu Gly Phe Pro Ile Thr Ala Ile Arg Glu Ile Lys Ile	
762 767 772 777	
ctt cgt cag tta atc cac cga agt gtt gtt aac atg aag gaa att gtc	2522
Leu Arg Gln Leu Ile His Arg Ser Val Val Asn Met Lys Glu Ile Val	
778 783 788 793	
aca gat aaa caa gat gca ctg gat ttc aag aag gac aaa ggt gcc ttt	2570
Thr Asp Lys Gln Asp Ala Leu Asp Phe Lys Lys Asp Lys Gly Ala Phe	
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Tyr Leu Val Phe Glu Tyr Met Asp His Asp Leu Met Gly Leu Leu Glu	
810 815 820 825	
tct ggt ttg gtg cac ttt tct gag gac cat atc aag tcg ttc atg aaa	2666
Ser Gly Leu Val His Phe Ser Glu Asp His Ile Lys Ser Phe Met Lys	
826 831 836 841	
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Gln Leu Met Glu Gly Leu Glu Tyr Cys His Lys Lys Asn Phe Leu His	
842 847 852 857	
cgg gat att aag tgt tct aac att ttg ctg aat aac agt ggg caa atc	2762
Arg Asp Ile Lys Cys Ser Asn Ile Leu Leu Asn Asn Ser Gly Gln Ile	
858 863 868 873	
aaa cta gca gat ttt gga ctt gct cgg ctc tat aac tct gaa gag agt	2810
Lys Leu Ala Asp Phe Gly Leu Ala Arg Leu Tyr Asn Ser Glu Glu Ser	
874 879 884 889	
cgc cct tac aca aac aaa gtc att act ttg tgg tac cga cct cca gaa	2858
Arg Pro Tyr Thr Asn Lys Val Ile Thr Leu Trp Tyr Arg Pro Pro Glu	

890	895	900	905	
cta ctg cta gga gag gaa cgt tac aca cca gcc ata gat gtt tgg agc				2906
Leu Leu Leu Gly Glu Glu Arg Tyr Thr Pro Ala Ile Asp Val Trp Ser				
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Cys Gly Cys Ile Leu Gly Glu Leu Phe Thr Lys Lys Pro Ile Phe Gln				
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gcc aat ctg gaa ctg gct cag cta gaa ctg atc agc cga ctt tgt ggt				3002
Ala Asn Leu Glu Leu Ala Gln Leu Glu Leu Ile Ser Arg Leu Cys Gly				
938	943	948	953	
agc cct tgt cca gct gtg tgg cct gat gtt atc aaa ctg ccc tac ttc				3050
Ser Pro Cys Pro Ala Val Trp Pro Asp Val Ile Lys Leu Pro Tyr Phe				
954	959	964	969	
aac acc atg aaa ccg aag aag caa tat cga agg cgt cta cga gaa gaa				3098
Asn Thr Met Lys Pro Lys Lys Gln Tyr Arg Arg Arg Leu Arg Glu Glu				
970	975	980	985	
ttc tct ttc att cct tct gca gca ctt gat tta ttg gac cac atg ctg				3146
Phe Ser Phe Ile Pro Ser Ala Ala Leu Asp Leu Leu Asp His Met Leu				
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aca cta gat cct agt aag cgg tgc aca gct gaa cag acc cta cag agc				3194
Thr Leu Asp Pro Ser Lys Arg Cys Thr Ala Glu Gln Thr Leu Gln Ser				
1002	1007	1012	1017	
gac ttc ctt aaa gat gtc gaa ctc agc aaa atg gct cct cca gac ctc				3242
Asp Phe Leu Lys Asp Val Glu Leu Ser Lys Met Ala Pro Pro Asp Leu				
1018	1023	1028	1033	
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Pro His Trp Gln Asp Cys His Glu Leu Trp Ser Lys Lys Arg Arg Arg				
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Gln Arg Gln Ser Gly Val Val Val Glu Glu Pro Pro Pro Ser Lys Thr				
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tct cga aaa gaa act acc tca ggg aca agt act gag cct gtg aag aac				3386
Ser Arg Lys Glu Thr Thr Ser Gly Thr Ser Thr Glu Pro Val Lys Asn				
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agc agc cca gca cca cct cag cct gct cct ggc aag gtg gag tct ggg				3434
Ser Ser Pro Ala Pro Pro Gln Pro Ala Pro Gly Lys Val Glu Ser Gly				
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gct ggg gat gca ata ggc ctt gct gac atc aca caa cag ctg aat caa				3482
Ala Gly Asp Ala Ile Gly Leu Ala Asp Ile Thr Gln Gln Leu Asn Gln				
1108	1103	1108	1113	
agt gaa ttg gca gtg tta tta aac ctg ctg cag agc caa acc gac ctg				3530
Ser Glu Leu Ala Val Leu Leu Asn Leu Leu Gln Ser Gln Thr Asp Leu				
1114	1119	1124	1129	

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Ser Ile Pro Gln Met Ala Gln Leu Leu Asn Ile His Ser Asn Pro Glu	
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Met Gln Gln Gln Leu Glu Ala Leu Asn Gln Ser Ile Ser Ala Leu Thr	
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gaa gct act tcc cag cag cag gac tca gag acc atg gcc cca gag gag	3674
Glu Ala Thr Ser Gln Gln Gln Asp Ser Glu Thr Met Ala Pro Glu Glu	
1162 1167 1172 1177	
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Ser Leu Lys Glu Ala Pro Ser Ala Pro Val Ile Leu Pro Ser Ala Glu	
1178 1183 1188 1193	
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Gln Met Thr Leu Glu Ala Ser Ser Thr Pro Ala Asp Met Gln Asn Ile	
1194 1199 1204 1209	
ttg gca gtt ctc ttg agt cag ctg atg aaa acc caa gag cca gca ggc	3818
Leu Ala Val Leu Leu Ser Gln Leu Met Lys Thr Gln Glu Pro Ala Gly	
1210 1215 1220 1225	
agt ctg gag gaa aac aac agt gac aag aac agt ggg cca cag ggg ccc	3866
Ser Leu Glu Glu Asn Asn Ser Asp Lys Asn Ser Gly Pro Gln Gly Pro	
1226 1231 1236 1241	
cga aga act ccc aca atg cca cag gag gag gca gca gca tgt cct cct	3914
Arg Arg Thr Pro Thr Met Pro Gln Glu Glu Ala Ala Ala Cys Pro Pro	
1242 1247 1252 1257	
cac att ctt cca cca gag aag agg ccc cct gag ccc ccc gga cct cca	3962
His Ile Leu Pro Pro Glu Lys Arg Pro Pro Glu Pro Pro Gly Pro Pro	
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Pro Pro Pro Pro Pro Pro Pro Leu Val Glu Gly Asp Leu Ser Ser Ala	
1274 1279 1284 1289	
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Pro Gln Glu Leu Asn Pro Ala Val Thr Ala Ala Leu Leu Gln Leu Leu	
1290 1295 1300 1305	
tcc cag cct gaa gca gag cct cct ggc cac ctg cca cat gag cac cag	4106
Ser Gln Pro Glu Ala Glu Pro Pro Gly His Leu Pro His Glu His Gln	
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gcc ttg aga cca atg gag tac tcc acc cga ccc cgt cca aac agg act	4154
Ala Leu Arg Pro Met Glu Tyr Ser Thr Arg Pro Arg Pro Asn Arg Thr	
1322 1327 1332 1337	
tat gga aac act gat ggg cct gaa aca ggg ttc agt gcc att gac act	4202
Tyr Gly Asn Thr Asp Gly Pro Glu Thr Gly Phe Ser Ala Ile Asp Thr	
1338 1343 1348 1353	

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 Met Pro His Gln Arg Pro Arg Thr Cys Ala Met Asn Pro Glu Leu Thr
 1 5 10 15

atg gaa agt ctg ggc act ttg cac ggc gcg cgc ggc ggc ggc agt ggc 154
 Met Glu Ser Leu Gly Thr Leu His Gly Ala Arg Gly Gly Gly Ser Gly
 17 22 27 32

ggg ggc ggc ggc ggg ggc ggc ggg ggc ggc ggc ggg ggc ccg ggc cat 202
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Pro Gly His
 33 38 43 48

gag cag gag ctg ctg gcc agc ccc agc ccc cac cac gcg cgc cgc ggc 250
 Glu Gln Glu Leu Leu Ala Ser Pro Ser Pro His His Ala Arg Arg Gly
 49 54 59 64

ccg cgt ggc tcg ctg cgg ggc cct ccg ccg cct cca acc gcg cac cag 298
 Pro Arg Gly Ser Leu Arg Gly Pro Pro Pro Pro Pro Thr Ala His Gln
 65 70 75 80

gag ctg ggc acg gcg gca gcg gcg gca gcg gcg gcg tcg cgc tcg gcc 346
 Glu Leu Gly Thr Ala Ala Ala Ala Ala Ala Ala Ala Ser Arg Ser Ala
 81 86 91 96

atg gtc acc agc atg gcc tcg atc ctg gac ggc ggc gac tac cgg ccc 394
 Met Val Thr Ser Met Ala Ser Ile Leu Asp Gly Gly Asp Tyr Arg Pro
 97 102 107 112

gag ctc tcc atc ccg ctg cac cac gcc atg agc atg tcc tgc gac tcg 442
 Glu Leu Ser Ile Pro Leu His His Ala Met Ser Met Ser Cys Asp Ser
 113 118 123 128

tct ccg cct ggc atg ggc atg agc aac acc tac acc acg ctg aca ccg 490
 Ser Pro Pro Gly Met Gly Met Ser Asn Thr Tyr Thr Thr Leu Thr Pro

129	134	139	144	
ctc cag ccg ctg cca ccc atc tcc acc gtg tct gac aag ttc cac cac				538
Leu Gln Pro Leu Pro Pro Ile Ser Thr Val Ser Asp Lys Phe His His				
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cct cac ccg cac cac cat ccg cac cac cac cac cac cac cac cag				586
Pro His Pro His His His Pro His His His His His His His His Gln				
161	166	171	176	
cgc ctg tcc ggc aac gtc agc ggc agc ttc acc ctc atg cgc gac gag				634
Arg Leu Ser Gly Asn Val Ser Gly Ser Phe Thr Leu Met Arg Asp Glu				
177	182	187	192	
cgc ggg ctc ccg gcc atg aac aac ctc tac agt ccc tac aag gag atg				682
Arg Gly Leu Pro Ala Met Asn Asn Leu Tyr Ser Pro Tyr Lys Glu Met				
193	198	203	208	
ccc ggc atg agc cag agc ctg tcc ccg ctg gcc gcc acg ccg ctg ggc				730
Pro Gly Met Ser Gln Ser Leu Ser Pro Leu Ala Ala Thr Pro Leu Gly				
209	214	219	224	
aac ggg cta ggc ggc ctc cac aac gcg cag cag agt ctg ccc aac tac				778
Asn Gly Leu Gly Gly Leu His Asn Ala Gln Gln Ser Leu Pro Asn Tyr				
225	230	235	240	
ggc ccg ccg ggc cac gac aaa atg ctc agc ccc aac ttc gac gcg cac				826
Gly Pro Pro Gly His Asp Lys Met Leu Ser Pro Asn Phe Asp Ala His				
241	246	251	256	
cac act gcc atg ctg acc cgc ggt gag caa cac ctg tcc cgc ggc ctg				874
His Thr Ala Met Leu Thr Arg Gly Glu Gln His Leu Ser Arg Gly Leu				
257	262	267	272	
ggc acc cca cct gcg gcc atg atg tcg cac ctg aac ggc ctg cac cac				922
Gly Thr Pro Pro Ala Ala Met Met Ser His Leu Asn Gly Leu His His				
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ccg ggc cac act cag tct cac ggg ccg gtg ctg gca ccc agt cgc gag				970
Pro Gly His Thr Gln Ser His Gly Pro Val Leu Ala Pro Ser Arg Glu				
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Arg Pro Pro Ser Ser Ser Ser Gly Ser Gln Val Ala Thr Ser Gly Gln				
305	310	315	320	
ctg gaa gaa atc aac acc aaa gag gtg gcc cag cgc atc aca gcg gag				1066
Leu Glu Glu Ile Asn Thr Lys Glu Val Ala Gln Arg Ile Thr Ala Glu				
321	326	331	336	
ctg aag cgc tac agt atc ccc cag gcg atc ttt gcg cag agg gtg ctg				1114
Leu Lys Arg Tyr Ser Ile Pro Gln Ala Ile Phe Ala Gln Arg Val Leu				
337	342	347	352	
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Cys Arg Ser Gln Gly Thr Leu Ser Asp Leu Leu Arg Asn Pro Lys Pro				
353	358	363	368	

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Trp Ser Lys Leu Lys Ser Gly Arg Glu Thr Phe Arg Arg Met Trp Lys	
369 374 379 384	
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Trp Leu Gln Glu Pro Glu Phe Gln Arg Met Ser Ala Leu Arg Leu Ala	
385 390 395 400	
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Ala Cys Lys Arg Lys Glu Gln Glu Pro Asn Lys Asp Arg Asn Asn Ser	
401 406 411 416	
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Gln Lys Lys Ser Arg Leu Val Phe Thr Asp Leu Gln Arg Arg Thr Leu	
417 422 427 432	
ttc gcc atc ttc aag gag aac aaa cgc ccg tca aag gag atg cag atc	1402
Phe Ala Ile Phe Lys Glu Asn Lys Arg Pro Ser Lys Glu Met Gln Ile	
433 438 443 448	
acc att tcc cag cag ctg ggc ctg gag ctc aca acc gtc agc aac ttc	1450
Thr Ile Ser Gln Gln Leu Gly Leu Glu Leu Thr Thr Val Ser Asn Phe	
449 454 459 464	
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Phe Met Asn Ala Arg Arg Arg Ser Leu Glu Lys Trp Gln Asp Asp Leu	
465 470 475 480	
agc aca ggg ggc tcc tcg tcc acc tcc agc acg tgt acc aaa gca tga	1546
Ser Thr Gly Gly Ser Ser Ser Thr Ser Ser Thr Cys Thr Lys Ala *	
481 486 491 496	
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caattctctt gcaaagaaac ttatattcta gctgtaatca taggccaggt gttcttcttt	1726
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cttggttccc cctccctcag cttccgcccc aaaagcagaa gtagaaagta atgaaaagga	180
caacagacct gaggaagaag agcaagtaat acatgaagat gatgaaagac cttctgagaa	240
aaatgaatth tctagacgaa aacgtttctaa atcagaagac atg gac aat gta cag	295
Met Asp Asn Val Gln	
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Ser Lys Arg Arg Arg Tyr Met Glu Glu Glu Tyr Glu Ala Glu Phe Gln	
6 11 16 21	
gta aag att aca gcc aaa gga gac att aac cag aaa ctt caa aag gtt	391
Val Lys Ile Thr Ala Lys Gly Asp Ile Asn Gln Lys Leu Gln Lys Val	
22 27 32 37	
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Ile Gln Trp Leu Leu Glu Glu Lys Leu Cys Ala Leu Gln Cys Ala Val	
38 43 48 53	
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Phe Asp Lys Thr Leu Ala Glu Leu Lys Thr Arg Val Glu Lys Ile Glu	
54 59 64 69	
tgt aac aag agg cat aaa aca gtt ctc act gaa cta cag gcc aag ata	535
Cys Asn Lys Arg His Lys Thr Val Leu Thr Glu Leu Gln Ala Lys Ile	
70 75 80 85	
gcc agg tta acc aaa cgc ttt gaa gca gcc aaa gaa gat ctt aag aaa	583
Ala Arg Leu Thr Lys Arg Phe Glu Ala Ala Lys Glu Asp Leu Lys Lys	
86 91 96 101	
aga cat gaa cat cca ccc aac cca cca gta tca cca gga aaa act gta	631
Arg His Glu His Pro Asn Pro Pro Val Ser Pro Gly Lys Thr Val	
102 107 112 117	
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Asn Asp Val Asn Ser Asn Asn Asn Met Ser Tyr Arg Asn Ala Gly Thr	
118 123 128 133	
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Val Arg Gln Met Leu Glu Ser Lys Arg Asn Val Ser Glu Ser Ala Pro	
134 139 144 149	
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Pro Ser Phe Gln Thr Pro Val Asn Thr Val Ser Ser Thr Asn Leu Val	
150 155 160 165	
act cct cca gca gtt gtc agt agt caa cct aaa ttg cag act cca gtg	823

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Thr	Ser	Gly	Ser	Leu	Thr	Ala	Thr	Ser	Val	Leu	Pro	Ala	Pro	Asn	Thr	
182					187					192					197	
gct	act	gta	gtt	gct	act	act	cag	gtg	cct	agt	gga	aat	ccc	cag	cct	919
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Val	Ser	Ser	Gln	Pro	Gln	Leu	Leu	Gln	Ser	His	Pro	Gly	Thr	Leu	Val	
230					235					240					245	
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246					251					256					261	
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294					299					304					309	
gct	gtg	cag	gct	gtt	cca	aca	gca	cac	tct	att	gta	caa	gcc	aca	agg	1255
Ala	Val	Gln	Ala	Val	Pro	Thr	Ala	His	Ser	Ile	Val	Gln	Ala	Thr	Arg	
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342					347					352					357	
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Ser	Ser	Ala	Ala	Glu	Gln	Asn	Ser	Asn	Thr	Thr	Pro	Arg	Ile	Glu	Asn	
358					363					368					373	
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Gln	Thr	Asn	Lys	Thr	Ile	Asp	Ala	Ser	Val	Ser	Lys	Lys	Ala	Ala	Asp	
374					379					384					389	
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Ser	Thr	Ser	Gln	Cys	Gly	Lys	Ala	Thr	Gly	Ser	Asp	Ser	Ser	Gly	Val	

390	395	400	405	
att gat ctc aca atg	gat gat gaa gag agt	gga gct tca caa gac	ccc	1543
Ile Asp Leu Thr Met	Asp Asp Glu Glu Ser	Gly Ala Ser Gln Asp	Pro	
406	411	416	421	
aaa aaa cta aat cac	act cct gta tca acc	atg agt tct tct cag	cct	1591
Lys Lys Leu Asn His	Thr Pro Val Ser Thr	Met Ser Ser Ser Gln	Pro	
422	427	432	437	
gtg tca cga cca ttg	caa ccc ata caa cca	gca ccg cct ctt caa	cca	1639
Val Ser Arg Pro Leu	Gln Pro Ile Gln Pro	Ala Pro Pro Leu Gln	Pro	
438	443	448	453	
tct ggg gtg cca aca	agt gga cca tct cag	acc acc ata cac tta	cta	1687
Ser Gly Val Pro Thr	Ser Gly Pro Ser Gln	Thr Thr Ile His Leu	Leu	
454	459	464	469	
cct aca gct cca act	acc gtg aat gta aca	cat cgt cca gta act	cag	1735
Pro Thr Ala Pro Thr	Thr Val Asn Val Thr	His Arg Pro Val Thr	Gln	
470	475	480	485	
gtg acc aca aga ctc	cct gta cca aga gct	cct gca aac cac cag	gtg	1783
Val Thr Thr Arg Leu	Pro Val Pro Arg Ala	Pro Ala Asn His Gln	Val	
486	491	496	501	
gtt tat aca act ctt	cct gca cca cca gct	cag gct ccc ttg cga	gga	1831
Val Tyr Thr Thr Leu	Pro Ala Pro Pro Ala	Gln Ala Pro Leu Arg	Gly	
502	507	512	517	
act gtt atg cag gct	cct gct gtt cgg cag	gtc aat ccc caa aat	agt	1879
Thr Val Met Gln Ala	Pro Ala Val Arg Gln	Val Asn Pro Gln Asn	Ser	
518	523	528	533	
gtt aca gtt cga gtg	cct caa aca acc aca	tat gtt gta aac aat	gga	1927
Val Thr Val Arg Val	Pro Gln Thr Thr Thr	Tyr Val Val Asn Asn	Gly	
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Leu Thr Leu Gly Ser	Thr Gly Pro Gln Leu	Thr Val His His Arg	Pro	
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cca caa gtg cat act	gag ccc cca cgc ccc	gtg cac cca gca ccc	tta	2023
Pro Gln Val His Thr	Glu Pro Pro Arg Pro	Val His Pro Ala Pro	Leu	
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cca gaa gct cca caa	cca cag cgt ctg ccc	cca gaa gct gcc agc	aca	2071
Pro Glu Ala Pro Gln	Pro Gln Arg Leu Pro	Pro Glu Ala Ala Ser	Thr	
582	587	592	597	
tct ctg cct cag aag	cca cac ttg aag tta	gca cgc gtt cag agt	caa	2119
Ser Leu Pro Gln Lys	Pro His Leu Lys Leu	Ala Arg Val Gln Ser	Gln	
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aat ggc ata gta ctg	tca tgg agt gtc ctg	gag gtg gat cga agc	tgt	2167
Asn Gly Ile Val Leu	Ser Trp Ser Val Leu	Glu Val Asp Arg Ser	Cys	
614	619	624	629	

gcc act gtt gat agc tac cat ctc tat gct tac cat gag gaa ccc agt	2215
Ala Thr Val Asp Ser Tyr His Leu Tyr Ala Tyr His Glu Glu Pro Ser	
630 635 640 645	
gcc act gtg ccc tca caa tgg aaa aag att ggg gaa gtc aag gca ctt	2263
Ala Thr Val Pro Ser Gln Trp Lys Lys Ile Gly Glu Val Lys Ala Leu	
646 651 656 661	
ccc ttg ccc atg gca tgt act ctc acc cag ttt gta tct ggt agc aaa	2311
Pro Leu Pro Met Ala Cys Thr Leu Thr Gln Phe Val Ser Gly Ser Lys	
662 667 672 677	
tac tac ttt gca gta cga gcc aag gat att tat gga cgt ttt ggg cct	2359
Tyr Tyr Phe Ala Val Arg Ala Lys Asp Ile Tyr Gly Arg Phe Gly Pro	
678 683 688 693	
ttc tgt gat cct cag tca aca gat gtg atc tct tct acc cag agc agt	2407
Phe Cys Asp Pro Gln Ser Thr Asp Val Ile Ser Ser Thr Gln Ser Ser	
694 699 704 709	
taa acct tggagccttt atattttcct cttttaaaat ttccaccttt tgggtcttgtt	2464
* 710	
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aaccacgtgg ctagcctgcc tgaagttctc acctctccag gaaggcgggg ggtttcta      180
ggctgcagct gcgctggggg ctgggggctc ccgctgggac tccacttcg tggatgtcta      240
agcttcacct ttcttgcgcc cgcaggggca tgactcaggt gaaagggagc cattttctca      300
gacccctggc ctc      atg cag ccc ttc agc atc ccc gtg caa atc aca ctt      349
                        Met Gln Pro Phe Ser Ile Pro Val Gln Ile Thr Leu
                        1             5             10

cag ggc agc cgg agg cgc cag ggg agg aca gcc ttt cct gcc tca ggg      397
Gln Gly Ser Arg Arg Arg Gln Gly Arg Thr Ala Phe Pro Ala Ser Gly
 13             18             23             28

aag aag aga gag aca gac tac agt gat gga gac cca cta gat gtg cac      445
Lys Lys Arg Glu Thr Asp Tyr Ser Asp Gly Asp Pro Leu Asp Val His
 29             34             39             44

aag agg ctg cca tcc agt act gga gag gac cga gcc gtg atg ctg ggg      493
Lys Arg Leu Pro Ser Ser Thr Gly Glu Asp Arg Ala Val Met Leu Gly
 45             50             55             60

ttt gcc atg atg ggc ttc tca gtc cta atg ttc ttc ttg ctc gga aca      541
Phe Ala Met Met Gly Phe Ser Val Leu Met Phe Phe Leu Leu Gly Thr
 61             66             71             76

acc att cta aag cct ttt atg ctc agc att cag aga gaa gaa tcg acc      589
Thr Ile Leu Lys Pro Phe Met Leu Ser Ile Gln Arg Glu Glu Ser Thr
 77             82             87             92

tgc act gcc atc cac aca gat atc atg gac gac tgg ctg gac tgt gcc      637
Cys Thr Ala Ile His Thr Asp Ile Met Asp Asp Trp Leu Asp Cys Ala
 93             98             103            108

ttc acc tgt ggt gtg cac tgc cac ggt cag ggg aag tac cca tgt ctt      685
Phe Thr Cys Gly Val His Cys His Gly Gln Gly Lys Tyr Pro Cys Leu
109            114            119            124

cag gtg ttt gtg aac ctc agc cat cca ggt cag aaa gct ctc cta cat      733
Gln Val Phe Val Asn Leu Ser His Pro Gly Gln Lys Ala Leu Leu His
125            130            135            140

tat aat gaa gag gct gtc cag ata aat ccc aag tgc ttt tac aca cct      781
Tyr Asn Glu Glu Ala Val Gln Ile Asn Pro Lys Cys Phe Tyr Thr Pro
141            146            151            156
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Lys Cys His Gln Asp Arg Asn Asp Leu Leu Asn Ser Ala Leu Asp Ile	
157 162 167 172	
aaa gaa ttc ttc gat cac aaa aat gga act ccc ttt tca tgc ttc tac	877
Lys Glu Phe Phe Asp His Lys Asn Gly Thr Pro Phe Ser Cys Phe Tyr	
173 178 183 188	
agt cca gcc agc caa tct gaa gat gtc att ctt ata aaa aag tat gac	925
Ser Pro Ala Ser Gln Ser Glu Asp Val Ile Leu Ile Lys Lys Tyr Asp	
189 194 199 204	
caa atg gct atc ttc cac tgt tta ttt tgg cct tca ctg act ctg cta	973
Gln Met Ala Ile Phe His Cys Leu Phe Trp Pro Ser Leu Thr Leu Leu	
205 210 215 220	
ggg ggt gcc ctg att gtt ggc atg gtg aga tta aca caa cac ctg tcc	1021
Gly Gly Ala Leu Ile Val Gly Met Val Arg Leu Thr Gln His Leu Ser	
221 226 231 236	
tta ctg tgt gaa aaa tat agc act gta gtc aga gat gag gta ggt gga	1069
Leu Leu Cys Glu Lys Tyr Ser Thr Val Val Arg Asp Glu Val Gly Gly	
237 242 247 252	
aaa gta cct tat ata gaa cag cat cag ttc aaa ctg tgc att atg agg	1117
Lys Val Pro Tyr Ile Glu Gln His Gln Phe Lys Leu Cys Ile Met Arg	
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atg gcc tgc ctg agc	113
Met Ala Cys Leu Ser	
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ccc tcg cag ctc cag aag ttc caa cag gat gga ttc ctg gtg ctg gaa	161
Pro Ser Gln Leu Gln Lys Phe Gln Gln Asp Gly Phe Leu Val Leu Glu	
6 11 16 21	
gga ttc ttg tct gcg gaa gag tgt gtg gcc atg caa caa agg att ggc	209

Gly	Phe	Leu	Ser	Ala	Glu	Glu	Cys	Val	Ala	Met	Gln	Gln	Arg	Ile	Gly		
22					27					32					37		
gag	ata	gtg	gct	gaa	atg	gat	gtt	cct	ctc	cac	tgc	cgc	aca	gaa	ttc	257	
Glu	Ile	Val	Ala	Glu	Met	Asp	Val	Pro	Leu	His	Cys	Arg	Thr	Glu	Phe		
38					43					48					53		
tcc	acc	cag	gaa	gag	gag	cag	ctt	cga	gcc	cag	ggc	agc	aca	gac	tat	305	
Ser	Thr	Gln	Glu	Glu	Glu	Gln	Leu	Arg	Ala	Gln	Gly	Ser	Thr	Asp	Tyr		
54					59					64					69		
ttc	ttg	agc	agt	ggg	gac	aag	att	cga	ttc	ttc	ttt	gag	aaa	ggc	gtt	353	
Phe	Leu	Ser	Ser	Gly	Asp	Lys	Ile	Arg	Phe	Phe	Phe	Glu	Lys	Gly	Val		
70					75					80					85		
ttt	gat	gag	aaa	gga	aat	ttc	ctg	gtc	cct	ccg	gag	aaa	tcc	atc	aac	401	
Phe	Asp	Glu	Lys	Gly	Asn	Phe	Leu	Val	Pro	Pro	Glu	Lys	Ser	Ile	Asn		
86					91					96					101		
aaa	att	ggc	cac	gct	ctg	cac	gcc	cac	gac	ccc	gtc	ttc	aag	agc	atc	449	
Lys	Ile	Gly	His	Ala	Leu	His	Ala	His	Asp	Pro	Val	Phe	Lys	Ser	Ile		
102					107					112					117		
aca	cac	tcc	ttc	aag	gtg	cag	acc	ttg	gcc	aga	agt	ctg	ggc	ctc	cag	497	
Thr	His	Ser	Phe	Lys	Val	Gln	Thr	Leu	Ala	Arg	Ser	Leu	Gly	Leu	Gln		
118					123					128					133		
atg	ccc	gtg	gtg	gtg	cag	agc	atg	tac	atc	ttt	aag	caa	cct	cac	ttt	545	
Met	Pro	Val	Val	Val	Gln	Ser	Met	Tyr	Ile	Phe	Lys	Gln	Pro	His	Phe		
134					139					144					149		
ggc	ggg	gaa	gtc	tcc	cct	cat	cag	gac	gcc	tcc	ttc	ctg	tac	acg	gag	593	
Gly	Gly	Glu	Val	Ser	Pro	His	Gln	Asp	Ala	Ser	Phe	Leu	Tyr	Thr	Glu		
150					155					160					165		
ccc	ctg	ggc	cgg	gtg	ctg	ggc	gtg	tgg	atc	gca	gtg	gag	gat	gcc	acg	641	
Pro	Leu	Gly	Arg	Val	Leu	Gly	Val	Trp	Ile	Ala	Val	Glu	Asp	Ala	Thr		
166					171					176					181		
ctg	gag	aac	ggc	tgt	ctc	tgg	ttc	atc	cct	ggc	tcc	cac	acc	agt	ggg	689	
Leu	Glu	Asn	Gly	Cys	Leu	Trp	Phe	Ile	Pro	Gly	Ser	His	Thr	Ser	Gly		
182					187					192					197		
gtg	tca	aga	agg	atg	gtc	cgg	gcc	cct	gtt	ggc	tca	gcg	cct	ggg	acc	737	
Val	Ser	Arg	Arg	Met	Val	Arg	Ala	Pro	Val	Gly	Ser	Ala	Pro	Gly	Thr		
198					203					208					213		
agc	ttc	ctt	ggg	tca	gag	cca	gcc	cgg	gat	aac	agc	ctc	ttt	gtg	ccc	785	
Ser	Phe	Leu	Gly	Ser	Glu	Pro	Ala	Arg	Asp	Asn	Ser	Leu	Phe	Val	Pro		
214					219					224					229		
acc	cca	gtg	cag	aga	ggg	gcc	ctg	gtc	ctc	atc	cat	gga	gaa	gtg	gta	833	
Thr	Pro	Val	Gln	Arg	Gly	Ala	Leu	Val	Leu	Ile	His	Gly	Glu	Val	Val		
230					235					240					245		
cac	aag	agc	aag	cag	aac	ctc	tct	gac	cgc	tcg	cgc	cag	gcc	tac	act	881	
His	Lys	Ser	Lys	Gln	Asn	Leu	Ser	Asp	Arg	Ser	Arg	Gln	Ala	Tyr	Thr		

246	251	256	261	
ttc cac ctc atg gag gcc tct ggc acc acc tgg agc ccg gag aac tgg				929
Phe His Leu Met Glu Ala Ser Gly Thr Thr Trp Ser Pro Glu Asn Trp				
262	267	272	277	
ctc cag cca aca gct gaa ctg ccc ttt ccc caa ctg tac acc taa agg				977
Leu Gln Pro Thr Ala Glu Leu Pro Phe Pro Gln Leu Tyr Thr *				
278	283	288		
ctctcgcagg gcaggagccc tcgcccctcc cgggtgaagc tgtgggctgt aaacaccagt				1037
gccttgctca gctcctggt tgcaacaggg aggtcttgct tcccctcctg ggctttcctc				1097
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gcctccctac tgccccaaca tagccttgag gaggcttctc agccaccaaa gggttctggc				1217
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aagacaggtc tcttgccaag gcaccaaga tgaaatcttg aaa atg aga aac aca	175
Met Arg Asn Thr	
1	

ttt gct gaa ctg aag aat tca tta gag gct ctc agc agt aga atg gac	223
Phe Ala Glu Leu Lys Asn Ser Leu Glu Ala Leu Ser Ser Arg Met Asp	
5 10 15 20	

cag gca gag gaa aga att ggg acc cag gct gga gtg cag tgg cgt gat	271
Gln Ala Glu Glu Arg Ile Gly Thr Gln Ala Gly Val Gln Trp Arg Asp	
21 26 31 36	

cat ggc tca ctg cag cct caa cct cct gaa ttc aag caa tgc ttc cac	319
His Gly Ser Leu Gln Pro Gln Pro Pro Glu Phe Lys Gln Cys Phe His	
37 42 47 52	

ctc agt ctc cca agt agc tgg gac tac agg gcg tgc ctt tct tag agc	367
Leu Ser Leu Pro Ser Ser Trp Asp Tyr Arg Ala Cys Leu Ser *	

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 gtgcaaggtc ttcattgtctg ctggcattgc tgcaacagt gcttgtgtga gagatcactt 487
 ttacggcaa tacccaattt attggagaga caaactgctc aagcaaggat gattagcatt 547
 ctatggcatt ttaaaaggat acttgcaatg cttgacctta ccacaatagc aacaggaggt 607
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 Met Gly Lys Ser Lys Ala Lys Pro Asn Gly Lys
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 Lys Pro Ala Ala Glu Arg Lys Ala Tyr Leu Glu Pro Glu His Thr
 12 17 22 27
 aag gcc agg atc acc gac ttc cag ttc aag gag ctg gtg gtg ctg ccc 206
 Lys Ala Arg Ile Thr Asp Phe Gln Phe Lys Glu Leu Val Val Leu Pro
 28 33 38 43
 cgc gag att gac ctt aac gag tgg ctg gcc agc aac acc acg acg ttt 254
 Arg Glu Ile Asp Leu Asn Glu Trp Leu Ala Ser Asn Thr Thr Thr Phe
 44 49 54 59
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 Phe His His Ile Asn Leu Gln Tyr Ser Thr Ile Ser Glu Phe Cys Thr
 60 65 70 75
 gga gag acg tgt cag acg atg gcc gtg tgc aac aca cag tac tac tgg 350
 Gly Glu Thr Cys Gln Thr Met Ala Val Cys Asn Thr Gln Tyr Tyr Trp
 76 81 86 91

tat gac gag cgg ggg aag aag gtc aag tgc acg gcc cca cag tac gtt	398
Tyr Asp Glu Arg Gly Lys Lys Val Lys Cys Thr Ala Pro Gln Tyr Val	
92 97 102 107	
gac ttc gtc atg agc tcc gtg cag aag ctg gtg acg gat gag gac gtg	446
Asp Phe Val Met Ser Ser Val Gln Lys Leu Val Thr Asp Glu Asp Val	
108 113 118 123	
ttc ccc aca aaa tac ggc aga gaa ttc ccc agc tcc ttt gag tcc ctg	494
Phe Pro Thr Lys Tyr Gly Arg Glu Phe Pro Ser Ser Phe Glu Ser Leu	
124 129 134 139	
gtg agg aag atc tgc aga cac ctg ttc cac gtg ctg gca cac atc tac	542
Val Arg Lys Ile Cys Arg His Leu Phe His Val Leu Ala His Ile Tyr	
140 145 150 155	
tgg gcc cac ttc aag gag acg ctg gcc ctg gag ctg cac gga cac ttg	590
Trp Ala His Phe Lys Glu Thr Leu Ala Leu Glu Leu His Gly His Leu	
156 161 166 171	
aac acg ctc tac gtc cac ttc atc ctc ttt gct cgg gag ttc aac ctg	638
Asn Thr Leu Tyr Val His Phe Ile Leu Phe Ala Arg Glu Phe Asn Leu	
172 177 182 187	
ctg gac ccc aaa gag acc gcc atc atg gac gac ctc acc gag gtg cta	686
Leu Asp Pro Lys Glu Thr Ala Ile Met Asp Asp Leu Thr Glu Val Leu	
188 193 198 203	
tgc agc ggg gcc ggc ggg gtc cac agt ggg ggc agt ggg gat ggg gcc	734
Cys Ser Gly Ala Gly Gly Val His Ser Gly Gly Ser Gly Asp Gly Ala	
204 209 214 219	
ggc agc ggg ggc ccg gga gca cag aac cac gtg aag gag aga tga gcc	782
Gly Ser Gly Gly Pro Gly Ala Gln Asn His Val Lys Glu Arg *	
220 225 230	
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tggccgaggg ggccggaccg cagccgccgc cctcccagga ccccgagctg ctgtcgggtga	360
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Gln Val His Ala Leu Arg Glu Asp Phe Arg Glu Lys Asn Ser Ser Thr	
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aac cag cac att atc cgg ctg gag agc ctt cag gcc gag atc aag atg	992
Asn Gln His Ile Ile Arg Leu Glu Ser Leu Gln Ala Glu Ile Lys Met	
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Leu Ser Asp Arg Lys Arg Glu Leu Glu His Arg Leu Ser Ala Thr Leu	
34 39 44 49	
gag gaa aat gac ctg ctc caa ggg acc gtg gag gag cta cag gac cgg	1088
Glu Glu Asn Asp Leu Leu Gln Gly Thr Val Glu Glu Leu Gln Asp Arg	
50 55 60 65	
gtg cta atc ctg gag agg cag ggc cat gac aag gac cta cag ctg cac	1136
Val Leu Ile Leu Glu Arg Gln Gly His Asp Lys Asp Leu Gln Leu His	
66 71 76 81	
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Gln Ser Gln Leu Glu Leu Gln Glu Val Arg Leu Ser Cys Arg Gln Leu	
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Gln Val Lys Val Glu Glu Leu Thr Glu Glu Arg Ser Leu Gln Ser Ser	

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gcc gcc acc agc aca tcc ctc ctg tca gag atc gag cag agc atg gag				1280
Ala Ala Thr Ser Thr Ser Leu Leu Ser Glu Ile Glu Gln Ser Met Glu				
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Ala Glu Glu Leu Glu Gln Glu Arg Glu Gln Val Thr Leu Leu Ser Val				
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Glu Met Thr Ala Leu Lys Glu Glu Arg Asp Arg Leu Arg Val Thr Ser				
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Glu Asp Lys Glu Pro Lys Glu Gln Leu Gln Lys Ala Ile Arg Asp Arg				
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gac gag gcc att gca aag aag aat gct gtg gag ctg gaa ctt gcc aag				1472
Asp Glu Ala Ile Ala Lys Lys Asn Ala Val Glu Leu Glu Leu Ala Lys				
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Cys Arg Met Asp Met Met Ser Leu Asn Ser Gln Leu Leu Asp Ala Ile				
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Gln Gln Lys Leu Asn Leu Ser Gln Gln Leu Glu Ala Trp Gln Asp Asp				
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atg cac agg gtc att gac cgg cag ctg atg gac acg cac ctg aaa gaa				1616
Met His Arg Val Ile Asp Arg Gln Leu Met Asp Thr His Leu Lys Glu				
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Arg Ser Gln Pro Ala Ala Ala Leu Cys Arg Gly His Ser Ala Gly Arg				
242	247	252	257	
ggg gat gag ccc agc atc gct gaa ggc aaa cga ctc ttc tca ttc ttc				1712
Gly Asp Glu Pro Ser Ile Ala Glu Gly Lys Arg Leu Phe Ser Phe Phe				
258	263	268	273	
agg aaa att taa gtt gggaggagtc aggccaccaa agatgggtgg actggaggca				1767
Arg Lys Ile *				
274				
gctggaaagg cgggtgcaggc aaggcctccc ctgcagcttg cacctcagca gctgccttgc				1827
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 Val Gly Gly Ser Arg Pro Gly Gln Thr Leu Arg Gly Ser Val Gln Asn
 17 22 27 32
 aaa ctc aat ccc cga cct gga aag gta gtg ata tat agt gaa ccc gac 144
 Lys Leu Asn Pro Arg Pro Gly Lys Val Val Ile Tyr Ser Glu Pro Asp
 33 38 43 48
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 Val Ser Glu Lys Cys Ile Glu Val Phe Ser Asp Ile Gln Asp Cys Ser
 49 54 59 64
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 Ser Trp Ser Leu Ser Pro Val Ile Leu Ile Lys Val Val Arg Gly Cys
 65 70 75 80
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 Trp Ile Leu Tyr Glu Gln Pro Asn Phe Glu Gly His Ser Ile Pro Leu
 81 86 91 96
 gaa gaa gga gaa ttg gaa ctc tct ggt ctc tgg ggt ata gaa gac att 336

Glu	Glu	Gly	Glu	Leu	Glu	Leu	Ser	Gly	Leu	Trp	Gly	Ile	Glu	Asp	Ile		
97					102					107					112		
gtg	gaa	agg	cac	gaa	gaa	gca	gag	tct	gat	aag	cca	gtg	gtg	att	ggc	384	
Val	Glu	Arg	His	Glu	Glu	Ala	Glu	Ser	Asp	Lys	Pro	Val	Val	Ile	Gly		
113					118					123					128		
tcc	atc	aga	cat	gtg	gtt	cag	gat	tac	aga	gtt	agt	cac	att	gac	tta	432	
Ser	Ile	Arg	His	Val	Val	Gln	Asp	Tyr	Arg	Val	Ser	His	Ile	Asp	Leu		
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Phe	Thr	Glu	Pro	Glu	Gly	Leu	Gly	Ile	Leu	Ser	Ser	Tyr	Phe	Asp	Asp		
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act	gaa	gaa	atg	cag	gga	ttt	ggc	gta	atg	cag	aag	act	tgt	tcc	atg	528	
Thr	Glu	Glu	Met	Gln	Gly	Phe	Gly	Val	Met	Gln	Lys	Thr	Cys	Ser	Met		
161					166					171					176		
aaa	gta	cat	tgg	ggc	acg	tgg	ctg	att	tat	gaa	gaa	cct	gga	ttt	cag	576	
Lys	Val	His	Trp	Gly	Thr	Trp	Leu	Ile	Tyr	Glu	Glu	Pro	Gly	Phe	Gln		
177					182					187					192		
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Gly	Val	Pro	Phe	Ile	Leu	Glu	Pro	Gly	Glu	Tyr	Pro	Asp	Leu	Ser	Phe		
193					198					203					208		
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Trp	Asp	Thr	Glu	Ala	Ala	Tyr	Ile	Gly	Ser	Met	Arg	Pro	Leu	Lys	Met		
209					214					219					224		
ggc	ggc	cgt	aaa	gtt	gaa	ttc	cct	aca	gat	cca	aag	tcc	aga	gca	caa	720	
Gly	Gly	Arg	Lys	Val	Glu	Phe	Pro	Thr	Asp	Pro	Lys	Ser	Arg	Ala	Gln		
225					230					235					240		
cct	cca	gaa	gac	aac	aga	agg	aag	cca	gtt	ttg	ggg	aaa	ctt	ggc	act	768	
Pro	Pro	Glu	Asp	Asn	Arg	Arg	Lys	Pro	Val	Leu	Gly	Lys	Leu	Gly	Thr		
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Leu	Phe	Thr	Ala	Gly	Arg	Arg	Arg	Asn	Ser	Arg	Asn	Gly	Leu	Glu	Ser		
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ccc	acc	aga	tca	aat	gcc	aaa	cca	ctc	tct	ccc	aaa	gat	gtg	gta	gcc	864	
Pro	Thr	Arg	Ser	Asn	Ala	Lys	Pro	Leu	Ser	Pro	Lys	Asp	Val	Val	Ala		
273					278					283					288		
tct	cct	aag	ctc	cca	gag	aga	gag	agt	gag	agg	agc	aga	tct	cag	agc	912	
Ser	Pro	Lys	Leu	Pro	Glu	Arg	Glu	Ser	Glu	Arg	Ser	Arg	Ser	Gln	Ser		
289					294					299					304		
agc	caa	ctg	aag	caa	acg	gac	aca	agc	gag	gag	ggc	tcc	ccg	cgg	gag	960	
Ser	Gln	Leu	Lys	Gln	Thr	Asp	Thr	Ser	Glu	Glu	Gly	Ser	Pro	Arg	Glu		
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aat	ccc	cga	gag	gca	gag	ggc	gag	ctc	ccc	gag	agc	ggc	ggc	ccc	gca	1008	
Asn	Pro	Arg	Glu	Ala	Glu	Gly	Glu	Leu	Pro	Glu	Ser	Gly	Gly	Pro	Ala		

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gcc ccc cct gac gcc gag ctg tca cct cgc tgg agc agc agt gca gcg				1056
Ala Pro Pro Asp Ala Glu Leu Ser Pro Arg Trp Ser Ser Ser Ala Ala				
337	342	347	352	
gct gtg gct gtg cag cag tgc cat gaa aat gat tca ccc caa tta gaa				1104
Ala Val Ala Val Gln Gln Cys His Glu Asn Asp Ser Pro Gln Leu Glu				
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cct ctg gag gca gag gga gag cct ttc cca gat gcc acc acc act gcc				1152
Pro Leu Glu Ala Glu Gly Glu Pro Phe Pro Asp Ala Thr Thr Thr Ala				
369	374	379	384	
aag cag ctg cat tcc tcg ccg gga aat tcc tcc agg caa gag aac gca				1200
Lys Gln Leu His Ser Ser Pro Gly Asn Ser Ser Arg Gln Glu Asn Ala				
385	390	395	400	
gag acg ccc gcc cgc agt ccg ggg gag gac gct tca cca ggt gct ggc				1248
Glu Thr Pro Ala Arg Ser Pro Gly Glu Asp Ala Ser Pro Gly Ala Gly				
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His Glu Gln Glu Ala Phe Leu Gly Val Arg Gly Ala Pro Gly Ser Pro				
417	422	427	432	
acc cag gag cgg ccc gcg gga gga cta ggc gag gcc cct aac gca gcc				1344
Thr Gln Glu Arg Pro Ala Gly Gly Leu Gly Glu Ala Pro Asn Ala Ala				
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ccc agt gtg tgt gcc gaa gaa ggc tcc ctg ggg ccc cgc aac gcc cgc				1392
Pro Ser Val Cys Ala Glu Glu Gly Ser Leu Gly Pro Arg Asn Ala Arg				
449	454	459	464	
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Ser Gln Pro Pro Lys Gly Ala Ser Asp Leu Pro Gly Glu Pro Pro Ala				
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Glu Gly Ala Ala His Thr Ala Ser Ser Ala Gln Ala Asp Cys Thr Ala				
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cgc ccc aag ggt cac gcc cac cct gct aag gtg cta act ttg gac atc				1536
Arg Pro Lys Gly His Ala His Pro Ala Lys Val Leu Thr Leu Asp Ile				
497	502	507	512	
tac ttg agt aag act gag ggg gca caa gtg gac gag ccg gtc gtg att				1584
Tyr Leu Ser Lys Thr Glu Gly Ala Gln Val Asp Glu Pro Val Val Ile				
513	518	523	528	
act ccc aga gcg gaa gat tgc ggt gac tgg gac gac atg gag aag agg				1632
Thr Pro Arg Ala Glu Asp Cys Gly Asp Trp Asp Asp Met Glu Lys Arg				
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Ser Ser Gly Arg Arg Ser Gly Arg Arg Arg Gly Ser Gln Lys Ser Thr				
545	550	555	560	

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Asp Ser Pro Gly Ala Asp Ala Glu Leu Pro Glu Ser Ala Ala Arg Asp	
561 566 571 576	
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Asp Ala Val Phe Asp Asp Glu Val Ala Pro Asn Ala Ala Ser Asp Asn	
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Ala Ser Ala Glu Lys Lys Val Lys Ser Pro Arg Ala Ala Leu Asp Gly	
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Gly Val Ala Ser Ala Ala Ser Pro Glu Ser Lys Pro Ser Pro Gly Thr	
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Lys Gly Gln Leu Arg Gly Glu Ser Asp Arg Ser Lys Lys Gln Pro Pro Pro	
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Ala Ser Ser Pro Thr Lys Arg Lys Gly Arg Ser Arg Ala Leu Glu Ala	
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Pro Pro Lys Arg Val Pro Asp Pro Ser Pro Val Thr Lys Gly Thr Ala	
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Ala Glu Ser Gly Glu Glu Ala Ala Arg Ala Ile Pro Arg Glu Leu Pro	
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Val Lys Ser Ser Ser Leu Leu Pro Glu Ile Lys Pro Glu His Lys Arg	
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Gly Pro Leu Pro Asn His Phe Asn Gly Arg Ala Glu Gly Gly Arg Ser	
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Arg Glu Leu Gly Arg Ala Ala Gly Ala Pro Gly Ala Ser Asp Ala Asp	
737 742 747 752	
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Gly Leu Lys Pro Arg Asn His Phe Gly Val Gly Arg Ser Thr Val Thr	
753 758 763 768	
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Thr Lys Val Thr Leu Pro Ala Lys Pro Lys His Val Glu Leu Asn Leu	
769 774 779 784	

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Glu Asn Lys Arg Thr Asn Ser Ser Pro Arg His Thr Asp Ile Arg Gly	
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Gln Arg Asn Thr Pro Ala Ser Ser Lys Thr Phe Val Gly Arg Ala Lys	
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Leu Asn Leu Ala Lys Lys Ala Lys Glu Met Glu Gln Pro Glu Lys Lys	
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Lys Glu Ser Gln Pro Glu Met Ser Pro Ala Leu His Leu Met Gln Asn				
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Leu Asp Thr Lys Ser Lys Leu Arg Pro Lys Arg Ala Ser Ala Glu Gln				
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Ser Val Leu Phe Lys Ser Leu His Thr Asn Thr Asn Gly Asn Ser Glu				
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Pro Leu Val Met Pro Glu Ile Asn Asp Lys Glu Asn Arg Asp Val Thr				
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Asn Gly Gly Ile Lys Arg Ser Arg Leu Glu Lys Ser Ala Leu Phe Ser				
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Pro Cys Gly Leu Asn Lys Glu Gln Ser Asn Leu Leu Pro Asp Asn Ser				
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Lys Ser Pro Ser His Met Glu Lys Tyr Pro Gln Lys Glu Lys Thr Lys				
1457	1462	1467	1472	

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Phe Asp Asp Thr Glu Glu Met Gln Gly Phe Gly Val Met Gln Lys Thr	
1681 1686 1691 1696	

tgt tcc atg aaa gta cat tgg ggc acg tgg ctg att tat gaa gaa cct	5136
Cys Ser Met Lys Val His Trp Gly Thr Trp Leu Ile Tyr Glu Glu Pro	
1697 1702 1707 1712	
gga ttt cag ggt gtt cct ttc atc ctg gaa cct ggt gaa tac cct gac	5184
Gly Phe Gln Gly Val Pro Phe Ile Leu Glu Pro Gly Glu Tyr Pro Asp	
1713 1718 1723 1728	
ttg tcc ttc tgg gat aca gaa gca gcg tac att gga tcc atg cgg cct	5232
Leu Ser Phe Trp Asp Thr Glu Ala Ala Tyr Ile Gly Ser Met Arg Pro	
1729 1734 1739 1744	
ctg aaa atg ggt ggc cgt aaa gtt gaa ttc cct aca gat cca aag gta	5280
Leu Lys Met Gly Gly Arg Lys Val Glu Phe Pro Thr Asp Pro Lys Val	
1745 1750 1755 1760	
gtt gtt tat gaa aag cct ttc ttt gaa gga aaa tgt gtg gaa cta gaa	5328
Val Val Tyr Glu Lys Pro Phe Phe Glu Gly Lys Cys Val Glu Leu Glu	
1761 1766 1771 1776	
aca gga atg tgt agt ttt gtc atg gag gga ggt gaa aca gaa gag gcg	5376
Thr Gly Met Cys Ser Phe Val Met Glu Gly Gly Glu Thr Glu Glu Ala	
1777 1782 1787 1792	
act gga gac gat cat ttg ccg ttt acg tca gtg ggg tct atg aaa gtt	5424
Thr Gly Asp Asp His Leu Pro Phe Thr Ser Val Gly Ser Met Lys Val	
1793 1798 1803 1808	
cta aga ggc att tgg gtt gca tat gag aag cct gga ttt acc ggt cat	5472
Leu Arg Gly Ile Trp Val Ala Tyr Glu Lys Pro Gly Phe Thr Gly His	
1809 1814 1819 1824	
cag tat ttg cta gaa gaa gga gaa tac agg gac tgg aaa gcc tgg gga	5520
Gln Tyr Leu Leu Glu Glu Gly Glu Tyr Arg Asp Trp Lys Ala Trp Gly	
1825 1830 1835 1840	
ggg tac aat gga gag ctt cag tct tta cga cct ata tta ggt gat ttt	5568
Gly Tyr Asn Gly Glu Leu Gln Ser Leu Arg Pro Ile Leu Gly Asp Phe	
1841 1846 1851 1856	
tca aat gct cac atg ata atg tac agt gaa aaa aac ttt gga tcc aaa	5616
Ser Asn Ala His Met Ile Met Tyr Ser Glu Lys Asn Phe Gly Ser Lys	
1857 1862 1867 1872	
ggg tcc agt att gat gta ttg gga att gtt gct aat tta aag gag act	5664
Gly Ser Ser Ile Asp Val Leu Gly Ile Val Ala Asn Leu Lys Glu Thr	
1873 1878 1883 1888	
gga tat gga gtg aag aca cag tct att aat gta ctg agt gga gta tgg	5712
Gly Tyr Gly Val Lys Thr Gln Ser Ile Asn Val Leu Ser Gly Val Trp	
1889 1894 1899 1904	
gta gcc tat gaa aat cct gac ttc aca gga gaa cag tat ata ctg gat	5760
Val Ala Tyr Glu Asn Pro Asp Phe Thr Gly Glu Gln Tyr Ile Leu Asp	
1905 1910 1915 1920	
aaa gga ttt tat acc agt ttt gag gac tgg gga ggc aaa aat tat aag	5808

Lys Gly Phe Tyr Thr Ser Phe Glu Asp Trp Gly Gly Lys Asn Tyr Lys	
1921 1926 1931 1936	
atc tct tct gtt caa cct ata tgt ttg gat tct ttc act ggc cca agg	5856
Ile Ser Ser Val Gln Pro Ile Cys Leu Asp Ser Phe Thr Gly Pro Arg	
1937 1942 1947 1952	
aga cga aat cag att cac ttg ttt tca gaa cca cag ttt caa ggt cac	5904
Arg Arg Asn Gln Ile His Leu Phe Ser Glu Pro Gln Phe Gln Gly His	
1953 1958 1963 1968	
agt caa agt ttt gaa gaa aca aca agt caa att gat gat tca ttt tct	5952
Ser Gln Ser Phe Glu Glu Thr Thr Ser Gln Ile Asp Asp Ser Phe Ser	
1969 1974 1979 1984	
acc aag tct tgc aga gtt tca gga ggc agc tgg gtt gta tat gat gga	6000
Thr Lys Ser Cys Arg Val Ser Gly Gly Ser Trp Val Val Tyr Asp Gly	
1985 1990 1995 2000	
gaa aat ttc act ggt aat caa tac gtg ttg gaa gaa ggc cat tat cct	6048
Glu Asn Phe Thr Gly Asn Gln Tyr Val Leu Glu Glu Gly His Tyr Pro	
2001 2006 2011 2016	
tgt ctg tct gca atg gga tgc ccg cct gga gca act ttc aag tct ctt	6096
Cys Leu Ser Ala Met Gly Cys Pro Pro Gly Ala Thr Phe Lys Ser Leu	
2017 2022 2027 2032	
cgt ttt ata gat gtt gaa ttt tct gaa cca aca att att ctc ttt gaa	6144
Arg Phe Ile Asp Val Glu Phe Ser Glu Pro Thr Ile Ile Leu Phe Glu	
2033 2038 2043 2048	
aga gaa gac ttc aaa gga aaa aag att gaa ctt aat gca gaa act gtc	6192
Arg Glu Asp Phe Lys Gly Lys Lys Ile Glu Leu Asn Ala Glu Thr Val	
2049 2054 2059 2064	
aat ctc cga tcc ctg gga ttc aac aca caa ata cgc tct gtt cag gtt	6240
Asn Leu Arg Ser Leu Gly Phe Asn Thr Gln Ile Arg Ser Val Gln Val	
2065 2070 2075 2080	
att ggt ggc ata tgg gtt act tat gaa tat ggc agt tac aga ggg cga	6288
Ile Gly Gly Ile Trp Val Thr Tyr Glu Tyr Gly Ser Tyr Arg Gly Arg	
2081 2086 2091 2096	
cag ttc cta ttg tca cct gca gaa gta cct aat tgg tat gaa ttc agt	6336
Gln Phe Leu Leu Ser Pro Ala Glu Val Pro Asn Trp Tyr Glu Phe Ser	
2097 2102 2107 2112	
ggc tgt cgc caa ata ggt tct cta cga cct ttt gtt cag aag cga att	6384
Gly Cys Arg Gln Ile Gly Ser Leu Arg Pro Phe Val Gln Lys Arg Ile	
2113 2118 2123 2128	
tat ttc aga ctt cga aac aaa gca aca ggg tta ttc atg tca acc aat	6432
Tyr Phe Arg Leu Arg Asn Lys Ala Thr Gly Leu Phe Met Ser Thr Asn	
2129 2134 2139 2144	
gga aac tta gag gat ctg aag ctt ctg agg ata cag gtc atg gag gat	6480
Gly Asn Leu Glu Asp Leu Lys Leu Leu Arg Ile Gln Val Met Glu Asp	

2145	2150	2155	2160	
gtc ggg gcc gat gat cag att tgg atc tat caa gaa gga tgt atc aaa				6528
Val Gly Ala Asp Asp Gln Ile Trp Ile Tyr Gln Glu Gly Cys Ile Lys				
2161	2166	2171	2176	
tgc agg ata gca gaa gac tgc tgc ctg acg att gtg ggc agc ctg gta				6576
Cys Arg Ile Ala Glu Asp Cys Cys Leu Thr Ile Val Gly Ser Leu Val				
2177	2182	2187	2192	
aca tct ggc tcc aag cta ggc ctg gcc ctg gac cag aat gct gac agc				6624
Thr Ser Gly Ser Lys Leu Gly Leu Ala Leu Asp Gln Asn Ala Asp Ser				
2193	2198	2203	2208	
cag ttc tgg agc ttg aag tcc gat ggc agg att tac agc aag ttg aag				6672
Gln Phe Trp Ser Leu Lys Ser Asp Gly Arg Ile Tyr Ser Lys Leu Lys				
2209	2214	2219	2224	
cca aat tta gtt tta gac att aaa ggg ggc aca cag tat gat caa aat				6720
Pro Asn Leu Val Leu Asp Ile Lys Gly Gly Thr Gln Tyr Asp Gln Asn				
2225	2230	2235	2240	
cac att atc ctc aac act gtc agc aaa gag aag ttt aca caa gtg tgg				6768
His Ile Ile Leu Asn Thr Val Ser Lys Glu Lys Phe Thr Gln Val Trp				
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Glu Ala Met Val Leu Tyr Thr *				
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tcgaaggccc ggcgcgccat gtcctgggtg ccgcggtgcg ggcagtgaac gcgcgccggg	180
cggg atg ggc cgg cgc cgg gcg cca gag ctg tac cgg gct ccg ttc ccg	229
Met Gly Arg Arg Arg Ala Pro Glu Leu Tyr Arg Ala Pro Phe Pro	
1 5 10	
ttg tac gcg ctt cag gtc gac ccc agc act ggg ctg ctc atc gct gcg	277
Leu Tyr Ala Leu Gln Val Asp Pro Ser Thr Gly Leu Leu Ile Ala Ala	
16 21 26 31	

ggc gga gga ggc gcc gcc aag aca ggc ata aag aat ggc gtg cac ttt Gly Gly Gly Gly Ala Ala Lys Thr Gly Ile Lys Asn Gly Val His Phe 32 37 42 47	325
ctg cag cta gag ctg att aat ggg cgc ttg agt gcc tcc ttg ctg cac Leu Gln Leu Glu Leu Ile Asn Gly Arg Leu Ser Ala Ser Leu Leu His 48 53 58 63	373
tcc cat gac aca gag aca cgg gcc acc atg aac ttg gca ctg gct ggt Ser His Asp Thr Glu Thr Arg Ala Thr Met Asn Leu Ala Leu Ala Gly 64 69 74 79	421
gac atc ctt gct gca ggg cag gat gcc cac tgt cag ctc ctg cgc ttc Asp Ile Leu Ala Ala Gly Gln Asp Ala His Cys Gln Leu Leu Arg Phe 80 85 90 95	469
cag gca cat caa cag cag ggc aac aag gca gag aag gcc ggt tcc aag Gln Ala His Gln Gln Gln Gly Asn Lys Ala Glu Lys Ala Gly Ser Lys 96 101 106 111	517
gag cag ggg cct cga caa agg aag gga gca gcc cca gca gag aag aaa Glu Gln Gly Pro Arg Gln Arg Lys Gly Ala Ala Pro Ala Glu Lys Lys 112 117 122 127	565
tgt gga gcg gaa acc cag cac gag ggg cta gaa ctc agg gta gag aat Cys Gly Ala Glu Thr Gln His Glu Gly Leu Glu Leu Arg Val Glu Asn 128 133 138 143	613
ttg cag gcg gtg cag aca gac ttt agc tcc gat cca ctg cag aaa gtt Leu Gln Ala Val Gln Thr Asp Phe Ser Ser Asp Pro Leu Gln Lys Val 144 149 154 159	661
gtg tgc ttc aac cac gat aat acc ctg ctt gcc act gga gga aca gat Val Cys Phe Asn His Asp Asn Thr Leu Leu Ala Thr Gly Gly Thr Asp 160 165 170 175	709
ggc tac gtc cgt gtc tgg aag gtg ccc agc ctg gag aag gtt ctg gag Gly Tyr Val Arg Val Trp Lys Val Pro Ser Leu Glu Lys Val Leu Glu 176 181 186 191	757
ttc aaa gcc cac gaa ggg gag att gaa gac ctg gct tta ggg cct gat Phe Lys Ala His Glu Gly Glu Ile Glu Asp Leu Ala Leu Gly Pro Asp 192 197 202 207	805
ggc aag ttg gta acc gtg ggc cgg gac ctt aag gcc tct gtg tgg cag Gly Lys Leu Val Thr Val Gly Arg Asp Leu Lys Ala Ser Val Trp Gln 208 213 218 223	853
aag gat cag ctg gtg aca cag ctg cac tgg caa gaa aat gga ccc acc Lys Asp Gln Leu Val Thr Gln Leu His Trp Gln Glu Asn Gly Pro Thr 224 229 234 239	901
ttt tcc agc aca cct tac cgc tac cag gcc tgc agg ttt ggg cag gtt Phe Ser Ser Thr Pro Tyr Arg Tyr Gln Ala Cys Arg Phe Gly Gln Val 240 245 250 255	949

cca gac cag cct gct ggc ctg cga ctc ttc aca gtg caa att ccc cac	997
Pro Asp Gln Pro Ala Gly Leu Arg Leu Phe Thr Val Gln Ile Pro His	
256 261 266 271	
aag cgc ctg cgc cag ccc cct ccc tgc tac ctc aca gcc tgg gat ggc	1045
Lys Arg Leu Arg Gln Pro Pro Pro Cys Tyr Leu Thr Ala Trp Asp Gly	
272 277 282 287	
tcc aac ttc ttg ccc ctt cgg acc aag tcc tgt ggc cat gaa gtc gtc	1093
Ser Asn Phe Leu Pro Leu Arg Thr Lys Ser Cys Gly His Glu Val Val	
288 293 298 303	
tcc tgc ctc gat gtc agt gaa tcc ggc acc ttc cta ggc ctg ggc aca	1141
Ser Cys Leu Asp Val Ser Glu Ser Gly Thr Phe Leu Gly Leu Gly Thr	
304 309 314 319	
gtc act ggc tct gtt gcc atc tac ata gct ttc tct ctc cag tgc ctc	1189
Val Thr Gly Ser Val Ala Ile Tyr Ile Ala Phe Ser Leu Gln Cys Leu	
320 325 330 335	
tac tac gtg agg gag gcc cat ggc att gtg gtg acg gat gtg gcc ttt	1237
Tyr Tyr Val Arg Glu Ala His Gly Ile Val Val Thr Asp Val Ala Phe	
336 341 346 351	
cta cct gag aag ggt cgt ggt cca gag ctc ctt ggg tcc cat gaa act	1285
Leu Pro Glu Lys Gly Arg Gly Pro Glu Leu Leu Gly Ser His Glu Thr	
352 357 362 367	
gcc ctg ttc tct gtg gct gtg gac agt cgt tgc cag ctg cat ctg ttg	1333
Ala Leu Phe Ser Val Ala Val Asp Ser Arg Cys Gln Leu His Leu Leu	
368 373 378 383	
ccc tca cgg cgg agt gtt cct gtg tgg ctc ctg ctc ctg ctg tgt gtc	1381
Pro Ser Arg Arg Ser Val Pro Val Trp Leu Leu Leu Leu Cys Val	
384 389 394 399	
ggg ctt att att gtg acc atc ctg ctg ctc cag agt gcc ttt cca ggt	1429
Gly Leu Ile Ile Val Thr Ile Leu Leu Leu Gln Ser Ala Phe Pro Gly	
400 405 410 415	
ttc ctt tag cttccct gcttcctggg aatcaggagc ctggacactg ccatctctag	1485
Phe Leu *	
416	
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catgaagccc ctggcatttg ctggggaagg gactggcctg gtacttgctg ttagggcagg	1905

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gctggcctaa agatgcaata agttcctagg tagtctaccc ttaccttgag gaatgggaaa 2025
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ggcggtagca ggtggtcctg cagcaggttg tctggccaca gctggggcgg cagcaggtgg 180
gctggcagta cacagactgg cagcactggg gtctgaagca gctggacaca cagcagctgg 240
gacggcagca ggtggtcctg cagcaagtgg tctggcagca gctggggctg cagcaggtgg 300
gctggcagca cacagactgg cagcactgcg gtctgcagca gctggacaca cagcagctgg 360
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tttcatatca tgggatggtg actggctcat ggttgatagt ccaatatgag gttcaacaag 480
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gtggacggca gcagctggac acaccacagc tggggcggca ggtggtctga caacagagtg 600
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aagagttaac catggtgtca gaggggtggag gttagaagct gcggcagcag caagcgggtct 960
tgcagcaggt ggtctggcag cagctgggat ggcagcagat ctcttggcag aggtcttaac 1020
cacacctctc tgaacaggag cccacccttc acccctgaca cc atg acc cac tgc 1074

Met Thr His Cys

1

tgt tcc cct tgc tgt cag cct aca tgc tgc agg acc acc tgc tgc agg	1122
Cys Ser Pro Cys Cys Gln Pro Thr Cys Cys Arg Thr Thr Cys Cys Arg	
5 10 15 20	
aca acc tgc tgg aag ccc acc act gtg acc acc tgc agc agc aca ccc	1170
Thr Thr Cys Trp Lys Pro Thr Thr Val Thr Thr Cys Ser Ser Thr Pro	
21 26 31 36	
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Cys Cys Gln Pro Ser Cys Cys Val Pro Ser Cys Cys Gln Pro Cys Cys	
37 42 47 52	
cac cca act tgc tgt caa aac acc tgc tgc agg acc acc tgc tgc cag	1266
His Pro Thr Cys Cys Gln Asn Thr Cys Cys Arg Thr Thr Cys Cys Gln	
53 58 63 68	
ccc act tgt gtg gcc agc tgc tgc cag cct tcc tgc tgc agc aca ccc	1314
Pro Thr Cys Val Ala Ser Cys Cys Gln Pro Ser Cys Cys Ser Thr Pro	
69 74 79 84	
tgc tgc cag ccc acc tgc tgt ggg tcc agc tgc tgt ggc caa acc agc	1362
Cys Cys Gln Pro Thr Cys Cys Gly Ser Ser Cys Cys Gly Gln Thr Ser	
85 90 95 100	
tgt ggg tcc agc tgc tgt cag cct att tgt ggg tcc agt tgc tgt cag	1410
Cys Gly Ser Ser Cys Cys Gln Pro Ile Cys Gly Ser Ser Cys Cys Gln	
101 106 111 116	
cct tgc tgt cac ccg act tgc tat caa act atc tgc ttc agg acc acc	1458
Pro Cys Cys His Pro Thr Cys Tyr Gln Thr Ile Cys Phe Arg Thr Thr	
117 122 127 132	
tgc tgc cag cct acc tgc tgc cag ccc acc tgc tgc agg aac acc tct	1506
Cys Cys Gln Pro Thr Cys Cys Gln Pro Thr Cys Cys Arg Asn Thr Ser	
133 138 143 148	
tgc cag ccc acc tgc tgt ggg tcc agc tgc tgc cag cct tgc tgc cac	1554
Cys Gln Pro Thr Cys Cys Gly Ser Ser Cys Cys Gln Pro Cys Cys His	
149 154 159 164	
cca aca tgc tgt caa acc att tgt aga tcc acc tgc tgc caa cca tcc	1602
Pro Thr Cys Cys Gln Thr Ile Cys Arg Ser Thr Cys Cys Gln Pro Ser	
165 170 175 180	
tgt gtg acc aga tgc tgc agc aca ccc tgt tgc cag cca acc tgt ggt	1650
Cys Val Thr Arg Cys Cys Ser Thr Pro Cys Cys Gln Pro Thr Cys Gly	
181 186 191 196	
ggg tcc agc tgc tgt agc caa acc tgc aat gag tcc agc tat tgt ctg	1698
Gly Ser Ser Cys Cys Ser Gln Thr Cys Asn Glu Ser Ser Tyr Cys Leu	
197 202 207 212	
cct tgc tgc cgt ccc acc tgc tgc cag acc acc tgc tac agg acc acc	1746
Pro Cys Cys Arg Pro Thr Cys Cys Gln Thr Thr Cys Tyr Arg Thr Thr	

213	218	223	228	
tgt tgc cgc ccc agc	tgt tgc tgc agt cct	tgc tgt gtc tcc agc	tgc	1794
Cys Cys Arg Pro Ser	Cys Cys Cys Ser Pro	Cys Cys Val Ser Ser	Cys	
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tgc cag cct tcc tgc	tgc taa tc cacttgctgc	agacccacca	cccaccagag	1847
Cys Gln Pro Ser Cys	Cys *			
245	250			
acat				1851

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 agcctcccaa aaagggtggga ttacagggtt tagcccccg cccgggcctg caaaaccctt 180
 ttttactttt ggggccc aaa aagatcccc atttccccgt ccttttccgg tagactattc 240
 gctactgaaa cgattttttt ttttttttga gacgagggtg aggggcgggg gttctcgcta 300
 tcttgctcaa gctgatctcg aactcctggg ttgatcaat actcagacaa tcttggcagg 360
 cgcaggagga ccaaattcta gtgaatgaga tcgagtctct cggctctttc ccttccatgt 420
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acccagcagc ccctgccgcc aggetcaacg tggacgggct cctggtctac ttcccgtacg 1020
 actacatcta ccccgagcag ttctcctac atg cgg gag ctc aaa cgc acg ctg 1073
 Met Arg Glu Leu Lys Arg Thr Leu
 1 5
 gac gcc aag ggt cat gga gtc ctg gag atg ccc tca ggc acc ggg aag 1121
 Asp Ala Lys Gly His Gly Val Leu Glu Met Pro Ser Gly Thr Gly Lys
 9 14 19 24
 aca gta tcc ctg ttg gcc ctg atc atg gca tac cag aga gca tat ccg 1169
 Thr Val Ser Leu Leu Ala Leu Ile Met Ala Tyr Gln Arg Ala Tyr Pro
 25 30 35 40
 ctg gag gtg acc aaa ctc atc tac tgc tca aga act gtg cca gag att 1217
 Leu Glu Val Thr Lys Leu Ile Tyr Cys Ser Arg Thr Val Pro Glu Ile
 41 46 51 56
 gag aag gtg att gaa gag ctt cga aag ttg ctc aac ttc tat gag aag 1265
 Glu Lys Val Ile Glu Glu Leu Arg Lys Leu Leu Asn Phe Tyr Glu Lys
 57 62 67 72
 cag gag ggc gag aag ctg ccg ttt ctg gga ctg gct ctg agc tcc cgc 1313
 Gln Glu Gly Glu Lys Leu Pro Phe Leu Gly Leu Ala Leu Ser Ser Arg
 73 78 83 88
 aaa aac ttg tgt att cac cct gag gtg aca ccc ctg cgc ttt ggg aag 1361
 Lys Asn Leu Cys Ile His Pro Glu Val Thr Pro Leu Arg Phe Gly Lys
 89 94 99 104
 gac gtc gat ggg aaa tgc cac agc ctc aca gcc tcc tat gtg cgg gcg 1409
 Asp Val Asp Gly Lys Cys His Ser Leu Thr Ala Ser Tyr Val Arg Ala
 105 110 115 120
 cag tac cag cat gac acc agc ctg ccc cac tgc cga ttc tat gag gaa 1457
 Gln Tyr Gln His Asp Thr Ser Leu Pro His Cys Arg Phe Tyr Glu Glu
 121 126 131 136
 ttt gat gcc cat ggg cgt gag gtg ccc ctc ccc gct ggc atc tac aac 1505
 Phe Asp Ala His Gly Arg Glu Val Pro Leu Pro Ala Gly Ile Tyr Asn
 137 142 147 152
 ctg gat gac ctg aag gcc ctg ggg cgg cgc cag ggc tgg tgc cca tac 1553
 Leu Asp Asp Leu Lys Ala Leu Gly Arg Arg Gln Gly Trp Cys Pro Tyr
 153 158 163 168
 ttc ctt gct cga tac tca atc ctg cat gcc aat gtg gtg gtt tat agc 1601
 Phe Leu Ala Arg Tyr Ser Ile Leu His Ala Asn Val Val Val Tyr Ser
 169 174 179 184
 tac cac tac ctc ctg gac ccc aag att gca gac ctg gtg tcc aag gaa 1649
 Tyr His Tyr Leu Leu Asp Pro Lys Ile Ala Asp Leu Val Ser Lys Glu
 185 190 195 200
 ctg gcc cgc aag gcc gtc gtg gtc ttc gac gag gcc cac aac att gac 1697
 Leu Ala Arg Lys Ala Val Val Val Phe Asp Glu Ala His Asn Ile Asp
 201 206 211 216

aac gtc tgc atc gac tcc atg agc gtc aac ctc acc cgc cgg acc ctt	1745
Asn Val Cys Ile Asp Ser Met Ser Val Asn Leu Thr Arg Arg Thr Leu	
217 222 227 232	
gac cgg tgc cag ggc aac ctg gag acc ctg cag aag acg gtg ctc agg	1793
Asp Arg Cys Gln Gly Asn Leu Glu Thr Leu Gln Lys Thr Val Leu Arg	
233 238 243 248	
atc aaa gag aca gac gag cag cgc ctg cgg gac gag tac cgg cgt ctg	1841
Ile Lys Glu Thr Asp Glu Gln Arg Leu Arg Asp Glu Tyr Arg Arg Leu	
249 254 259 264	
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Val Glu Gly Leu Arg Glu Ala Ser Ala Ala Arg Glu Thr Asp Ala His	
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Leu Ala Asn Pro Val Leu Pro Asp Glu Val Leu Gln Glu Ala Val Pro	
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Gly Ser Ile Arg Thr Ala Glu His Phe Leu Gly Phe Leu Arg Arg Leu	
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Leu Glu Tyr Val Lys Trp Arg Leu Arg Val Gln His Val Val Gln Glu	
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Arg Lys Pro Leu Arg Phe Cys Ala Glu Arg Leu Arg Ser Leu Leu His	
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Thr Leu Glu Ile Thr Asp Leu Ala Asp Phe Ser Pro Leu Thr Leu Leu	
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Ala Asn Phe Ala Thr Leu Val Ser Thr Tyr Ala Lys Gly Phe Thr Ile	
377 382 387 392	
atc atc gag ccc ttt gac gac aga acc ccg acc att gcc aac ccc atc	2273
Ile Ile Glu Pro Phe Asp Asp Arg Thr Pro Thr Ile Ala Asn Pro Ile	
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Leu His Phe Ser Cys Met Asp Ala Ser Leu Ala Ile Lys Pro Val Phe	
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 Cys Phe Ser *
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Ser Ile Cys Thr Met Gly Ala Asn Ala Ser Ala Leu Glu Lys Glu Ile
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ttt ggg aat acc tgc tac tgc aat tca gtt ctt caa gca ctt tat ttt      315
Phe Gly Asn Thr Cys Tyr Cys Asn Ser Val Leu Gln Ala Leu Tyr Phe
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tgt cgt cca ttt cgg gaa aaa gtt ctt gcg tat aag agt caa cct agg      363
Cys Arg Pro Phe Arg Glu Lys Val Leu Ala Tyr Lys Ser Gln Pro Arg
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aaa aag gag agc ctt ctt aca tgc tta gca gat ctc ttc cat agc ata      411
Lys Lys Glu Ser Leu Leu Thr Cys Leu Ala Asp Leu Phe His Ser Ile
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gcc act cag aag aaa aag gtt gga gta ata ccc cct aag aag ttc atc      459
Ala Thr Gln Lys Lys Lys Val Gly Val Ile Pro Pro Lys Lys Phe Ile
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aca aga tta cgg aaa gaa aat gag ctt ttt gac aac tac atg caa caa      507
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gat gcc cat gaa ttc tta aat tac cta cta aat aca att gct gat att      555
Asp Ala His Glu Phe Leu Asn Tyr Leu Leu Asn Thr Ile Ala Asp Ile
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tta caa gaa gag aga aag cag gaa aaa caa aat ggt cgt tta cct aat      603
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148 153 158 163	
tgc gcg cta cct ttc atg ggc ttc ggg aag ttc gtg cag tac tgc ccc	702
Cys Ala Leu Pro Phe Met Gly Phe Gly Lys Phe Val Gln Tyr Cys Pro	
164 169 174 179	
ggc acc tgg tgc ttt atc cag atg gtc cac gag gag ggc tgc ctg tgc	750
Gly Thr Trp Cys Phe Ile Gln Met Val His Glu Glu Gly Ser Leu Ser	
180 185 190 195	
gtg ctg ggg tac tct gtg ctc tac tcc agc ctc atg gcg ctg ctg gtc	798
Val Leu Gly Tyr Ser Val Leu Tyr Ser Ser Leu Met Ala Leu Leu Val	
196 201 206 211	
ctc gcc acc gtg ctg tgc aac ctc ggc gcc atg cgc aac ctc tat gcg	846
Leu Ala Thr Val Leu Cys Asn Leu Gly Ala Met Arg Asn Leu Tyr Ala	
212 217 222 227	
atg cac cgg cgg ctg cag cgg cac ccg cgc tcc tgc acc agg gac tgt	894
Met His Arg Arg Leu Gln Arg His Pro Arg Ser Cys Thr Arg Asp Cys	
228 233 238 243	
gcc gag ccg cgc gcg gac ggg agg gaa gcg tcc cct cag ccc ctg gag	942
Ala Glu Pro Arg Ala Asp Gly Arg Glu Ala Ser Pro Gln Pro Leu Glu	
244 249 254 259	
gag ctg gat cac ctc ctg ctg ctg gcg ctg atg acc gtg ctc ttc act	990
Glu Leu Asp His Leu Leu Leu Leu Ala Leu Met Thr Val Leu Phe Thr	
260 265 270 275	
atg tgt tct ctg ccc gta att tat cgc gct tac tat gga gca ttt aag	1038
Met Cys Ser Leu Pro Val Ile Tyr Arg Ala Tyr Tyr Gly Ala Phe Lys	
276 281 286 291	
gat gtc aag gag aaa aac agg acc tct gaa gaa gca gaa gac ctc cga	1086
Asp Val Lys Glu Lys Asn Arg Thr Ser Glu Glu Ala Glu Asp Leu Arg	
292 297 302 307	
gcc ttg cga ttt cta tct gtg att tca att gtg gac cct tgg att ttt	1134
Ala Leu Arg Phe Leu Ser Val Ile Ser Ile Val Asp Pro Trp Ile Phe	
308 313 318 323	
atc att ttc aga tct cca gta ttt cgg ata ttt ttt cac aag att ttc	1182
Ile Ile Phe Arg Ser Pro Val Phe Arg Ile Phe Phe His Lys Ile Phe	
324 329 334 339	
att aga cct ctt agg tac agg agc cgg tgc agc aat tcc act aac atg	1230
Ile Arg Pro Leu Arg Tyr Arg Ser Arg Cys Ser Asn Ser Thr Asn Met	
340 345 350 355	
gaa tcc agt ctg tga cagtgttttt cactctgtgg taagctgagg aatatgtcac	1285
Glu Ser Ser Leu *	
356	
attttcagcg gcaccagc	1303

<210> 341
 <211> 1023
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (121) .. (846)

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 atttgccct cgagcagcaa ttcggcacga ggtgagttgg ctgccggtga gttgggtgcc 60
 ggtggagtcg tggttggtcct cagaatcccc gcgtagccgc tgcctcctcc taccctcgcc 120
 atg ttt ctt acc cgg tct gag tac gac agg ggc gtg aat act ttt tct 168
 Met Phe Leu Thr Arg Ser Glu Tyr Asp Arg Gly Val Asn Thr Phe Ser
 1 5 10 15
 ccc gaa gga aga tta ttt caa gtg gaa tat gcc att gag gct atc aag 216
 Pro Glu Gly Arg Leu Phe Gln Val Glu Tyr Ala Ile Glu Ala Ile Lys
 17 22 27 32
 ctt ggt tct aca gcc att ggg atc cag aca tca gag ggt gtg tgc cta 264
 Leu Gly Ser Thr Ala Ile Gly Ile Gln Thr Ser Glu Gly Val Cys Leu
 33 38 43 48
 gct gtg gag aag aga att act tcc cca ctg atg gag ccc agc agc att 312
 Ala Val Glu Lys Arg Ile Thr Ser Pro Leu Met Glu Pro Ser Ser Ile
 49 54 59 64
 gag aaa att gta gag att gat gct cac ata ggt tgt gcc atg agt ggg 360
 Glu Lys Ile Val Glu Ile Asp Ala His Ile Gly Cys Ala Met Ser Gly
 65 70 75 80
 cta att gct gat gct aag act tta att gat aaa gcc aga gtg gag aca 408
 Leu Ile Ala Asp Ala Lys Thr Leu Ile Asp Lys Ala Arg Val Glu Thr
 81 86 91 96
 cag aac cac tgg ttc acc tac aat gag aca atg aca gtg gag agt gtg 456
 Gln Asn His Trp Phe Thr Tyr Asn Glu Thr Met Thr Val Glu Ser Val
 97 102 107 112
 acc caa gct gtg tcc aat ctg gct ttg cag ttt gga gaa gaa gat gca 504
 Thr Gln Ala Val Ser Asn Leu Ala Leu Gln Phe Gly Glu Glu Asp Ala
 113 118 123 128
 gat cca ggt gcc atg tct cgt ccc ttt gga gta gca tta tta ttt gga 552
 Asp Pro Gly Ala Met Ser Arg Pro Phe Gly Val Ala Leu Leu Phe Gly
 129 134 139 144
 gga gtt gat gag aaa gga ccc cag ctg ttt cat atg gac cca tct ggg 600
 Gly Val Asp Glu Lys Gly Pro Gln Leu Phe His Met Asp Pro Ser Gly
 145 150 155 160

acc ttt gta cag tgt gat gct cga gca att ggc tct gct tca gag ggt	648
Thr Phe Val Gln Cys Asp Ala Arg Ala Ile Gly Ser Ala Ser Glu Gly	
161 166 171 176	
gcc cag agc tcc ttg caa gaa gtt tac cac aag tct atg act ttg aaa	696
Ala Gln Ser Ser Leu Gln Glu Val Tyr His Lys Ser Met Thr Leu Lys	
177 182 187 192	
gaa gcc atc aag tct tca ctc atc atc ctc aaa caa gta atg gag gag	744
Glu Ala Ile Lys Ser Ser Leu Ile Ile Leu Lys Gln Val Met Glu Glu	
193 198 203 208	
aag ctg aat gca aca aac att gag cta gcc aca gtg cag cct ggc cag	792
Lys Leu Asn Ala Thr Asn Ile Glu Leu Ala Thr Val Gln Pro Gly Gln	
209 214 219 224	
aat ttc cac atg ttc aca aag gaa gaa ctt gaa gag gtt atc aag gac	840
Asn Phe His Met Phe Thr Lys Glu Glu Leu Glu Glu Val Ile Lys Asp	
225 230 235 240	
att taa ggaatcctga tcttcagaac ttctctggga caatttcagt tctaataatg	896
Ile *	
241	
tccttaaaatt ttatttccag ctctgttcc ttggaaaatc tccattgtat gtgcattttt	956
taaatgatgt ctgtacataa aggcagttct gaaataaaga aaatttttaa atattaaaaa	1016
aaaaaaaa	1023

<210> 342
 <211> 2132
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (59) .. (1255)

<400> 342	
gccactggc caggagggc gccgcgcgga ggcgcgttcg tgtctcctgt caaaagcc	58
atg ctc ggc agg tct ggg tac cgg gcg ctg ccc ctg ggt gat ttt gac	106
Met Leu Gly Arg Ser Gly Tyr Arg Ala Leu Pro Leu Gly Asp Phe Asp	
1 5 10 15	
cgc ttc cag cag tcg agc ttc ggc ttt ctg ggc tcg cag aag ggc tgc	154
Arg Phe Gln Gln Ser Ser Phe Gly Phe Leu Gly Ser Gln Lys Gly Cys	
17 22 27 32	
ttg tcc ccg gag cgg ggc ggc gtg ggg aca ggg gcc gat gta ccc cag	202
Leu Ser Pro Glu Arg Gly Gly Val Gly Thr Gly Ala Asp Val Pro Gln	
33 38 43 48	

agc tgg ccc tcc tgc ctc tgt cat ggc ctc atc agt ttc ctg ggg ttc	250
Ser Trp Pro Ser Cys Leu Cys His Gly Leu Ile Ser Phe Leu Gly Phe	
49 54 59 64	
ttg ctg ctg ttg gtc acc ttc ccc att tct ggc tgg ttt gcc ctg aag	298
Leu Leu Leu Leu Val Thr Phe Pro Ile Ser Gly Trp Phe Ala Leu Lys	
65 70 75 80	
att gtg ccc acc tac gag cgg atg att gtg ttc cgc ctg ggc cgg atc	346
Ile Val Pro Thr Tyr Glu Arg Met Ile Val Phe Arg Leu Gly Arg Ile	
81 86 91 96	
cgc acc ccc cag gga cct ggc atg gtt ctg ctc ttg ccc ttc att gac	394
Arg Thr Pro Gln Gly Pro Gly Met Val Leu Leu Leu Pro Phe Ile Asp	
97 102 107 112	
tcc ttt cag agg gtg gat ctg agg aca cga gcc ttc aac gtc cct ccc	442
Ser Phe Gln Arg Val Asp Leu Arg Thr Arg Ala Phe Asn Val Pro Pro	
113 118 123 128	
tgc aag ctg gcc tct aag gac ggg gct gtg ctg tcc gtg gga gcc gat	490
Cys Lys Leu Ala Ser Lys Asp Gly Ala Val Leu Ser Val Gly Ala Asp	
129 134 139 144	
gtc cag ttt cgc atc tgg gac ccg gtg ctg tgc gtg atg act gtg aaa	538
Val Gln Phe Arg Ile Trp Asp Pro Val Leu Ser Val Met Thr Val Lys	
145 150 155 160	
gac ctg aac aca gcc aca cgc atg aca gcc cag aac gcc atg acc aag	586
Asp Leu Asn Thr Ala Thr Arg Met Thr Ala Gln Asn Ala Met Thr Lys	
161 166 171 176	
gcc ctg ctc aag agg ccg ctg cgg gag atc cag atg gag aag ctc aag	634
Ala Leu Leu Lys Arg Pro Leu Arg Glu Ile Gln Met Glu Lys Leu Lys	
177 182 187 192	
atc agc gac cag ctt ctg ctg gag atc aac gat gtg acc agg gcc tgg	682
Ile Ser Asp Gln Leu Leu Leu Glu Ile Asn Asp Val Thr Arg Ala Trp	
193 198 203 208	
ggg ctg gag gta gac cgc gtg gag ctg gca gtg gag gcc gtg ctc cag	730
Gly Leu Glu Val Asp Arg Val Glu Leu Ala Val Glu Ala Val Leu Gln	
209 214 219 224	
ccg ccc cag gac agc cca gct ggg ccc aac ctg gac agc acc ctc cag	778
Pro Pro Gln Asp Ser Pro Ala Gly Pro Asn Leu Asp Ser Thr Leu Gln	
225 230 235 240	
cag ctg gcc ctg cac ttc ctg gga gga agc atg aac tca atg gca gga	826
Gln Leu Ala Leu His Phe Leu Gly Gly Ser Met Asn Ser Met Ala Gly	
241 246 251 256	
ggg gcc ccg tcc ccg ggg cca gca gac acc gtg gag atg gtg agt gaa	874
Gly Ala Pro Ser Pro Gly Pro Ala Asp Thr Val Glu Met Val Ser Glu	
257 262 267 272	
gtt gag cca cct gcc cct caa gtt ggt gcc agg tcc agt ccg aag cag	922

Val Glu Pro Pro Ala Pro Gln Val Gly Ala Arg Ser Ser Pro Lys Gln	
273 278 283 288	
cct ctg gcg gag ggg cta ctg act gct cta cag ccc ttc ctg tct gag	970
Pro Leu Ala Glu Gly Leu Leu Thr Ala Leu Gln Pro Phe Leu Ser Glu	
289 294 299 304	
gcc ctg gtc agc caa gtc ggg gcc tgc tac cag ttc aat gtc gtc ctg	1018
Ala Leu Val Ser Gln Val Gly Ala Cys Tyr Gln Phe Asn Val Val Leu	
305 310 315 320	
ccc agc ggc acc caa agc gcc tac ttc ctg gac ctc act aca gga cga	1066
Pro Ser Gly Thr Gln Ser Ala Tyr Phe Leu Asp Leu Thr Thr Gly Arg	
321 326 331 336	
gga aga gtg gga cac ggg gtg cct gat ggc atc cct gat gtg gtg gtg	1114
Gly Arg Val Gly His Gly Val Pro Asp Gly Ile Pro Asp Val Val Val	
337 342 347 352	
gag atg gcc gag gca gac ctg cgg gcc ctg cta tgc aga gag ctg cgg	1162
Glu Met Ala Glu Ala Asp Leu Arg Ala Leu Leu Cys Arg Glu Leu Arg	
353 358 363 368	
ccc ctg ggg gcc tac atg agt gga cgg ctg aag gtg aag ggc gac ctg	1210
Pro Leu Gly Ala Tyr Met Ser Gly Arg Leu Lys Val Lys Gly Asp Leu	
369 374 379 384	
gct atg gcc atg aag ctg gag gct gtc ctc agg gcc ttg aag tag cag	1258
Ala Met Ala Met Lys Leu Glu Ala Val Leu Arg Ala Leu Lys *	
385 390 395	
ccttggtga ctttccagag ccagtcacca agcctggcac caagcctgag gggcctcttg	1318
gaggaggagg tgttcatctg caccacagag agttgaggcc ctaacaaatt tcaggcccag	1378
ccaagagccc atgaatggag gctgcaggag gctgagtcgg gctgccatgc acgtctcccc	1438
tacagtgggt ctctggacaa ggctttgtcc atcccgggtcc ccagctgagt gccagcgct	1498
gagctgggtg cacggtgtga ttccaggagg agagccaggc ctgccttgcc ctgctggctt	1558
cctgactgga gagacaggac ccacagaaac agcctgacag cagctgggtt ggtccttggtg	1618
tgagggacca agcatgtggc ccaggctcta agctctgcgg ggattggaga gggatgggga	1678
gggaaggga ggcagctcca agaagaggtc cctgtggcga agttacctgg ggatcctggc	1738
tgggccacct tcctggctgc agtccaggcc cgtgctggcg ggattgggca tgggaaggag	1798
cagggcctgc tgcttccctg gcgctgctcc caaagatttc tgactcatct gccagctccg	1858
tcctgcatgc ctggcgagct ggggcccagg gcagcatgaa ggagagccct gcgttctgtg	1918
cttcttacca gaggtttgca agcctcagac aaataaatgt ggtgtttaca atgtaaaaaa	1978
aagacttcag tcatcccagc aatcgcttgg ttcagtttca ttcagctctc tatggaccag	2038

taatctgata aataaccgag ctcttctttg gggatcacta cttcttgact tgtagtaact 2098
gccaccaatc aagcagtctc tcccctgcaa aaca 2132

<210> 343
<211> 575
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (134) .. (499)

<400> 343
acggccagtg aattgaattt aggtgacact atagaagagc tatgacgtcg catgcacgcg 60
tacgtaagct tggatcctct agagcggccg cctactacta ctaaattcgc ggcggcgcgcg 120
tggtgaaata gat atg gcg acc gag ggg gat gtg gag ctg gag ttg gag 169
Met Ala Thr Glu Gly Asp Val Glu Leu Glu Leu Glu
1 5 10
act gag acc agt gga cca gag cgg cct ccg gag aag cca cgg aaa cat 217
Thr Glu Thr Ser Gly Pro Glu Arg Pro Pro Glu Lys Pro Arg Lys His
13 18 23 28
gac agc ggt gcg gcg gac ttg gag cgg gtc acc gac tat gca gag gag 265
Asp Ser Gly Ala Ala Asp Leu Glu Arg Val Thr Asp Tyr Ala Glu Glu
29 34 39 44
aag gag atc cag agt tcc aat ctg gag acg gcc atg tct gtg att gga 313
Lys Glu Ile Gln Ser Ser Asn Leu Glu Thr Ala Met Ser Val Ile Gly
45 50 55 60
gac aga agg tcc cgg gag cag aaa gcc aaa cag gag cgg gag aaa gaa 361
Asp Arg Arg Ser Arg Glu Gln Lys Ala Lys Gln Glu Arg Glu Lys Glu
61 66 71 76
ctg gca aaa gtc act atc aag aag gaa gat ctg gag cta ata atg act 409
Leu Ala Lys Val Thr Ile Lys Lys Glu Asp Leu Glu Leu Ile Met Thr
77 82 87 92
gag atg gag ata tct cga gca gca gca gaa cgc agt ttg cgg gaa cac 457
Glu Met Glu Ile Ser Arg Ala Ala Ala Glu Arg Ser Leu Arg Glu His
93 98 103 108
atg ggc aac gtg gta gag gcg ctt att gcc cta acc aac tga tgcgtgc 506
Met Gly Asn Val Val Glu Ala Leu Ile Ala Leu Thr Asn *
109 114 119
tttctcaaat atacctactg gattaattta tggcaataaa attttttttt gtctttttaa 566
aaaaaaaaa 575

<210> 344
 <211> 642
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (52)..(471)

<400> 344
 atttggccct cgaggccaag aattcggcac gagcggcgac ggaggaggag g atg gag 57
 Met Glu
 1

gcg gtg gtg ttc gtc ttc tct ctc ctc gat tgt tgc gcg ctc atc ttc 105
 Ala Val Val Phe Val Phe Ser Leu Leu Asp Cys Cys Ala Leu Ile Phe
 3 8 13 18

ctc tcg gtc tac ttc ata att aca ttg tct gat tta gaa tgt gat tac 153
 Leu Ser Val Tyr Phe Ile Ile Thr Leu Ser Asp Leu Glu Cys Asp Tyr
 19 24 29 34

att aat gct aga tca tgt tgc tca aaa tta aac aag tgg gta att cca 201
 Ile Asn Ala Arg Ser Cys Cys Ser Lys Leu Asn Lys Trp Val Ile Pro
 35 40 45 50

gaa ttg att ggc cat acc att gtc act gta tta ctg ctc atg tca ttg 249
 Glu Leu Ile Gly His Thr Ile Val Thr Val Leu Leu Leu Met Ser Leu
 51 56 61 66

cac tgg ttc atc ttc ctt ctc aac tta cct gtt gcc act tgg aat ata 297
 His Trp Phe Ile Phe Leu Leu Asn Leu Pro Val Ala Thr Trp Asn Ile
 67 72 77 82

tat cga tac att atg gtg ccg agt ggt aac atg gga gtg ttt gat cca 345
 Tyr Arg Tyr Ile Met Val Pro Ser Gly Asn Met Gly Val Phe Asp Pro
 83 88 93 98

aca gaa ata cac aat cga ggg cag ctg aag tca cac atg aaa gaa gcc 393
 Thr Glu Ile His Asn Arg Gly Gln Leu Lys Ser His Met Lys Glu Ala
 99 104 109 114

atg atc aag ctt ggt ttc cac ttg ctc tgc ttc ttc atg tat ctt tat 441
 Met Ile Lys Leu Gly Phe His Leu Leu Cys Phe Phe Met Tyr Leu Tyr
 115 120 125 130

agt atg atc tta gct ttg ata aat gac tga a gccgtggttg aagtcagcct 492
 Ser Met Ile Leu Ala Leu Ile Asn Asp *
 131 136

acactacagt gcacagttga ggagccagag atttcttaaa tcatacttag aaccgtgacc 552

atagcagtat atattttcct cttggaacaa aaaactatctt ttgctgtatt tttaccatat 612

aaagtatttta aaaaacataa aaaaaaaaaa

642

<210> 345
<211> 3135
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (489) .. (2900)

<400> 345

aagagatgac cgctgtagca ggcctcaatt taaccctcac taaagggaat aagcttgcg 60
ccgcaatgct ttttttaggtg tttttttttg gggctgggggt gtgtttattt gggatatatac 120
aatgagtcac ggattaaaat tgcttcacgc ggatagatac ctaggtgttc cacagcatta 180
ctgaacaagc tgctgtcatt tccccattac ctcagaagac ccccttaatt acttacttat 240
attaactgta gaacgtattt atgcatacca ggctctacct ctgggctttc tattctgttc 300
cagagacca gtaccagaat atttaaata ctagggggcgt taaatacggt ttaatatctg 360
atagggccag tttctgcgca ttgcacattt ttttttcccc tttcaggaac gtgttcaggc 420
ccgcggcagg gggcgggac gcgcctctc ctcggctctg gttccagccg agcctctcgg 480
acgcagag atg gaa atc ccg aag ctg ctc ccg gct cgc ggg aca cta cag 530
Met Glu Ile Pro Lys Leu Leu Pro Ala Arg Gly Thr Leu Gln
1 5 10
ggc ggc ggc ggc ggc ggt atc ccc gcg ggt ggc ggc cga gtc cac cga 578
Gly Gly Gly Gly Gly Gly Ile Pro Ala Gly Gly Gly Arg Val His Arg
15 20 25 30
ggc cct gac tcg ccg gct ggc cag gtc ccc acg cgc cgc ctc ctg ctg 626
Gly Pro Asp Ser Pro Ala Gly Gln Val Pro Thr Arg Arg Leu Leu Leu
31 36 41 46
ctc cgg ggc ccc caa gat ggc ggg ccc ggg cgg cgc gag gag gcc 674
Leu Arg Gly Pro Gln Asp Gly Gly Pro Gly Arg Arg Arg Glu Glu Ala
47 52 57 62
agc acg gca tca cgg ggc cct ggc cca agc ctg ttg gcg ccg agg acc 722
Ser Thr Ala Ser Arg Gly Pro Gly Pro Ser Leu Leu Ala Pro Arg Thr
63 68 73 78
gat caa cct agc ggc ggc ggc ggc ggc ggc ggc gac gac ttc ttc ctg 770
Asp Gln Pro Ser Gly Gly Gly Gly Gly Gly Gly Asp Asp Phe Phe Leu
79 84 89 94
gtg ctg ctt gac ccg gtg ggt ggc gac gtg gag acc gcg ggc tcc ggt 818
Val Leu Leu Asp Pro Val Gly Gly Asp Val Glu Thr Ala Gly Ser Gly

95	100	105	110	
cag gcc gca ggg cct	gtg ttg agg gag gag	gcc gag gag ggc ccg ggg	866	
Gln Ala Ala Gly Pro	Val Leu Arg Glu Glu	Ala Glu Glu Gly Pro Gly		
111	116	121	126	
ctc cag ggg ggc gag	agc ggc gcg aat ccc	gcg ggg ccc act gcg cta	914	
Leu Gln Gly Gly Glu	Ser Gly Ala Asn Pro	Ala Gly Pro Thr Ala Leu		
127	132	137	142	
ggc ccc cgc tgc ctg	tcc gcg gtt ccc act	ccg gcc ccg atc tcc gcc	962	
Gly Pro Arg Cys Leu	Ser Ala Val Pro Thr	Pro Ala Pro Ile Ser Ala		
143	148	153	158	
ccc ggc ccc gcc gcg	gcc ttc gcg ggc aca	gtc act atc cac aac cag	1010	
Pro Gly Pro Ala Ala	Ala Phe Ala Gly Thr	Val Thr Ile His Asn Gln		
159	164	169	174	
gac ctg ctg ttg cgc	ttt gag aac ggc gtc	ctc acc ctg gcc acg ccc	1058	
Asp Leu Leu Leu Arg	Phe Glu Asn Gly Val	Leu Thr Leu Ala Thr Pro		
175	180	185	190	
cca cca cac gcc tgg	gag cca ggg gcc gct	cct gcc cag cag ccc ggg	1106	
Pro Pro His Ala Trp	Glu Pro Gly Ala Ala	Pro Ala Gln Gln Pro Gly		
191	196	201	206	
tgt ctg atc gcc ccg	caa gct ggg ttc ccg	cat gcc gcg cac ccg ggt	1154	
Cys Leu Ile Ala Pro	Gln Ala Gly Phe Pro	His Ala Ala His Pro Gly		
207	212	217	222	
gac tgc cca gag ctg	ccg cca gac ctc ctg	cta gct gag ccg gcc gaa	1202	
Asp Cys Pro Glu Leu	Pro Pro Asp Leu Leu	Leu Ala Glu Pro Ala Glu		
223	228	233	238	
ccc gcg cca gct ccg	gcg cct gag gag gag	gcg gag ggc ccg gcc gcc	1250	
Pro Ala Pro Ala Pro	Ala Pro Glu Glu Glu	Ala Glu Gly Pro Ala Ala		
239	244	249	254	
gcc ctg ggc ccc cgc	gga ccg ctg ggc tcc	ggc cca ggc gtg gtg ctg	1298	
Ala Leu Gly Pro Arg	Gly Pro Leu Gly Ser	Gly Pro Gly Val Val Leu		
255	260	265	270	
tac ttg tgc ccc gag	gcg cag tgc ggg caa	acc ttc gcc aag aag cac	1346	
Tyr Leu Cys Pro Glu	Ala Gln Cys Gly Gln	Thr Phe Ala Lys Lys His		
271	276	281	286	
cag ctg aag gtg cac	ctg ctg acg cac agc	agc agc cag ggc cag agg	1394	
Gln Leu Lys Val His	Leu Leu Thr His Ser	Ser Ser Gln Gly Gln Arg		
287	292	297	302	
ccc ttc aaa tgc ccc	ctg ggt ggc tgc ggc	tgg acc ttc acc acc tct	1442	
Pro Phe Lys Cys Pro	Leu Gly Gly Cys Gly	Trp Thr Phe Thr Thr Ser		
303	308	313	318	
tac aag ctc aag agg	cac ctg cag tcg cac	gac aaa ctg cgg ccc ttt	1490	
Tyr Lys Leu Lys Arg	His Leu Gln Ser His	Asp Lys Leu Arg Pro Phe		
319	324	329	334	

ggc tgc ccg gca gag ggc tgt ggc aag agc ttc acc aca gtg tac aac	1538
Gly Cys Pro Ala Glu Gly Cys Gly Lys Ser Phe Thr Thr Val Tyr Asn	
335 340 345 350	
ctc aag gcg cac atg aag ggc cat gag cag gag aac tca ttc aaa tgc	1586
Leu Lys Ala His Met Lys Gly His Glu Gln Glu Asn Ser Phe Lys Cys	
351 356 361 366	
gag gtg tgc gag gag agc ttc ccc acg cag gcc aaa ctc agc gcc cac	1634
Glu Val Cys Glu Glu Ser Phe Pro Thr Gln Ala Lys Leu Ser Ala His	
367 372 377 382	
cag cgc agc cac ttc gaa ccg gag agg cct tac cag tgc gcg ttt tct	1682
Gln Arg Ser His Phe Glu Pro Glu Arg Pro Tyr Gln Cys Ala Phe Ser	
383 388 393 398	
ggc tgc aag aag aca ttt atc aca gtg agt gct ctg ttt tcc cat aac	1730
Gly Cys Lys Lys Thr Phe Ile Thr Val Ser Ala Leu Phe Ser His Asn	
399 404 409 414	
cgc gcc cat ttc agg gaa cag gaa ctg ttt tcc tgc tct ttt cct ggc	1778
Arg Ala His Phe Arg Glu Gln Glu Leu Phe Ser Cys Ser Phe Pro Gly	
415 420 425 430	
tgc agc aaa caa tat gac aag gct tgt agg ctg aaa att cac ctg cgg	1826
Cys Ser Lys Gln Tyr Asp Lys Ala Cys Arg Leu Lys Ile His Leu Arg	
431 436 441 446	
agt cac acc ggc gag aga cct ttc ctt tgt gac ttt gat ggc tgt ggc	1874
Ser His Thr Gly Glu Arg Pro Phe Leu Cys Asp Phe Asp Gly Cys Gly	
447 452 457 462	
tgg aac ttc act agc atg tcc aaa ctc tta agg cac aaa aga aag cac	1922
Trp Asn Phe Thr Ser Met Ser Lys Leu Leu Arg His Lys Arg Lys His	
463 468 473 478	
gac gat gac cgg agg ttc atg tgc cct gtg gaa ggc tgt ggg aaa tct	1970
Asp Asp Asp Arg Arg Phe Met Cys Pro Val Glu Gly Cys Gly Lys Ser	
479 484 489 494	
ttc acg agg gcg gaa cat ctg aaa ggc cac agc ata acc cac ctg ggc	2018
Phe Thr Arg Ala Glu His Leu Lys Gly His Ser Ile Thr His Leu Gly	
495 500 505 510	
aca aag cct ttc gtg tgt cct gtg gca ggc tgc tgt gcc agg ttc tct	2066
Thr Lys Pro Phe Val Cys Pro Val Ala Gly Cys Cys Ala Arg Phe Ser	
511 516 521 526	
gct cgc agt agc ctc tac att cac tcc aag aaa cac ctg cag gat gtg	2114
Ala Arg Ser Ser Leu Tyr Ile His Ser Lys Lys His Leu Gln Asp Val	
527 532 537 542	
gac act tgg aaa agc cgt tgc ccg atc tcc tct tgt aat aaa ctc ttc	2162
Asp Thr Trp Lys Ser Arg Cys Pro Ile Ser Ser Cys Asn Lys Leu Phe	
543 548 553 558	

aca tcc aag cac agc atg aag acg cac atg gtt aaa agg cat aag gtg	2210
Thr Ser Lys His Ser Met Lys Thr His Met Val Lys Arg His Lys Val	
559 564 569 574	
ggc cag gat ctc tta gct cag cta gaa gca gca aat tct ctc aca ccc	2258
Gly Gln Asp Leu Leu Ala Gln Leu Glu Ala Ala Asn Ser Leu Thr Pro	
575 580 585 590	
agc agt gaa ctt acc agc cag aga cag aat gat ctc agt gat gca gag	2306
Ser Ser Glu Leu Thr Ser Gln Arg Gln Asn Asp Leu Ser Asp Ala Glu	
591 596 601 606	
ata gtg tct ctc ttc tct gat gta cct gac agt act tct gct gca ttg	2354
Ile Val Ser Leu Phe Ser Asp Val Pro Asp Ser Thr Ser Ala Ala Leu	
607 612 617 622	
ctg gac aca gca ttg gtg aac tct gga atc ttg act att gat gtg gct	2402
Leu Asp Thr Ala Leu Val Asn Ser Gly Ile Leu Thr Ile Asp Val Ala	
623 628 633 638	
tct gtg agc tcg act ctg gca ggg cac ctc cct gct aat aat aat aat	2450
Ser Val Ser Ser Thr Leu Ala Gly His Leu Pro Ala Asn Asn Asn Asn	
639 644 649 654	
tcc gta ggg cag gct gtg gac cct ccg tcc ttg atg gcc acc agc gac	2498
Ser Val Gly Gln Ala Val Asp Pro Pro Ser Leu Met Ala Thr Ser Asp	
655 660 665 670	
cct cct caa agt ctg gat acc tct ctc ttt ttt gga acg gcg gcc act	2546
Pro Pro Gln Ser Leu Asp Thr Ser Leu Phe Phe Gly Thr Ala Ala Thr	
671 676 681 686	
ggc ttt cag cag agc tcc tta aat atg gat gag gtc tca agt gta agt	2594
Gly Phe Gln Gln Ser Ser Leu Asn Met Asp Glu Val Ser Ser Val Ser	
687 692 697 702	
gtg ggg cca ttg gga tct ctg gac tct ttg gcc atg aaa aac tcc agt	2642
Val Gly Pro Leu Gly Ser Leu Asp Ser Leu Ala Met Lys Asn Ser Ser	
703 708 713 718	
cca gag cct cag gct ttg aca ccc agc agt aag cta aca gtg gac aca	2690
Pro Glu Pro Gln Ala Leu Thr Pro Ser Ser Lys Leu Thr Val Asp Thr	
719 724 729 734	
gat gct ctg act cct tcg agc acc ctt tgt gaa aac agt gtc tca gaa	2738
Asp Ala Leu Thr Pro Ser Ser Thr Leu Cys Glu Asn Ser Val Ser Glu	
735 740 745 750	
cta ctg aca cca acc aaa gcg gag tgg aac gta cat cct gac tct gac	2786
Leu Leu Thr Pro Thr Lys Ala Glu Trp Asn Val His Pro Asp Ser Asp	
751 756 761 766	
ttc ttt gga cag gag gga gaa acc cag ttt gga ttc ccc aat gca gca	2834
Phe Phe Gly Gln Glu Gly Glu Thr Gln Phe Gly Phe Pro Asn Ala Ala	
767 772 777 782	
gga aac cat ggt tct cag aaa gaa aca gat ctt atc act gtg act ggc	2882

Gly Asn His Gly Ser Gln Lys Glu Thr Asp Leu Ile Thr Val Thr Gly
 783 788 793 798

agc tca ttt ttg gta tga accaac tctattcatt cctcatcatg tggcttactt 2936
 Ser Ser Phe Leu Val *
 799 804

ttattacagt caattttgag gatattctgg actaaatatt taagtgcagt catttctttt 2996

tggtttgcaa aaagagcaca gccctggact acaagtttgg agatttaaata ctgatcttga 3056

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tcggatccac tagtccagtg tgggtgaatt ccggtgcgt gagaggcgcg cggcgggcgca 120

gtgaacagtc tccttccaca aaacc atg gcg tcg ctc aaa tgt agc acc gtc 172
 Met Ala Ser Leu Lys Cys Ser Thr Val
 1 5

gtc tgc gtg atc tgc ttg gag aag ccc aaa tac cgc tgt cca gcc tgc 220
 Val Cys Val Ile Cys Leu Glu Lys Pro Lys Tyr Arg Cys Pro Ala Cys
 10 15 20 25

cgc gtg ccc tac tgc tcg gta gtc tgc ttc cgg aag cac aaa gaa cag 268
 Arg Val Pro Tyr Cys Ser Val Val Cys Phe Arg Lys His Lys Glu Gln
 26 31 36 41

tgc aac cct gaa act cgt cct gtt gag aaa aaa ata aga tca gct ctt 316
 Cys Asn Pro Glu Thr Arg Pro Val Glu Lys Lys Ile Arg Ser Ala Leu
 42 47 52 57

cct acc aaa acc gta aag cct gtg gaa aac aaa gat gat gat gac tct 364
 Pro Thr Lys Thr Val Lys Pro Val Glu Asn Lys Asp Asp Asp Asp Ser
 58 63 68 73

ata gct gat ttt ctc aat agt gat gag gaa gaa gac aga gtt tct ttg	412
Ile Ala Asp Phe Leu Asn Ser Asp Glu Glu Glu Asp Arg Val Ser Leu	
74 79 84 89	
cag aat tta aag aat tta ggg gaa tct gca aca tta aga agc tta ttg	460
Gln Asn Leu Lys Asn Leu Gly Glu Ser Ala Thr Leu Arg Ser Leu Leu	
90 95 100 105	
ctc aat cca cac ctc agg cag ttg atg gtc aac ctc gat cag gga gaa	508
Leu Asn Pro His Leu Arg Gln Leu Met Val Asn Leu Asp Gln Gly Glu	
106 111 116 121	
gac aaa gca aag ctc atg aga gct tac atg caa gag cct ttg ttt gtg	556
Asp Lys Ala Lys Leu Met Arg Ala Tyr Met Gln Glu Pro Leu Phe Val	
122 127 132 137	
gag ttt gca gac tgc tgt tta gga att gtg gag cca tcc cag aat gag	604
Glu Phe Ala Asp Cys Cys Leu Gly Ile Val Glu Pro Ser Gln Asn Glu	
138 143 148 153	
gag tct taa gatggat tattgtgctg cttgctcaag cgtgtgcttg actcctggaa	660
Glu Ser *	
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atgattgttt ttaaattgtt tacttttggg acagttgata gacatcataa acgatatcaa	900
gcttacactt catatggagt taaacttggg cagtgttaat aaaatcaaaa cgtgattcta	960
ctgtacattg cattattcat aatttaattg tttgaaatta cattaaataa atcaactaat	1020
taaataactaa agttttgttc ctttttaaag gaaataacca caagattttt cccagcccaa	1080
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tagtgaaatg tggccctgat gtttcttaac cctgatttgg taactaccag cctgacacc	1260
atcagtgctt gatgtagcct ggaaccccag gccactgac gcaactgggca cggggctctg	1320
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tggcagctgt gtgctgatta aatgtctttg gcaaggcagg gggcaggaaa aggccttgtg	1440
gaaacaaagg caccaaggat cccccagcc cagtgaaggc agaagaggtc acgtggatca	1500
gcctgtgtct ttccagcaga atctgattaa agcctgtaat gctgtagggt gaaggttcag	1560
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<400> 347

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acc cag gcc atg agg gac aaa tgt gga gca agg gat gga gct gga act	96
Thr Gln Ala Met Arg Asp Lys Cys Gly Ala Arg Asp Gly Ala Gly Thr	
17 22 27 32	
tgc tat tat ggg acg tta aag ctg gca gga cct gag agc ctt aga tgg	144
Cys Tyr Tyr Gly Thr Leu Lys Leu Ala Gly Pro Glu Ser Leu Arg Trp	
33 38 43 48	
ctt gcc tta gat ggc gaa agg gat gtt gca gat aca atg aag aat ttt	192
Leu Ala Leu Asp Gly Glu Arg Asp Val Ala Asp Thr Met Lys Asn Phe	
49 54 59 64	
gag atg cgg att ctc ctg gat tac cca ggt ggg ccc agc aca atc act	240
Glu Met Arg Ile Leu Leu Asp Tyr Pro Gly Gly Pro Ser Thr Ile Thr	
65 70 75 80	
gga tca gag aga gta gaa gat gcc tct ttg ctg gct ttg aag atg gag	288
Gly Ser Glu Arg Val Glu Asp Ala Ser Leu Leu Ala Leu Lys Met Glu	
81 86 91 96	
gaa ggg gct atg agt gaa gga gga ggg aag aat agc cac tgt cta ctg	336
Glu Gly Ala Met Ser Glu Gly Gly Gly Lys Asn Ser His Cys Leu Leu	
97 102 107 112	
acc tct acc gtg agg ccc aga gca aca gct tac gga gcc agt ggc cca	384
Thr Ser Thr Val Arg Pro Arg Ala Thr Ala Tyr Gly Ala Ser Gly Pro	
113 118 123 128	
gac cct ggc cca gcc cgt gtg gcc tcc aga cgt ctg ggg gcc gca gtt	432
Asp Pro Gly Pro Ala Arg Val Ala Ser Arg Arg Leu Gly Ala Ala Val	
129 134 139 144	
ggg ctt ctg agt gca gac acg ctg tgg cct ctc aat ggc ctt gcc agg	480
Gly Leu Leu Ser Ala Asp Thr Leu Trp Pro Leu Asn Gly Leu Ala Arg	
145 150 155 160	
gca ata gat gag gaa att gag gct ctg aga gat gac tct ggg gac gac	528
Ala Ile Asp Glu Glu Ile Glu Ala Leu Arg Asp Asp Ser Gly Asp Asp	
161 166 171 176	

gac gag gct acc acc cca gcc gac aag agc gag ctg cac cac acc ctg Asp Glu Ala Thr Thr Pro Ala Asp Lys Ser Glu Leu His His Thr Leu 177 182 187 192	576
aag aat ctt tcc ctg aag tta gat gac ctc agc acg tgc aat gac ctc Lys Asn Leu Ser Leu Lys Leu Asp Asp Leu Ser Thr Cys Asn Asp Leu 193 198 203 208	624
atc gcc aag cac ggc gct gca ctc cag cgc tcc ctg aca gag ctg gac Ile Ala Lys His Gly Ala Ala Leu Gln Arg Ser Leu Thr Glu Leu Asp 209 214 219 224	672
ggc ctc aag atc cca tct gag agt ggg gag aag ctg aag gtg gtg aat Gly Leu Lys Ile Pro Ser Glu Ser Gly Glu Lys Leu Lys Val Val Asn 225 230 235 240	720
gag cgg gcc acc ctc ttc cgc atc aca tcc aat gct atg atc aac ggc Glu Arg Ala Thr Leu Phe Arg Ile Thr Ser Asn Ala Met Ile Asn Gly 241 246 251 256	768
gct gca gcc atc ctc acc tca tat cag gaa tgg ctt cag ccc cag ggg Ala Ala Ala Ile Leu Thr Ser Tyr Gln Glu Trp Leu Gln Pro Gln Gly 257 262 267 272	816
ttt gag gga aca agg tgc tca gag gtg gtt tct gga ttg gga atc tgg Phe Glu Gly Thr Arg Cys Ser Glu Val Val Ser Gly Leu Gly Ile Trp 273 278 283 288	864
aac agc aac gct gtg ttt caa ccc ccc acg cct tta cca gtg ctg tac Asn Ser Asn Ala Val Phe Gln Pro Pro Thr Pro Leu Pro Val Leu Tyr 289 294 299 304	912
ctt cta gaa cac ccc ttc ctc acc ctt cag cac agc cag gat ggg gcc Leu Leu Glu His Pro Phe Leu Thr Leu Gln His Ser Gln Asp Gly Ala 305 310 315 320	960
tgg aga agg ccg gca gca gca gag gag acc ctg gga gtc agg gat gga Trp Arg Arg Pro Ala Ala Ala Glu Glu Thr Leu Gly Val Arg Asp Gly 321 326 331 336	1008
cac cag gtg agg act ggt gtg ccc atc ttc ctc ctt tgg ggt ggg aca His Gln Val Arg Thr Gly Val Pro Ile Phe Leu Leu Trp Gly Gly Thr 337 342 347 352	1056
gcc tgt gat gtg cat gga gct cag tgg gtg ctc cag gcc tgc agg gac Ala Cys Asp Val His Gly Ala Gln Trp Val Leu Gln Ala Cys Arg Asp 353 358 363 368	1104
ttc ttg gaa cta gca gag ata cac agt cgg aaa tgg cag cgg gca ctg Phe Leu Glu Leu Ala Glu Ile His Ser Arg Lys Trp Gln Arg Ala Leu 369 374 379 384	1152
cag tat gag cag gag cag cgc gtg cac ttg gag gaa acc att gag cag Gln Tyr Glu Gln Glu Gln Arg Val His Leu Glu Glu Thr Ile Glu Gln 385 390 395 400	1200

ctg gcg aag cag cac aac agc ctc gag cgg gcc ttc cac agt gcc cct	1248
Leu Ala Lys Gln His Asn Ser Leu Glu Arg Ala Phe His Ser Ala Pro	
401 406 411 416	
ggc cgg ccg gcc aac ccc tcc aag agc ttc att gag gga agc ctc ttg	1296
Gly Arg Pro Ala Asn Pro Ser Lys Ser Phe Ile Glu Gly Ser Leu Leu	
417 422 427 432	
act ccc aaa gga gag gac agt gag gaa gat gaa gat acc gag tac ttt	1344
Thr Pro Lys Gly Glu Asp Ser Glu Glu Asp Glu Asp Thr Glu Tyr Phe	
433 438 443 448	
gat gcc atg gaa gac tcc aca tcc ttc atc acc gtg atc acc gag gcc	1392
Asp Ala Met Glu Asp Ser Thr Ser Phe Ile Thr Val Ile Thr Glu Ala	
449 454 459 464	
aag gaa gac agc aga aaa gct gaa ggt agc acc ggg aca agt tcc gtg	1440
Lys Glu Asp Ser Arg Lys Ala Glu Gly Ser Thr Gly Thr Ser Ser Val	
465 470 475 480	
gac tgg agc tca gca gac aat gta cta gat ggt gcc tcg ctc gtg ccc	1488
Asp Trp Ser Ser Ala Asp Asn Val Leu Asp Gly Ala Ser Leu Val Pro	
481 486 491 496	
aag ggt tca tcc aaa gtc aag agg cga gtc cgc att ccc aac aag ccc	1536
Lys Gly Ser Ser Lys Val Lys Arg Arg Val Arg Ile Pro Asn Lys Pro	
497 502 507 512	
aac tac agc ctt aac ctc tgg agc atc atg aag aac tgc atc ggc cgg	1584
Asn Tyr Ser Leu Asn Leu Trp Ser Ile Met Lys Asn Cys Ile Gly Arg	
513 518 523 528	
gag ctc tcc agg atc ccc atg ccg gtg aac ttc aat gag ccc ctg tcc	1632
Glu Leu Ser Arg Ile Pro Met Pro Val Asn Phe Asn Glu Pro Leu Ser	
529 534 539 544	
atg ctc cag cgg ctg aca gag gac ctg gag tac cac cac ctg ctg gac	1680
Met Leu Gln Arg Leu Thr Glu Asp Leu Glu Tyr His His Leu Leu Asp	
545 550 555 560	
aag gca gtg cac tgc acc agc tca gtg gag cag atg tgc ctg gtg gcc	1728
Lys Ala Val His Cys Thr Ser Ser Val Glu Gln Met Cys Leu Val Ala	
561 566 571 576	
gcc ttc tct gtg tcc tcc tac tcc acc aca gtg cac cgc atc gcc aag	1776
Ala Phe Ser Val Ser Ser Tyr Ser Thr Thr Val His Arg Ile Ala Lys	
577 582 587 592	
ccc ttc aac ccc atg ctg ggg gag acc ttc gag ctg gac cgc ctc gac	1824
Pro Phe Asn Pro Met Leu Gly Glu Thr Phe Glu Leu Asp Arg Leu Asp	
593 598 603 608	
gac atg ggc ctg cgc tcc ctc tgt gag cag gtg agc cac cac ccc ccc	1872
Asp Met Gly Leu Arg Ser Leu Cys Glu Gln Val Ser His His Pro Pro	
609 614 619 624	
tca gct gcg cac tac gtg ttc tcc aag cat ggc tgg agc ctc tgg cag	1920

Ser	Ala	Ala	His	Tyr	Val	Phe	Ser	Lys	His	Gly	Trp	Ser	Leu	Trp	Gln	
625					630					635					640	
gag	atc	acc	atc	tcc	agc	aag	ttc	cgg	gga	aaa	tac	atc	tcc	atc	atg	1968
Glu	Ile	Thr	Ile	Ser	Ser	Lys	Phe	Arg	Gly	Lys	Tyr	Ile	Ser	Ile	Met	
641					646					651					656	
ccg	cta	ggt	gcc	atc	cac	tta	gaa	ttc	cag	gcc	agt	ggg	aat	cac	tac	2016
Pro	Leu	Gly	Ala	Ile	His	Leu	Glu	Phe	Gln	Ala	Ser	Gly	Asn	His	Tyr	
657					662					667					672	
gtg	tgg	agg	aag	agc	acc	tca	act	gtt	cac	aac	atc	atc	gtg	ggc	aag	2064
Val	Trp	Arg	Lys	Ser	Thr	Ser	Thr	Val	His	Asn	Ile	Ile	Val	Gly	Lys	
673					678					683					688	
ctc	tgg	atc	gac	cag	tca	ggg	gac	atc	gag	att	gtg	aac	cat	aag	acc	2112
Leu	Trp	Ile	Asp	Gln	Ser	Gly	Asp	Ile	Glu	Ile	Val	Asn	His	Lys	Thr	
689					694					699					704	
aat	gac	cgg	tgc	cag	ctg	aag	ttc	ctg	ccc	tac	agc	tac	ttc	tcc	aaa	2160
Asn	Asp	Arg	Cys	Gln	Leu	Lys	Phe	Leu	Pro	Tyr	Ser	Tyr	Phe	Ser	Lys	
705					710					715					720	
gag	gca	gcc	cgg	aag	gtg	aca	gga	gtg	gtg	agt	gac	agc	cag	ggc	aag	2208
Glu	Ala	Ala	Arg	Lys	Val	Thr	Gly	Val	Val	Ser	Asp	Ser	Gln	Gly	Lys	
721					726					731					736	
gcc	cat	tac	gtg	ctg	tcc	ggc	tcg	tgg	gat	gaa	caa	atg	gag	tgc	tcc	2256
Ala	His	Tyr	Val	Leu	Ser	Gly	Ser	Trp	Asp	Glu	Gln	Met	Glu	Cys	Ser	
737					742					747					752	
aag	gtc	atg	cat	agc	agt	ccc	agc	agc	ccc	agc	tct	gac	ggg	aag	cag	2304
Lys	Val	Met	His	Ser	Ser	Pro	Ser	Ser	Pro	Ser	Ser	Asp	Gly	Lys	Gln	
753					758					763					768	
aag	aca	gtg	tac	cag	acc	ctg	tca	gcc	aag	ctg	ctg	tgg	aag	aag	tac	2352
Lys	Thr	Val	Tyr	Gln	Thr	Leu	Ser	Ala	Lys	Leu	Leu	Trp	Lys	Lys	Tyr	
769					774					779					784	
ccg	ctg	ccg	gag	aac	gcg	gag	aac	atg	tac	tac	ttc	tca	gag	ctg	gcc	2400
Pro	Leu	Pro	Glu	Asn	Ala	Glu	Asn	Met	Tyr	Tyr	Phe	Ser	Glu	Leu	Ala	
785					790					795					800	
ctg	acc	ctc	aac	gag	cac	gag	gag	ggc	gta	gcg	cca	acc	gac	agc	cgc	2448
Leu	Thr	Leu	Asn	Glu	His	Glu	Glu	Gly	Val	Ala	Pro	Thr	Asp	Ser	Arg	
801					806					811					816	
ctg	cgg	ccc	gac	cag	cgg	ctg	atg	gag	aag	ggc	cgt	tgg	gac	gag	gcc	2496
Leu	Arg	Pro	Asp	Gln	Arg	Leu	Met	Glu	Lys	Gly	Arg	Trp	Asp	Glu	Ala	
817					822					827					832	
aat	acc	gag	aag	cag	cgg	ctg	gag	gag	aag	cag	cgc	ctg	tcg	cgg	cgc	2544
Asn	Thr	Glu	Lys	Gln	Arg	Leu	Glu	Glu	Lys	Gln	Arg	Leu	Ser	Arg	Arg	
833					838					843					848	
cgg	cgg	ctg	gag	gcc	tgc	ggg	ccg	ggc	agc	agc	tgc	agc	tcg	gag	gaa	2592
Arg	Arg	Leu	Glu	Ala	Cys	Gly	Pro	Gly	Ser	Ser	Cys	Ser	Ser	Glu	Glu	

849	854	859	864	
gaa ggt gta aag gca ttt gac aaa att cag cca gtt tcc agg ggg cac				2640
Glu Gly Val Lys Ala Phe Asp Lys Ile Gln Pro Val Ser Arg Gly His				
865	870	875	880	
agc cca cgt ttc att ctg tgt gac tgc tgc ccc ctg gcg ccc aac tca				2688
Ser Pro Arg Phe Ile Leu Cys Asp Cys Cys Pro Leu Ala Pro Asn Ser				
881	886	891	896	
ggc agg act ggc aac tac cgg aag ctc gcg agg ctt cca aag cgc atg				2736
Gly Arg Thr Gly Asn Tyr Arg Lys Leu Ala Arg Leu Pro Lys Arg Met				
897	902	907	912	
cgc agg tca cgg tac ggg cac gtg cgg cgc gcc agc aaa acc acg cag				2784
Arg Arg Ser Arg Tyr Gly His Val Arg Arg Ala Ser Lys Thr Thr Gln				
913	918	923	928	
gcg tct tgt cgc ttc cgc ctc gag cgt gtg gcg gga ttg cgg aag ccc				2832
Ala Ser Cys Arg Phe Arg Leu Glu Arg Val Ala Gly Leu Arg Lys Pro				
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Met Gly Ile	
1	
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Phe Val Lys Thr Ile Phe Pro Asn Gly Ser Ala Ala Glu Asp Gly Arg	
4 9 14 19	
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Leu Lys Glu Gly Asp Glu Ile Leu Asp Val Asn Gly Ile Pro Ile Lys	
20 25 30 35	
ggc ttg aca ttt caa gaa gcc att cat acc ttt aag caa atc cgg agt	321

260	265	270	275	
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Ser His Arg Ala Ser Gly Leu Phe His Lys	Gln Val Thr Val Ala Arg			
276	281	286	291	
caa gcc agt ctc ccc gga agc cca cag gcc ctc	cga aac cct ctc ctc	1089		
Gln Ala Ser Leu Pro Gly Ser Pro Gln Ala	Leu Arg Asn Pro Leu Leu			
292	297	302	307	
cgc cag agg aag gta ggc tgc tac gat gcc aac	gat gcc agt gat gag	1137		
Arg Gln Arg Lys Val Gly Cys Tyr Asp Ala	Asn Asp Ala Ser Asp Glu			
308	313	318	323	
gaa gag ttt gac aga gaa ggg gac tgc att tca	ctc cca ggg gcc ctc	1185		
Glu Glu Phe Asp Arg Glu Gly Asp Cys Ile	Ser Leu Pro Gly Ala Leu			
324	329	334	339	
ccg ggt ccc atc agg cct ctg tca gag gat gac	ccg agg cgt gtc tca	1233		
Pro Gly Pro Ile Arg Pro Leu Ser Glu Asp	Asp Pro Arg Arg Val Ser			
340	345	350	355	
att tcc tct tcc aag ggc atg gac gtc cac aac	caa gag gaa cga ccc	1281		
Ile Ser Ser Ser Lys Gly Met Asp Val His	Asn Gln Glu Glu Arg Pro			
356	361	366	371	
cgg aaa aca ctg gtg agc aag gcc atc tgc gca	cct ctt ctt ggt agc	1329		
Arg Lys Thr Leu Val Ser Lys Ala Ile Ser	Ala Pro Leu Leu Gly Ser			
372	377	382	387	
tca gtg gac tta gag gag agt atc cca gag ggc	atg gtg gat gct gcg	1377		
Ser Val Asp Leu Glu Glu Ser Ile Pro Glu	Gly Met Val Asp Ala Ala			
388	393	398	403	
tcc tat gca gcc aac ctc acg gac tct gca gag	gcc ccc aag ggg agc	1425		
Ser Tyr Ala Ala Asn Leu Thr Asp Ser Ala	Glu Ala Pro Lys Gly Ser			
404	409	414	419	
cct gga agc tgg tgg aag aag gaa ctg tca gga	tca agt agc gca ccc	1473		
Pro Gly Ser Trp Trp Lys Lys Glu Leu Ser	Gly Ser Ser Ser Ala Pro			
420	425	430	435	
aaa ttg gaa tac aca gtc cgt aca gac acc	cag agt ccg acg aac act	1521		
Lys Leu Glu Tyr Thr Val Arg Thr Asp Thr	Gln Ser Pro Thr Asn Thr			
436	441	446	451	
ggg agc ccc agt tcc ccc cag cag aaa agt	gaa ggc ctg ggc tcc agg	1569		
Gly Ser Pro Ser Ser Pro Gln Gln Lys Ser	Glu Gly Leu Gly Ser Arg			
452	457	462	467	
cac aga cca gtg gcc agg gta agc ccc cac	tgc aag aga tcc gag gct	1617		
His Arg Pro Val Ala Arg Val Ser Pro His	Cys Lys Arg Ser Glu Ala			
468	473	478	483	
gag gcc aag ccc agt ggc tca cag aca gtg	aac ctg act ggc aga gcc	1665		
Glu Ala Lys Pro Ser Gly Ser Gln Thr Val	Asn Leu Thr Gly Arg Ala			
484	489	494	499	

aat gat cca tgc gat ctg gac tcg aga gtc cag gcc act tct gtc aaa	1713
Asn Asp Pro Cys Asp Leu Asp Ser Arg Val Gln Ala Thr Ser Val Lys	
500 505 510 515	
gtg act gtc gct ggc ttt cag cca ggt gga gct gtg gag aag gaa tct	1761
Val Thr Val Ala Gly Phe Gln Pro Gly Gly Ala Val Glu Lys Glu Ser	
516 521 526 531	
ctg gga aag ctg acc act gga gat gct tgt gtc tct acc agc tgt gaa	1809
Leu Gly Lys Leu Thr Thr Gly Asp Ala Cys Val Ser Thr Ser Cys Glu	
532 537 542 547	
cta gcc agt gct ctg tcc cat ctg gat gcc agc cac ctc aca gag aac	1857
Leu Ala Ser Ala Leu Ser His Leu Asp Ala Ser His Leu Thr Glu Asn	
548 553 558 563	
ctg ccc aaa gct gca tca gag ctg ggg caa caa ccc atg act gaa ctg	1905
Leu Pro Lys Ala Ala Ser Glu Leu Gly Gln Gln Pro Met Thr Glu Leu	
564 569 574 579	
gac agc tcc tcg gac ctc atc tct tcc cca ggg aag aag ggg gcc gct	1953
Asp Ser Ser Ser Asp Leu Ile Ser Ser Pro Gly Lys Lys Gly Ala Ala	
580 585 590 595	
cat cct gac ccc agc aag acc tct gta gac aca ggg aaa gtc agt cgg	2001
His Pro Asp Pro Ser Lys Thr Ser Val Asp Thr Gly Lys Val Ser Arg	
596 601 606 611	
cca gag aat ccc agc cag cct gca tcg ccc agg gtc gcc aag tgc aag	2049
Pro Glu Asn Pro Ser Gln Pro Ala Ser Pro Arg Val Ala Lys Cys Lys	
612 617 622 627	
gcc agg tct cca gtc agg ctc ccc cat gag ggc agc ccc tcc cca ggg	2097
Ala Arg Ser Pro Val Arg Leu Pro His Glu Gly Ser Pro Ser Pro Gly	
628 633 638 643	
gag aaa gca gcg gct ccc cct gac tac agc aag act cga tca gca tcg	2145
Glu Lys Ala Ala Ala Pro Pro Asp Tyr Ser Lys Thr Arg Ser Ala Ser	
644 649 654 659	
gaa acc agc aca ccc cac aat acc agg agg gtg gct gcc ctc agg gga	2193
Glu Thr Ser Thr Pro His Asn Thr Arg Arg Val Ala Ala Leu Arg Gly	
660 665 670 675	
gcg gga cct gga gca gag gga atg aca cca gct ggt gct gtc ctg cca	2241
Ala Gly Pro Gly Ala Glu Gly Met Thr Pro Ala Gly Ala Val Leu Pro	
676 681 686 691	
gga gac ccc ctc aca tcc cag gag cag aga cag gga gct cca ggt aac	2289
Gly Asp Pro Leu Thr Ser Gln Glu Gln Arg Gln Gly Ala Pro Gly Asn	
692 697 702 707	
cac agt aag gct ctg gaa atg aca gga atc cat gca cct gaa agc tcc	2337
His Ser Lys Ala Leu Glu Met Thr Gly Ile His Ala Pro Glu Ser Ser	
708 713 718 723	

cag gag cct tcc ctg ctg gag gga gca gat tct gtg tcc tca agg gca	2385
Gln Glu Pro Ser Leu Leu Glu Gly Ala Asp Ser Val Ser Ser Arg Ala	
724 729 734 739	
ccg cag gcc agc ctc tcc atg ctg cca tcc act gac aac acc aaa gaa	2433
Pro Gln Ala Ser Leu Ser Met Leu Pro Ser Thr Asp Asn Thr Lys Glu	
740 745 750 755	
gca tgt ggc cat gtc tgc ggg cac tgc tgc ccg ggg ggg agt aga gag	2481
Ala Cys Gly His Val Ser Gly His Cys Cys Pro Gly Gly Ser Arg Glu	
756 761 766 771	
agc cct gtg acg gac att gac agc ttc atc aag gag ctg gat gct tct	2529
Ser Pro Val Thr Asp Ile Asp Ser Phe Ile Lys Glu Leu Asp Ala Ser	
772 777 782 787	
gca gca agg tct ccg tct tcc cag acg ggg gac agt ggc tct cag gag	2577
Ala Ala Arg Ser Pro Ser Ser Gln Thr Gly Asp Ser Gly Ser Gln Glu	
788 793 798 803	
ggc agt gct cag ggc cac cca cca gcc ggg gct gga ggt ggg agc tcc	2625
Gly Ser Ala Gln Gly His Pro Pro Ala Gly Ala Gly Gly Gly Ser Ser	
804 809 814 819	
tgc cgt gcc gaa cca gtc ccg ggg ggc cag acc tcc tcc ccg agg agg	2673
Cys Arg Ala Glu Pro Val Pro Gly Gly Gln Thr Ser Ser Pro Arg Arg	
820 825 830 835	
gcc tgg gct gct ggt gcc ccc gcc tac cca caa tgg gcc tcc cag cct	2721
Ala Trp Ala Ala Gly Ala Pro Ala Tyr Pro Gln Trp Ala Ser Gln Pro	
836 841 846 851	
tgc gtt tta gat tca att aat ccc gac aaa cat ttt act gtg aac aaa	2769
Ser Val Leu Asp Ser Ile Asn Pro Asp Lys His Phe Thr Val Asn Lys	
852 857 862 867	
aac ttt ctg agc aac tac tct aga aat ttt agc agt ttt cat gaa gac	2817
Asn Phe Leu Ser Asn Tyr Ser Arg Asn Phe Ser Ser Phe His Glu Asp	
868 873 878 883	
agc acc tcc cta tca ggc ctg ggt gac agc acg gag ccg tct ctg tca	2865
Ser Thr Ser Leu Ser Gly Leu Gly Asp Ser Thr Glu Pro Ser Leu Ser	
884 889 894 899	
tcc atg tat ggc gat gct gag gat tct tct tct gac cct gag tca ctc	2913
Ser Met Tyr Gly Asp Ala Glu Asp Ser Ser Ser Asp Pro Glu Ser Leu	
900 905 910 915	
act gaa gcc cca cga gct tct gcc agg gac ggc tgg tcc cct cct cgt	2961
Thr Glu Ala Pro Arg Ala Ser Ala Arg Asp Gly Trp Ser Pro Pro Arg	
916 921 926 931	
tcc cgt gtg tct ttg cac aag gaa gat cct tgc gag tca gaa gag gaa	3009
Ser Arg Val Ser Leu His Lys Glu Asp Pro Ser Glu Ser Glu Glu Glu	
932 937 942 947	
cag att gag att tgt tcc aca cgt ggc tgc ccc aat cca ccc tgc agt	3057

Gln Ile Glu Ile Cys Ser Thr Arg Gly Cys Pro Asn Pro Pro Ser Ser	
948 953 958 963	
cct gct cat ctt ccc acc cag gct gcc atc tgt cct gcc tca gcc aaa	3105
Pro Ala His Leu Pro Thr Gln Ala Ala Ile Cys Pro Ala Ser Ala Lys	
964 969 974 979	
gtt ctg tca tta aaa tac agc act ccg aga gag tcg gtg gcc agt ccc	3153
Val Leu Ser Leu Lys Tyr Ser Thr Pro Arg Glu Ser Val Ala Ser Pro	
980 985 990 995	
cgt gag aag gcc gcc tgc ttg cca ggc tca tac act tca ggc cca gac	3201
Arg Glu Lys Ala Ala Cys Leu Pro Gly Ser Tyr Thr Ser Gly Pro Asp	
996 1001 1006 1011	
tct tcc cag cca tca tca ctc ttg gag atg agc tct cag gag cat gaa	3249
Ser Ser Gln Pro Ser Ser Leu Leu Glu Met Ser Ser Gln Glu His Glu	
1012 1017 1022 1027	
act cat gcg gac ata agc act tca cag aac cac agg ccc tcg tgt gca	3297
Thr His Ala Asp Ile Ser Thr Ser Gln Asn His Arg Pro Ser Cys Ala	
1028 1033 1038 1043	
gaa gaa acc aca gaa gtc acc agc gct agc tca gcc atg gaa aac agt	3345
Glu Glu Thr Thr Glu Val Thr Ser Ala Ser Ser Ala Met Glu Asn Ser	
1044 1049 1054 1059	
ccg ctg tct aaa gta gcc agg cat ttt cac agt ccg ccc atc att ctc	3393
Pro Leu Ser Lys Val Ala Arg His Phe His Ser Pro Pro Ile Ile Leu	
1060 1065 1070 1075	
agc tcc ccc aac atg gta aat ggc ttg gaa cat gac ctg cta gat gac	3441
Ser Ser Pro Asn Met Val Asn Gly Leu Glu His Asp Leu Leu Asp Asp	
1076 1081 1086 1091	
gaa acc ctg aat caa tac gaa aca agc att aat gca gct gcc agt ctg	3489
Glu Thr Leu Asn Gln Tyr Glu Thr Ser Ile Asn Ala Ala Ala Ser Leu	
1092 1097 1102 1107	
tcc tcc ttc agt gtg gat gtc cct aag aat gga gaa tct gtt ttg gaa	3537
Ser Ser Phe Ser Val Asp Val Pro Lys Asn Gly Glu Ser Val Leu Glu	
1108 1113 1118 1123	
aac ctc cac atc tct gaa agt caa gac ctg gat gac ttg cta cag aaa	3585
Asn Leu His Ile Ser Glu Ser Gln Asp Leu Asp Asp Leu Leu Gln Lys	
1124 1129 1134 1139	
cca aaa atg atc gct agg agg ccc atc atg gcc tgg ttt aaa gaa ata	3633
Pro Lys Met Ile Ala Arg Arg Pro Ile Met Ala Trp Phe Lys Glu Ile	
1140 1145 1150 1155	
aat aaa cat aac caa ggc aca cat ttg agg agc aaa acc gag aag gaa	3681
Asn Lys His Asn Gln Gly Thr His Leu Arg Ser Lys Thr Glu Lys Glu	
1156 1161 1166 1171	
caa cct cta atg cct gcc aga agt ccc gac tcc aag att cag atg gtg	3729
Gln Pro Leu Met Pro Ala Arg Ser Pro Asp Ser Lys Ile Gln Met Val	

1172	1177	1182	1187	
agt tca agc caa aaa aag ggc gtt act gtg cct cat agc cct cct cag				3777
Ser Ser Ser Gln Lys Lys Gly Val Thr Val Pro His Ser Pro Pro Gln				
1188	1193	1198	1203	
ccg aaa aca aac ctg gaa aat aag gac ctg tct aag aag agt ccg gca				3825
Pro Lys Thr Asn Leu Glu Asn Lys Asp Leu Ser Lys Lys Ser Pro Ala				
1204	1209	1214	1219	
gaa atg ctt ctg act aat ggt cag aag gca aag tgt ggt ccg aag ctg				3873
Glu Met Leu Leu Thr Asn Gly Gln Lys Ala Lys Cys Gly Pro Lys Leu				
1220	1225	1230	1235	
aag agg ctc agc ctc aag ggc aag gcc aaa gtc aac tct gag gcc cct				3921
Lys Arg Leu Ser Leu Lys Gly Lys Ala Lys Val Asn Ser Glu Ala Pro				
1236	1241	1246	1251	
gct gcg aat gct gtg aag gct ggg ggg acg gac cac agg aaa ccc ttg				3969
Ala Ala Asn Ala Val Lys Ala Gly Gly Thr Asp His Arg Lys Pro Leu				
1252	1257	1262	1267	
atc tca ccc cag acc tcc cac aaa aca ctt tct aag gca gtg tca cag				4017
Ile Ser Pro Gln Thr Ser His Lys Thr Leu Ser Lys Ala Val Ser Gln				
1268	1273	1278	1283	
cgg ctc cat gta gcc gac cac gag gac cct gac aga aac acc aca gct				4065
Arg Leu His Val Ala Asp His Glu Asp Pro Asp Arg Asn Thr Thr Ala				
1284	1289	1294	1299	
gcc ccc agg tcc ccc cag tgt gtg ctg gaa agc aag cca cct ctt gcc				4113
Ala Pro Arg Ser Pro Gln Cys Val Leu Glu Ser Lys Pro Pro Leu Ala				
1300	1305	1310	1315	
acc tct ggg cca ctg aaa ccc tca gtg tct gac acg agc atc agg aca				4161
Thr Ser Gly Pro Leu Lys Pro Ser Val Ser Asp Thr Ser Ile Arg Thr				
1316	1321	1326	1331	
ttt gtc tcg ccc ctg acc tct ccc aag cct gtt cct gag caa ggc atg				4209
Phe Val Ser Pro Leu Thr Ser Pro Lys Pro Val Pro Glu Gln Gly Met				
1332	1337	1342	1347	
tgg agc agg ttc cac atg gct gtc ctc tct gaa ccc gac aga ggt tgc				4257
Trp Ser Arg Phe His Met Ala Val Leu Ser Glu Pro Asp Arg Gly Cys				
1348	1353	1358	1363	
cca acc acc cct aaa tct cct aag tgt aga gca gag ggc agg gcg ccc				4305
Pro Thr Thr Pro Lys Ser Pro Lys Cys Arg Ala Glu Gly Arg Ala Pro				
1364	1369	1374	1379	
cgt gct gac tcc ggg ccg gtg agt ccg gca gcg tct agg aac ggc atg				4353
Arg Ala Asp Ser Gly Pro Val Ser Pro Ala Ala Ser Arg Asn Gly Met				
1380	1385	1390	1395	
tcc gtg gca ggg aac aga cag agt gag ccg cgc ctg gcc agc cat gtg				4401
Ser Val Ala Gly Asn Arg Gln Ser Glu Pro Arg Leu Ala Ser His Val				
1396	1401	1406	1411	

aca tcg agg aat ctt cca gcc aca gat gaa ggg gat atc att tca gtc	5121
Thr Ser Arg Asn Leu Pro Ala Thr Asp Glu Gly Asp Ile Ile Ser Val	
1636 1641 1646 1651	
cag gag acg agc tgc cta gtc aca gac aaa atc aaa gtc acc aga cga	5169
Gln Glu Thr Ser Cys Leu Val Thr Asp Lys Ile Lys Val Thr Arg Arg	
1652 1657 1662 1667	
cac tac tgc tat gag cag aac tgg ccc cat gaa tct acc tca ttt ttc	5217
His Tyr Cys Tyr Glu Gln Asn Trp Pro His Glu Ser Thr Ser Phe Phe	
1668 1673 1678 1683	
tct gtg aag cag cgg atc aag tct ttt gag aac ctg gcc aat gct gac	5265
Ser Val Lys Gln Arg Ile Lys Ser Phe Glu Asn Leu Ala Asn Ala Asp	
1684 1689 1694 1699	
cgg cct gta gcc aag tcc ggg gct tcc cca ttt ttg tcg gtg agc tcc	5313
Arg Pro Val Ala Lys Ser Gly Ala Ser Pro Phe Leu Ser Val Ser Ser	
1700 1705 1710 1715	
aag cct ccc att ggg agg cgg tct tcc ggc agc att gtt tcc ggg agc	5361
Lys Pro Pro Ile Gly Arg Arg Ser Ser Gly Ser Ile Val Ser Gly Ser	
1716 1721 1726 1731	
ctg ggc cac cca ggt gac gca gca gca agg ttg ttg aga cgc agc ttg	5409
Leu Gly His Pro Gly Asp Ala Ala Ala Arg Leu Leu Arg Arg Ser Leu	
1732 1737 1742 1747	
agt tcc tgc agc gaa aac caa agc gaa gcc ggc acc ctc ctg ccc cag	5457
Ser Ser Cys Ser Glu Asn Gln Ser Glu Ala Gly Thr Leu Leu Pro Gln	
1748 1753 1758 1763	
atg gcc aag tct ccc tca atc atg aca ctg acc atc tct cgg cag aac	5505
Met Ala Lys Ser Pro Ser Ile Met Thr Leu Thr Ile Ser Arg Gln Asn	
1764 1769 1774 1779	
cca cca gag acc agt agc aag ggc tct gat tcg gaa cta aag aaa tca	5553
Pro Pro Glu Thr Ser Ser Lys Gly Ser Asp Ser Glu Leu Lys Lys Ser	
1780 1785 1790 1795	
ctt ggt cct ttg gga att ccc acc cca acg atg acc ctg gct tct cct	5601
Leu Gly Pro Leu Gly Ile Pro Thr Pro Thr Met Thr Leu Ala Ser Pro	
1796 1801 1806 1811	
gtt aag agg aac aag tcc tcg gta cgc cac acg cag ccc tcg ccc gtg	5649
Val Lys Arg Asn Lys Ser Ser Val Arg His Thr Gln Pro Ser Pro Val	
1812 1817 1822 1827	
tcc cgc tcc aag ctc cag gag ctg aga gcc ttg agc atg cct gac ctt	5697
Ser Arg Ser Lys Leu Gln Glu Leu Arg Ala Leu Ser Met Pro Asp Leu	
1828 1833 1838 1843	
gac aag ctc tgc agc gag gat tac tca gca ggg ccg agc gcc gtg ctc	5745
Asp Lys Leu Cys Ser Glu Asp Tyr Ser Ala Gly Pro Ser Ala Val Leu	
1844 1849 1854 1859	
ttc aaa act gag ctg gag atc acc ccc agg agg tca cct ggc cct cct	5793

Phe Lys Thr Glu Leu Glu Ile Thr Pro Arg Arg Ser Pro Gly Pro Pro	
1860 1865 1870 1875	
gct gga ggc gtt tgc tgt ccc gag aag ggc ggg aac agg gcc tgt cca	5841
Ala Gly Gly Val Ser Cys Pro Glu Lys Gly Gly Asn Arg Ala Cys Pro	
1876 1881 1886 1891	
gga gga agt ggc cct aaa acc agt gct gct gag aca ccc agt tca gcc	5889
Gly Gly Ser Gly Pro Lys Thr Ser Ala Ala Glu Thr Pro Ser Ser Ala	
1892 1897 1902 1907	
agt gat acg ggt gaa gct gcc cag gat ctg cct ttt aga aga agc tgg	5937
Ser Asp Thr Gly Glu Ala Ala Gln Asp Leu Pro Phe Arg Arg Ser Trp	
1908 1913 1918 1923	
tca gtt aat ttg gat caa ctt cta gtc tca gcg ggg gac cag caa aga	5985
Ser Val Asn Leu Asp Gln Leu Leu Val Ser Ala Gly Asp Gln Gln Arg	
1924 1929 1934 1939	
tta cag tct gtt tta tgc tca gtg gga tgc aaa tct acc atc cta act	6033
Leu Gln Ser Val Leu Ser Ser Val Gly Ser Lys Ser Thr Ile Leu Thr	
1940 1945 1950 1955	
ctc att cag gaa gcg aaa gca caa tca gag aat gaa gaa gat gtt tgc	6081
Leu Ile Gln Glu Ala Lys Ala Gln Ser Glu Asn Glu Glu Asp Val Cys	
1956 1961 1966 1971	
ttc ata gtc ttg aat aga aaa gaa ggc tca ggt ctg gga ttc agt gtg	6129
Phe Ile Val Leu Asn Arg Lys Glu Gly Ser Gly Leu Gly Phe Ser Val	
1972 1977 1982 1987	
gca gga ggg aca gat gtg gag cca aaa tca atc acg gtc cac agg gtg	6177
Ala Gly Gly Thr Asp Val Glu Pro Lys Ser Ile Thr Val His Arg Val	
1988 1993 1998 2003	
ttt tct cag ggg gcg gct tct cag gaa ggg act atg aac cga ggg gat	6225
Phe Ser Gln Gly Ala Ala Ser Gln Glu Gly Thr Met Asn Arg Gly Asp	
2004 2009 2014 2019	
ttc ctt ctg tca gtc aac ggc gcc tca ctg gct ggc tta gcc cac ggg	6273
Phe Leu Leu Ser Val Asn Gly Ala Ser Leu Ala Gly Leu Ala His Gly	
2020 2025 2030 2035	
aat gtc ctg aag gtt ctg cac cag gca cag ctg cac aaa gat gcc ctc	6321
Asn Val Leu Lys Val Leu His Gln Ala Gln Leu His Lys Asp Ala Leu	
2036 2041 2046 2051	
gtg gtc atc aag aaa ggg atg gat cag ccc agg ccc tct gcc cgg cag	6369
Val Val Ile Lys Lys Gly Met Asp Gln Pro Arg Pro Ser Ala Arg Gln	
2052 2057 2062 2067	
gag cct ccc aca gcc aat ggg aag ggt ttg ctg tcc aga aag acc atc	6417
Glu Pro Pro Thr Ala Asn Gly Lys Gly Leu Leu Ser Arg Lys Thr Ile	
2068 2073 2078 2083	
ccc ctg gag cct ggc att ggg aga agt gtg gct gta cac gat gct ctg	6465
Pro Leu Glu Pro Gly Ile Gly Arg Ser Val Ala Val His Asp Ala Leu	

2084	2089	2094	2099	
tgt gtt gaa gtg ctg aag acc tcg gct ggg ctg gga ctg agt ctg gat				6513
Cys Val Glu Val Leu Lys Thr Ser Ala Gly Leu Gly Leu Ser Leu Asp				
2100	2105	2110	2115	
ggg gga aaa tca tcg gtg acg gga gat ggg ccc ttg gtc att aaa aga				6561
Gly Gly Lys Ser Ser Val Thr Gly Asp Gly Pro Leu Val Ile Lys Arg				
2116	2121	2126	2131	
gtg tac aaa ggt ggt gtg gct gaa caa gct gga ata ata gaa gct gga				6609
Val Tyr Lys Gly Gly Val Ala Glu Gln Ala Gly Ile Ile Glu Ala Gly				
2132	2137	2142	2147	
gat gaa att ctt gct att aat ggg aaa cct ctg gtt ggg ctc atg cac				6657
Asp Glu Ile Leu Ala Ile Asn Gly Lys Pro Leu Val Gly Leu Met His				
2148	2153	2158	2163	
ttt gat gcc tgg aat att atg aag tct gtc cca gaa gga cct gtg cag				6705
Phe Asp Ala Trp Asn Ile Met Lys Ser Val Pro Glu Gly Pro Val Gln				
2164	2169	2174	2179	
tta tta att aga aag cat agg aat tct tca tga attttaac aagaatcatt				6756
Leu Leu Ile Arg Lys His Arg Asn Ser Ser *				
2180	2185	2190		
ttctcagttc tcttctttct ttagcaaadc agagtgcatt ctttaaacca caggttgttg				6816
aaatggccaa cactggtaca gacacggact ataaaaatct ccaagcttgt gcttacacat				6876
gaagcctgac ttaactgtat gtgcaacagc aatgaaatta actccagaag ccttcacact				6936
gcgtcaccga ggccgggagg gttccttcgt tccagtgcct gtccctacc tttatgttat				6996
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caacatgagt	ggagagtgca	tttgccatac	ctgtgtgcat	gacactaaga	ttttatgttg	8316
gagatacttc	tttaaataac	ctacagcttg	ggtctatggc	tgtgaccccc	agattcatgg	8376
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agtccagatt	tctcatcaac	tggcaataca	aaggaaaata	tggtagagga	gttagttaga	8556
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aactttgtat	gatattatac	attaaccttt	atttatgtaa	agtaaaatgc	cttatatatt	9396

aaagagtaag tgcaataata tgaaatagcc tgtacatttt aaaaatgttg tcaccaagtt 9456
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ctgctccagg ccaggcactg ttctaggagc caggatacag aggtggagac agaaacaaac 180
aaaccgataa ctgtatacaa tactctaacg tcagaggagc cacagagcac cagcctgcat 240
ggaacttcct tcctcactca gcttcccaag ttgccagctg ggacagggga gatggagtaa 300
ttttgctgtg gaaagacttc acgtcttgcc gaatgaaagt cccgcctgtc tgtcacgctg 360
atg ccc gtg cag ctg tct gag cac ccg gaa tgg aat gag tct atg cac 408
Met Pro Val Gln Leu Ser Glu His Pro Glu Trp Asn Glu Ser Met His
1 5 10 15
tcc ctc cgg atc agt gtg ggg ggc ctt cct gtg ctg gcg tcc atg acc 456
Ser Leu Arg Ile Ser Val Gly Gly Leu Pro Val Leu Ala Ser Met Thr
17 22 27 32
aag gcc gcg gac ccc cgc ttc cgc ccc cgc tgg aag gtg atc ctg acg 504
Lys Ala Ala Asp Pro Arg Phe Arg Pro Arg Trp Lys Val Ile Leu Thr
33 38 43 48
ttc ttt gtg ggt gcc gcc atc ctc tgg ctg ctc tgc tcc cac cgc ccg 552
Phe Phe Val Gly Ala Ala Ile Leu Trp Leu Leu Cys Ser His Arg Pro
49 54 59 64
gcc ccc ggc agg ccc ccc acc cac aat gca cac aac tgg agg ctc ggc 600
Ala Pro Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg Leu Gly
65 70 75 80
cag gcg ccc gcc aac tgg tac aat gac acc tac ccc ctg tct ccc cca 648
Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser Pro Pro
81 86 91 96
caa agg aca ccg gct ggg att cgg tat cga atc gca gtt atc gca gac 696
Gln Arg Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile Ala Asp

97	102	107	112	
ctg gac aca gag tca agg gcc caa gag gaa aac acc tgg ttc agt tac				744
Leu Asp Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe Ser Tyr				
113	118	123	128	
ctg aaa aag ggc tac ctg acc ctg tca gac agt ggg gac aag gtg gcc				792
Leu Lys Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys Val Ala				
129	134	139	144	
gtg gaa tgg gac aaa gac cat ggg gtc ctg gag tcc cac ctg gcg gag				840
Val Glu Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu Ala Glu				
145	150	155	160	
aag ggg aga ggc atg gag cta tcc gac ctg att gtt ttc aat ggg aaa				888
Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn Gly Lys				
161	166	171	176	
ctc tac tcc gtg gat gac cgg acg ggg gtc gtc tac cag atc gaa ggc				936
Leu Tyr Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile Glu Gly				
177	182	187	192	
agc aaa gcc gtg ccc tgg gtg att ctg tcc gac ggc gac ggc acc gtg				984
Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly Thr Val				
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gag aaa ggc ttc aag gcc gaa tgg ctg gca gtg aag gac gag cgt ctg				1032
Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Lys Asp Glu Arg Leu				
209	214	219	224	
tac gtg ggc ggc ctg ggc aag gag tgg acg acc act acg ggt gat gtg				1080
Tyr Val Gly Gly Leu Gly Lys Glu Trp Thr Thr Thr Thr Gly Asp Val				
225	230	235	240	
gtg aac gag aac ccg gag tgg gtg aag gtg gtg ggc tac aag ggc agc				1128
Val Asn Glu Asn Pro Glu Trp Val Lys Val Val Gly Tyr Lys Gly Ser				
241	246	251	256	
gtg gac cac gag aac tgg gtg tcc aac tac aac gcc ctg cgg gct gct				1176
Val Asp His Glu Asn Trp Val Ser Asn Tyr Asn Ala Leu Arg Ala Ala				
257	262	267	272	
gcc ggc atc cag ccg cca ggc tac ctc atc cat gag tct gcc tgc tgg				1224
Ala Gly Ile Gln Pro Pro Gly Tyr Leu Ile His Glu Ser Ala Cys Trp				
273	278	283	288	
agt gac acg ctg cag cgc tgg ttc ttc ctg ccg cgc cgc gcc agc cag				1272
Ser Asp Thr Leu Gln Arg Trp Phe Phe Leu Pro Arg Arg Ala Ser Gln				
289	294	299	304	
gag cgc tac agc gag aag gac gac gag cgc aag ggc gcc aac ctg ctg				1320
Glu Arg Tyr Ser Glu Lys Asp Asp Glu Arg Lys Gly Ala Asn Leu Leu				
305	310	315	320	
ctg agc gcc tcc cct gac ttc ggc gac atc gct gtg agc cac gtc ggg				1368
Leu Ser Ala Ser Pro Asp Phe Gly Asp Ile Ala Val Ser His Val Gly				
321	326	331	336	

gcg gtg gtc ccc act cac ggc ttc tcg tcc ttc aag ttc atc ccc aac	1416
Ala Val Val Pro Thr His Gly Phe Ser Ser Phe Lys Phe Ile Pro Asn	
337 342 347 352	
acc gac gac cag atc att gtg gcc ctc aaa tcc gag gag gac agc ggc	1464
Thr Asp Asp Gln Ile Ile Val Ala Leu Lys Ser Glu Glu Asp Ser Gly	
353 358 363 368	
aga gtc gcc tcc tac atc atg gcc ttc acg ctg gac ggg cgc ttc ctg	1512
Arg Val Ala Ser Tyr Ile Met Ala Phe Thr Leu Asp Gly Arg Phe Leu	
369 374 379 384	
ttg ccg gag acc aag atc gga agc gtg aaa tac gaa ggc atc gag ttc	1560
Leu Pro Glu Thr Lys Ile Gly Ser Val Lys Tyr Glu Gly Ile Glu Phe	
385 390 395 400	
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Ile *	
401	
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gatccagaca aaagagaagt aaacctcttc tgttacaatc agttcaggcc aatcactcca	180
caactctgcc ctccccttac ttgccaaggt tctagcccag tcctagaggg tgatgtcaga	240
tccttcagaa actgggtctga g atg aat gga gaa gaa gaa tac gga agc gga	291
Met Asn Gly Glu Glu Glu Tyr Gly Ser Gly	
1 5	
agt gcc ggt gga gcg cga gta gga agt ggt gag ttc gga gta gag atg	339
Ser Ala Gly Gly Ala Arg Val Gly Ser Gly Glu Phe Gly Val Glu Met	
11 16 21 26	
gcc gcg ctt gca ccg ctg ccc ccg ctc ccc gca cag ttc aag agc ata	387
Ala Ala Leu Ala Pro Leu Pro Pro Leu Pro Ala Gln Phe Lys Ser Ile	
27 32 37 42	
cag cat cat ctg agg acg gct cag gag cat gac aag cga gac cct gtg	435
Gln His His Leu Arg Thr Ala Gln Glu His Asp Lys Arg Asp Pro Val	
43 48 53 58	
gtg gct tat tac tgt cgt tta tac gca atg cag act gga atg aag atc	483
Val Ala Tyr Tyr Cys Arg Leu Tyr Ala Met Gln Thr Gly Met Lys Ile	
59 64 69 74	
gat agt aaa act cct gaa tgt cgc aaa ttt tta tca aag tta atg gat	531
Asp Ser Lys Thr Pro Glu Cys Arg Lys Phe Leu Ser Lys Leu Met Asp	
75 80 85 90	
cag tta gaa gct cta aag aag cag ttg ggt gat aat gaa gct att act	579
Gln Leu Glu Ala Leu Lys Lys Gln Leu Gly Asp Asn Glu Ala Ile Thr	
91 96 101 106	
caa gaa ata gtg ggc tgt gcc cat ttg gag aat tat gct ttg aaa atg	627
Gln Glu Ile Val Gly Cys Ala His Leu Glu Asn Tyr Ala Leu Lys Met	
107 112 117 122	
ttt ttg tat gca gac aat gaa gat cgt gct gga cga ttt cac aaa aac	675
Phe Leu Tyr Ala Asp Asn Glu Asp Arg Ala Gly Arg Phe His Lys Asn	
123 128 133 138	
atg atc aag tcc ttc tat act gca agt ctt ttg ata gat gtc ata aca	723
Met Ile Lys Ser Phe Tyr Thr Ala Ser Leu Leu Ile Asp Val Ile Thr	
139 144 149 154	
gta ttt gga gaa ctc act gat gaa aat gtg aaa cac agg aag tat gcc	771
Val Phe Gly Glu Leu Thr Asp Glu Asn Val Lys His Arg Lys Tyr Ala	
155 160 165 170	
aga tgg aag gca aca tac atc cat aat tgt tta aag aat ggg gag act	819
Arg Trp Lys Ala Thr Tyr Ile His Asn Cys Leu Lys Asn Gly Glu Thr	
171 176 181 186	

cct caa gca ggc cct gtt gga att gaa gaa gat aat gat att gaa gaa	867
Pro Gln Ala Gly Pro Val Gly Ile Glu Glu Asp Asn Asp Ile Glu Glu	
187 192 197 202	
aat gaa gat gct gga gca gcc tct ctg ccc act cag cca act cag cca	915
Asn Glu Asp Ala Gly Ala Ala Ser Leu Pro Thr Gln Pro Thr Gln Pro	
203 208 213 218	
tca tca tct tca act tat gac cca agc aac atg cca tca ggc aac tat	963
Ser Ser Ser Ser Thr Tyr Asp Pro Ser Asn Met Pro Ser Gly Asn Tyr	
219 224 229 234	
act gga ata cag att cct ccg ggt gca cac gct cca gct aat aca cca	1011
Thr Gly Ile Gln Ile Pro Pro Gly Ala His Ala Pro Ala Asn Thr Pro	
235 240 245 250	
gca gaa gtg cct cac agc aca ggt gta gca agt aat act atc caa cct	1059
Ala Glu Val Pro His Ser Thr Gly Val Ala Ser Asn Thr Ile Gln Pro	
251 256 261 266	
act cca cag act ata cct gcc att gat ccc gca ctt ttc aat aca att	1107
Thr Pro Gln Thr Ile Pro Ala Ile Asp Pro Ala Leu Phe Asn Thr Ile	
267 272 277 282	
tcc cag ggg gat gtt cgt cta acc cca gaa gac ttt gct aga gct cag	1155
Ser Gln Gly Asp Val Arg Leu Thr Pro Glu Asp Phe Ala Arg Ala Gln	
283 288 293 298	
aag tac tgc aaa tat gct ggc agt gct ttg cag tat gaa gat gta agc	1203
Lys Tyr Cys Lys Tyr Ala Gly Ser Ala Leu Gln Tyr Glu Asp Val Ser	
299 304 309 314	
act gct gtc cag aat cta caa aag gct ctc aag tta ctg acg aca ggc	1251
Thr Ala Val Gln Asn Leu Gln Lys Ala Leu Lys Leu Leu Thr Thr Gly	
315 320 325 330	
aga gaa tga agccttt gtatgacaga cccatgtatt tttggcatga ggaactaaca	1307
Arg Glu *	
331	
gtccattact ctatcttcag cctatcagga tcacagtttt aaggaagact tggttttggt	1367
gaatatgaca atgaaatctg tgtgtatcag atttttattg aagcattcat cagcagcctc	1427
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aattttattct catattaaat ataactccat taaaagttta aaatttcatg ggagaaaata	1847

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Val Asp Thr Tyr Pro Asn Glu Glu Lys Gln Gln Glu Arg Val Phe Pro	
123 128 133 138	
tac atc tca gcc atg gtg aac aac ggc tcc ctc agc tat gat cat gag	484
Tyr Ile Ser Ala Met Val Asn Asn Gly Ser Leu Ser Tyr Asp His Glu	
139 144 149 154	
cgg gat ggg cgg cct aca gag ctg gga ggc tgc aca gcc att gtc cgc	532
Arg Asp Gly Arg Pro Thr Glu Leu Gly Gly Cys Thr Ala Ile Val Arg	
155 160 165 170	
aat ctt cat tac gac acc ttc ctg gtg att cgc tac gtc aag agg cat	580
Asn Leu His Tyr Asp Thr Phe Leu Val Ile Arg Tyr Val Lys Arg His	
171 176 181 186	
ttg acg ata atg atg gat att gat ggc aag cat gag tgg agg gac tgc	628
Leu Thr Ile Met Met Asp Ile Asp Gly Lys His Glu Trp Arg Asp Cys	
187 192 197 202	
att gaa gtg ccc gga gtc cgc ctg ccc cgc ggc tac tac ttc ggc acc	676
Ile Glu Val Pro Gly Val Arg Leu Pro Arg Gly Tyr Tyr Phe Gly Thr	
203 208 213 218	
tcc tcc atc act ggg gat ctc tca gat aat cat gat gtc att tcc ttg	724
Ser Ser Ile Thr Gly Asp Leu Ser Asp Asn His Asp Val Ile Ser Leu	
219 224 229 234	
aag ttg ttt gaa ctg aca gtg gag aga acc cca gaa gag gaa aag ctc	772
Lys Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu Glu Glu Lys Leu	
235 240 245 250	
cat cga gat gtg ttc ttg ccc tca gtg gac aat atg aag ctg cct gag	820
His Arg Asp Val Phe Leu Pro Ser Val Asp Asn Met Lys Leu Pro Glu	
251 256 261 266	
atg aca gct cca ctg ccg ccc ctg agt ggc ctg gcc ctc ttc ctc atc	868
Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu Phe Leu Ile	
267 272 277 282	
gtc ttt ttc tcc ctg gtg ttt tct gta ttt gcc ata gtc att ggt atc	916
Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val Ile Gly Ile	
283 288 293 298	
ata ctc tac aac aaa tgg cag gaa cag agc cga aag cgc ttc tac tga	964
Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys Arg Phe Tyr *	
299 304 309 314	
gccctcctgc tgccaccact tttgtgactg tcacccatga ggtatggaag gagcaggcac	1024
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tctgtcactg gagttttgaa tgcagggacc ccgcattccc atggttgtgc atggggacat	1144

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 Met Gln Pro Pro Pro Pro Gly Pro Leu Gly Asp Cys Leu Arg Asp Trp
 1 5 10 15
 gag gat cta cag cag gac ttc cag aac atc cag gag acc cat cgg ctc 152
 Glu Asp Leu Gln Gln Asp Phe Gln Asn Ile Gln Glu Thr His Arg Leu
 17 22 27 32
 tac cgc ctg aag ctg gag gag ctg acc aaa ctt cag aac aat tgc acc 200
 Tyr Arg Leu Lys Leu Glu Glu Leu Thr Lys Leu Gln Asn Asn Cys Thr
 33 38 43 48
 agc tcc atc acg cgg cag aag aag cgg ctc cag gag ctg gcc ctc gcc 248
 Ser Ser Ile Thr Arg Gln Lys Lys Arg Leu Gln Glu Leu Ala Leu Ala
 49 54 59 64
 ctg aag aaa tgc aaa ccc tcc ctc cca gca gag gcc gag ggg gcc gca 296
 Leu Lys Lys Cys Lys Pro Ser Leu Pro Ala Glu Ala Glu Gly Ala Ala
 65 70 75 80
 cag gag ctg gag aac cag atg aaa gag cgc caa ggc ctc ttc ttt gac 344
 Gln Glu Leu Glu Asn Gln Met Lys Glu Arg Gln Gly Leu Phe Phe Asp
 81 86 91 96
 atg gag gcc tat ttg cct aag aag aat gga ttg tac ctg agc ctg gtt 392
 Met Glu Ala Tyr Leu Pro Lys Lys Asn Gly Leu Tyr Leu Ser Leu Val
 97 102 107 112
 ctg ggg aac gtc aac gtc acg ctc ctg agc aag cag gct aag ttt gcc 440
 Leu Gly Asn Val Asn Val Thr Leu Leu Ser Lys Gln Ala Lys Phe Ala
 113 118 123 128
 tac aag gac gag tat gag aag ttc aag ctc tac ctc acc atc atc ctc 488
 Tyr Lys Asp Glu Tyr Glu Lys Phe Lys Leu Tyr Leu Thr Ile Ile Leu
 129 134 139 144

atc ctc atc tcc ttc act tgc cgc ttc ctg ctc aac tcc agg gtg aca	536
Ile Leu Ile Ser Phe Thr Cys Arg Phe Leu Leu Asn Ser Arg Val Thr	
145 150 155 160	
gat gct gcc ttc aac ttc ctg ctg gtc tgg tac tac tgc acc ctg acc	584
Asp Ala Ala Phe Asn Phe Leu Leu Val Trp Tyr Tyr Cys Thr Leu Thr	
161 166 171 176	
atc cgg gag agc atc ctc atc aac aac ggc tcc cgg atc aaa ggc tgg	632
Ile Arg Glu Ser Ile Leu Ile Asn Asn Gly Ser Arg Ile Lys Gly Trp	
177 182 187 192	
tgg gtg ttc cat cac tac gtg tcc acc ttc ctg tcg gga gtc atg ctg	680
Trp Val Phe His His Tyr Val Ser Thr Phe Leu Ser Gly Val Met Leu	
193 198 203 208	
acg tgg ccc gac ggt ctc atg tac cag aaa ttc cgg aac caa ttc ctc	728
Thr Trp Pro Asp Gly Leu Met Tyr Gln Lys Phe Arg Asn Gln Phe Leu	
209 214 219 224	
tcc ttt tcc atg tac cag agc ttc gtg cag ttt ctc cag tac tac tac	776
Ser Phe Ser Met Tyr Gln Ser Phe Val Gln Phe Leu Gln Tyr Tyr Tyr	
225 230 235 240	
cag agc ggc tgc ctc tac cgc ctg cgg gcg ctg ggc gag cgg cac acc	824
Gln Ser Gly Cys Leu Tyr Arg Leu Arg Ala Leu Gly Glu Arg His Thr	
241 246 251 256	
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Met Asp Leu Thr Val Glu Gly Phe Gln Ser Trp Met Trp Arg Gly Leu	
257 262 267 272	
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Thr Phe Leu Leu Pro Phe Leu Phe Phe Gly His Phe Trp Gln Leu Phe	
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Asn Ala Leu Thr Leu Phe Asn Leu Ala Gln Asp Pro Gln Cys Lys Glu	
289 294 299 304	
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Trp Gln Val Leu Met Cys Gly Phe Pro Phe Leu Leu Leu Phe Leu Gly	
305 310 315 320	
aat ttc ttc acc acc ctg agg gtt gtg cac cag ctc cat cac gcg gca	1064
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321 326 331 336	
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Glu Glu Ala Ala Pro Gly Ala Gly Pro Ser Pro Glu Glu Met Gln Thr	
337 342 347 352	
ctc cct ccc agc aga ggc cga ggg ggc cgc aca gga gct gga gaa cca	1160
Leu Pro Pro Ser Arg Gly Arg Gly Gly Arg Thr Gly Ala Gly Glu Pro	
353 358 363 368	

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Asp Glu Arg Ala Pro Arg Pro Leu Leu *	
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gagtgtgcgt gtatcagggg gtctcttcta ttctcccttg ggttttatgg gcgctgtggg	2171
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aaaaa	2236

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cattatgcct tacaaactta cacagtgcct tgggaattcc aaagtactca gtggagagag 180

gtgttttcagg agccgtagag ccagatcgtc atc atg tct gca ttg tgg ctg ctg 234
Met Ser Ala Leu Trp Leu Leu
1 5

ctg ggc ctc ctt gcc ctg atg gac ttg tct gaa agc agc aac tgg gga 282
Leu Gly Leu Leu Ala Leu Met Asp Leu Ser Glu Ser Ser Asn Trp Gly
8 13 18 23

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Cys Tyr Gly Asn Ile Gln Ser Leu Asp Thr Pro Gly Ala Ser Cys Gly
24 29 34 39

att gga aga cgt cac ggc ctg aac tac tgt gga gtt cgt gct tct gaa 378
Ile Gly Arg Arg His Gly Leu Asn Tyr Cys Gly Val Arg Ala Ser Glu
40 45 50 55

agg ctg gct gaa ata gac atg cca tac ctc ctg aaa tat caa ccc atg 426
Arg Leu Ala Glu Ile Asp Met Pro Tyr Leu Leu Lys Tyr Gln Pro Met
56 61 66 71

atg caa acc att ggc caa aag tac tgc atg gat cct gcc gtg atc gct 474
Met Gln Thr Ile Gly Gln Lys Tyr Cys Met Asp Pro Ala Val Ile Ala
72 77 82 87

ggg gtc ttg tcc agg aag tct ccc ggt gac aaa att ctg gtc aac atg 522
Gly Val Leu Ser Arg Lys Ser Pro Gly Asp Lys Ile Leu Val Asn Met
88 93 98 103

ggc gat agg act agc atg gtg cag gac cct ggc tct caa gct ccc aca 570
Gly Asp Arg Thr Ser Met Val Gln Asp Pro Gly Ser Gln Ala Pro Thr
104 109 114 119

tcc tgg att agt gag tct cag gtt tcc cag aca act gaa gtt ctg act 618
Ser Trp Ile Ser Glu Ser Gln Val Ser Gln Thr Thr Glu Val Leu Thr
120 125 130 135

act aga atc aaa gaa atc cag agg agg ttt cca acc tgg acc cct gac 666
Thr Arg Ile Lys Glu Ile Gln Arg Arg Phe Pro Thr Trp Thr Pro Asp
136 141 146 151

cag tac ctg aga ggt gga ctc tgt gcc tac agt ggg ggt gct ggc tat 714
Gln Tyr Leu Arg Gly Gly Leu Cys Ala Tyr Ser Gly Gly Ala Gly Tyr
152 157 162 167

gtc cga agc agc cag gac ctg agc tgt gac ttc tgc aat gat gtc ctt 762
Val Arg Ser Ser Gln Asp Leu Ser Cys Asp Phe Cys Asn Asp Val Leu
168 173 178 183

gca cga gcc aag tac ctc aag aga cat ggc ttc taa catc tcagatgaaa 812
Ala Arg Ala Lys Tyr Leu Lys Arg His Gly Phe *
184 189 194

cccaagacca tgatcacata tgcagcctca aatgttacac agataaaact agccaagggc 872

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963

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Gly Lys Ala Thr Pro Pro Tyr Asp Val Gln Phe His Met Glu Ala Ser
9 14 19 24

gtt gaa aac tgc att att gtg agc atg aac acc gct gac cct ggc agc 147
Val Glu Asn Cys Ile Ile Val Ser Met Asn Thr Ala Asp Pro Gly Ser
25 30 35 40

cag ggc atc aca cac agc ctc ttg cta cag gtc att gat gac aag ggc 195
Gln Gly Ile Thr His Ser Leu Leu Leu Gln Val Ile Asp Asp Lys Gly
41 46 51 56

agc atc ctg cca cct aac aca gaa gga aac att ggc atc aga atc aaa 243
Ser Ile Leu Pro Pro Asn Thr Glu Gly Asn Ile Gly Ile Arg Ile Lys
57 62 67 72

cct gtc agg cct gtg agc ctc ttc atg tgc tat gag ggt gac cca gag 291
Pro Val Arg Pro Val Ser Leu Phe Met Cys Tyr Glu Gly Asp Pro Glu
73 78 83 88

aag aca gct aaa gtg gaa tgt ggg gac ttc tac aac act ggg gac aga 339
Lys Thr Ala Lys Val Glu Cys Gly Asp Phe Tyr Asn Thr Gly Asp Arg
89 94 99 104

gga aag atg gat gaa gag ggc tac att tgt ttc ctg ggg agg agt gat 387
Gly Lys Met Asp Glu Glu Gly Tyr Ile Cys Phe Leu Gly Arg Ser Asp
105 110 115 120

gac atc att aat gcc tct ggg tat cgc atc ggg cct gca gag gtt gaa 435
Asp Ile Ile Asn Ala Ser Gly Tyr Arg Ile Gly Pro Ala Glu Val Glu
121 126 131 136

agc gct ttg gtg gag cac cca gcg gtg gcg gag tca gcc gtg gtg ggc 483
Ser Ala Leu Val Glu His Pro Ala Val Ala Glu Ser Ala Val Val Gly
137 142 147 152

agc cca gac ccg att cga ggg gag gtg gtg aag gcc ttt att gtc ctg 531

Ser Pro Asp Pro Ile Arg Gly Glu Val Val Lys Ala Phe Ile Val Leu	
153 158 163 168	
acc cca cag ttc ctg tcc cat gac aag gat cag ctg acc aag gaa ctg	579
Thr Pro Gln Phe Leu Ser His Asp Lys Asp Gln Leu Thr Lys Glu Leu	
169 174 179 184	
cag cag cat gtc aag tca gtg aca gcc cca tac aag tac cca agg aag	627
Gln Gln His Val Lys Ser Val Thr Ala Pro Tyr Lys Tyr Pro Arg Lys	
185 190 195 200	
gtg gag ttt gtc tca gag ctg cca aaa acc atc act ggc aag att gaa	675
Val Glu Phe Val Ser Glu Leu Pro Lys Thr Ile Thr Gly Lys Ile Glu	
201 206 211 216	
cgg aag gaa ctt cgg aaa aag gag act ggt cag atg taa tcggcagtg	724
Arg Lys Glu Leu Arg Lys Lys Glu Thr Gly Gln Met *	
217 222 227	
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gttgcccaag gatcaggagg agtggaaaag acggacgggc cttctgctct acgagaacta	180
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Met Lys Ile Lys	
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ccg ggt ttc atg ggg aag gcc act cca ccc tat gac gtc cag gtc att	283
Pro Gly Phe Met Gly Lys Ala Thr Pro Pro Tyr Asp Val Gln Val Ile	
5 10 15 20	
gat gac aag ggc agc atc ctg cca cct aac aca gaa gga aac att ggc	331

Asp	Asp	Lys	Gly	Ser	Ile	Leu	Pro	Pro	Asn	Thr	Glu	Gly	Asn	Ile	Gly		
21					26					31					36		
atc	aga	atc	aaa	cct	gtc	agg	cct	gtg	agc	ctc	ttc	atg	tgc	tat	gag		379
Ile	Arg	Ile	Lys	Pro	Val	Arg	Pro	Val	Ser	Leu	Phe	Met	Cys	Tyr	Glu		
37					42					47					52		
ggc	gac	cca	gag	aag	aca	gct	aaa	gtg	gaa	tgt	ggg	gac	ttc	tac	aac		427
Gly	Asp	Pro	Glu	Lys	Thr	Ala	Lys	Val	Glu	Cys	Gly	Asp	Phe	Tyr	Asn		
53					58					63					68		
act	ggg	gac	aga	gga	aag	atg	gat	gaa	gag	ggc	tac	att	tgt	ttc	ctg		475
Thr	Gly	Asp	Arg	Gly	Lys	Met	Asp	Glu	Glu	Gly	Tyr	Ile	Cys	Phe	Leu		
69					74					79					84		
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Gly	Arg	Ser	Asp	Asp	Ile	Ile	Asn	Ala	Ser	Gly	Tyr	Arg	Ile	Gly	Pro		
85					90					95					100		
gca	gag	gtt	gaa	agc	gct	ttg	gtg	gag	cac	cca	gcg	gtg	gcg	gag	tca		571
Ala	Glu	Val	Glu	Ser	Ala	Leu	Val	Glu	His	Pro	Ala	Val	Ala	Glu	Ser		
101					106					111					116		
gcc	gtg	gtg	ggc	agc	cca	gac	ccg	att	cga	ggg	gag	gtg	gtg	aag	gcc		619
Ala	Val	Val	Gly	Ser	Pro	Asp	Pro	Ile	Arg	Gly	Glu	Val	Val	Lys	Ala		
117					122					127					132		
ttt	att	gtc	ctg	acc	cca	cag	ttc	ctg	tcc	cat	gac	aag	gat	cag	ctg		667
Phe	Ile	Val	Leu	Thr	Pro	Gln	Phe	Leu	Ser	His	Asp	Lys	Asp	Gln	Leu		
133					138					143					148		
acc	aag	gaa	ctg	cag	cag	cat	gtc	aag	tca	gtg	aca	gcc	cca	tac	aag		715
Thr	Lys	Glu	Leu	Gln	Gln	His	Val	Lys	Ser	Val	Thr	Ala	Pro	Tyr	Lys		
149					154					159					164		
tac	cca	agg	aag	gtg	gag	ttt	gtc	tca	gag	ctg	cca	aaa	acc	atc	act		763
Tyr	Pro	Arg	Lys	Val	Glu	Phe	Val	Ser	Glu	Leu	Pro	Lys	Thr	Ile	Thr		
165					170					175					180		
ggc	aag	att	gaa	cgg	aag	gaa	ctt	cgg	aaa	aag	gag	act	ggc	cag	atg		811
Gly	Lys	Ile	Glu	Arg	Lys	Glu	Leu	Arg	Lys	Lys	Glu	Thr	Gly	Gln	Met		
181					186					191					196		
taa	tcgg	cagtgaactc	agaacgcact	gcacacctga	ggcaaataccc	tgccacttt											868
*																	
197																	
agtctcccca	ctatggtgag	gacgagggtg	gggcattgag	agtgttgatt	tgggaaagta												928
tcaggagtgc	catgattcca	atgttttcct	tcttttaaat	taaattcagt	tgctctgctt												988
cctccaagtc	ctctgtatct	ttagaatttc	ccagggtgagc	actcataacg	caagtaataa												1048
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                                     Met Val Ala His
                                     1

ata aac aac agc cgg ctc aag gcc aag ggc gtg ggc cag cac gac aac      163
Ile Asn Asn Ser Arg Leu Lys Ala Lys Gly Val Gly Gln His Asp Asn
  5                      10                      15                      20

gcc cag aac ttt ggt aac cag agc ttt gag gag ctg cga gca gcc tgt      211
Ala Gln Asn Phe Gly Asn Gln Ser Phe Glu Glu Leu Arg Ala Ala Cys
  21                      26                      31                      36

cta aga aag ggg gag ctc ttc gag gac ccc tta ttc cct gct gaa ccc      259
Leu Arg Lys Gly Glu Leu Phe Glu Asp Pro Leu Phe Pro Ala Glu Pro
  37                      42                      47                      52

agc tca ctg ggc ttc aag gac ctg ggc ccc aac tcc aaa aat gtg cag      307
Ser Ser Leu Gly Phe Lys Asp Leu Gly Pro Asn Ser Lys Asn Val Gln
  53                      58                      63                      68

aac atc tcc tgg cag cgg ccc aag gat atc ata aac aac cct cta ttc      355
Asn Ile Ser Trp Gln Arg Pro Lys Asp Ile Ile Asn Asn Pro Leu Phe
  69                      74                      79                      84

atc atg gat ggg att tct cca aca gac atc tgc cag ggg atc ctc ggg      403
Ile Met Asp Gly Ile Ser Pro Thr Asp Ile Cys Gln Gly Ile Leu Gly
  85                      90                      95                      100

gac tgc tgg ctg ctg gct gcc atc ggc tcc ctt acc acc tgc ccc aaa      451
Asp Cys Trp Leu Leu Ala Ala Ile Gly Ser Leu Thr Thr Cys Pro Lys
  101                      106                      111                      116

ctg cta tac cgc gtg gtg ccc aga gga cag agc ttc aag aaa aac tat      499
Leu Leu Tyr Arg Val Val Pro Arg Gly Gln Ser Phe Lys Lys Asn Tyr
  117                      122                      127                      132

gct ggc atc ttc cat ttt cag att tgg cag ttt gga cag tgg gtg aac      547
Ala Gly Ile Phe His Phe Gln Ile Trp Gln Phe Gly Gln Trp Val Asn
  133                      138                      143                      148

gtg gtg gta gat gac cgg ctg ccc aca aag aat gac aag ctg gtg ttt      595
Val Val Val Asp Asp Arg Leu Pro Thr Lys Asn Asp Lys Leu Val Phe
  149                      154                      159                      164
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gtg cac tca acc gaa cgc agt gag ttc tgg agt gcc ctg ctg gag aag	643
Val His Ser Thr Glu Arg Ser Glu Phe Trp Ser Ala Leu Leu Glu Lys	
165 170 175 180	
gcg tat gcc aag ctg agt ggg tcc tat gaa gca ttg tca ggg ggc agt	691
Ala Tyr Ala Lys Leu Ser Gly Ser Tyr Glu Ala Leu Ser Gly Gly Ser	
181 186 191 196	
acc atg gag ggc ctt gag gac ttc aca gga ggc gtg gcc cag agc ttc	739
Thr Met Glu Gly Leu Glu Asp Phe Thr Gly Gly Val Ala Gln Ser Phe	
197 202 207 212	
caa ctc cag agg ccc cct cag aac ctg ctc agg ctc ctt agg aag gcc	787
Gln Leu Gln Arg Pro Pro Gln Asn Leu Leu Arg Leu Leu Arg Lys Ala	
213 218 223 228	
gtg gag cga tcc tcc ctc atg ggt tgc tcc att gaa gtc acc agt gat	835
Val Glu Arg Ser Ser Leu Met Gly Cys Ser Ile Glu Val Thr Ser Asp	
229 234 239 244	
agt gaa ctg gaa tcc atg act gac aag atg ctg gtg aga ggg cac gct	883
Ser Glu Leu Glu Ser Met Thr Asp Lys Met Leu Val Arg Gly His Ala	
245 250 255 260	
tac tct gtg act ggc ctt cag gat gtc cac tac aga ggc aaa atg gaa	931
Tyr Ser Val Thr Gly Leu Gln Asp Val His Tyr Arg Gly Lys Met Glu	
261 266 271 276	
aca ctg att cgg gtc cgg aat ccc tgg ggc cgg att gag tgg aat gga	979
Thr Leu Ile Arg Val Arg Asn Pro Trp Gly Arg Ile Glu Trp Asn Gly	
277 282 287 292	
gct tgg agt gac agt gcc agg gag tgg gaa gag gtg gcc tca gac atc	1027
Ala Trp Ser Asp Ser Ala Arg Glu Trp Glu Glu Val Ala Ser Asp Ile	
293 298 303 308	
cag atg cag ctg ctg cac aag acg gag gac ggg gag ttc tgg atg tcc	1075
Gln Met Gln Leu Leu His Lys Thr Glu Asp Gly Glu Phe Trp Met Ser	
309 314 319 324	
tac caa gat ttc ctg aac aac ttc acg ctc ctg gag atc tgc aac ctc	1123
Tyr Gln Asp Phe Leu Asn Asn Phe Thr Leu Leu Glu Ile Cys Asn Leu	
325 330 335 340	
acg cct gat aca ctc tct ggg gac tac aag agc tac tgg cac acc acc	1171
Thr Pro Asp Thr Leu Ser Gly Asp Tyr Lys Ser Tyr Trp His Thr Thr	
341 346 351 356	
ttc tac gag ggc agc tgg cgc aga ggc agc tcc gca ggg ggc tgc agg	1219
Phe Tyr Glu Gly Ser Trp Arg Arg Gly Ser Ser Ala Gly Gly Cys Arg	
357 362 367 372	
aac cac cct ggc acg ttc tgg acc aac ccc cag ttt aag atc tct ctt	1267
Asn His Pro Gly Thr Phe Trp Thr Asn Pro Gln Phe Lys Ile Ser Leu	
373 378 383 388	
cct gag ggg gat gac cca gag gat gac gca gag ggc aat gtt gtg gtc	1315

Pro Glu Gly Asp Asp	Pro Glu Asp Asp Ala	Glu Gly Asn Val Val Val	
389	394	399	404
tgc acc tgc ctg gtg gcc cta atg cag aag	aac tgg cgg cat gca cgg		1363
Cys Thr Cys Leu Val Ala Leu Met Gln Lys	Asn Trp Arg His Ala Arg		
405	410	415	420
cag cag gga gcc cag ctg cag acc att ggc	ttt gtc ctc tac gcg gtc		1411
Gln Gln Gly Ala Gln Leu Gln Thr Ile Gly	Phe Val Leu Tyr Ala Val		
421	426	431	436
cca aaa gag ttt cag aac att cag gat gtc	cac ttg aag aag gaa ttc		1459
Pro Lys Glu Phe Gln Asn Ile Gln Asp Val	His Leu Lys Lys Glu Phe		
437	442	447	452
ttc acg aag tat cag gac cac ggc ttc tca	gag atc ttc acc aac tca		1507
Phe Thr Lys Tyr Gln Asp His Gly Phe Ser	Glu Ile Phe Thr Asn Ser		
453	458	463	468
cgg gag gtg agc agc caa ctc cgg ctg cct	ccg ggg gaa tat atc att		1555
Arg Glu Val Ser Ser Gln Leu Arg Leu Pro	Pro Gly Glu Tyr Ile Ile		
469	474	479	484
att ccc tcc acc ttt gag cca cac aga gat	gct gac ttc ctg ctt cgg		1603
Ile Pro Ser Thr Phe Glu Pro His Arg Asp	Ala Asp Phe Leu Leu Arg		
485	490	495	500
gtc ttc acc gag aag cac agc gag tca tgg	gaa ttg gat gaa gtc aac		1651
Val Phe Thr Glu Lys His Ser Glu Ser Trp	Glu Leu Asp Glu Val Asn		
501	506	511	516
tat gct gag caa ctc caa gag gaa aag gtc	tct gag gat gac atg gac		1699
Tyr Ala Glu Gln Leu Gln Glu Glu Lys Val	Ser Glu Asp Asp Met Asp		
517	522	527	532
cag gac ttc cta cat ttg ttt aag ata gtg	gca gga gag ggc aag gag		1747
Gln Asp Phe Leu His Leu Phe Lys Ile Val	Ala Gly Glu Gly Lys Glu		
533	538	543	548
ata ggg gtg tat gag ctc cag agg ctg ctc	aac agg atg gcc atc aaa		1795
Ile Gly Val Tyr Glu Leu Gln Arg Leu Leu	Asn Arg Met Ala Ile Lys		
549	554	559	564
ttc aaa agc ttc aag acc aag ggc ttt ggc	ctg gat gct tgc cgc tgc		1843
Phe Lys Ser Phe Lys Thr Lys Gly Phe Gly	Leu Asp Ala Cys Arg Cys		
565	570	575	580
atg atc aac ctc atg gat aaa gat ggc tct	ggc aag ctg ggg ctt cta		1891
Met Ile Asn Leu Met Asp Lys Asp Gly Ser	Gly Lys Leu Gly Leu Leu		
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Glu Phe Lys Ile Leu Trp Lys Lys Leu Lys	Lys Trp Met Asp Ile Phe		
597	602	607	612
aga gag tgt gac cag gac cat tca ggc acc	ttg aac tcc tat gag atg		1987
Arg Glu Cys Asp Gln Asp His Ser Gly Thr	Leu Asn Ser Tyr Glu Met		

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cgc ctg gtt att gag aaa gca ggc atc aag	ctg aac aac aag gta atg	2035		
Arg Leu Val Ile Glu Lys Ala Gly Ile Lys	Leu Asn Asn Lys Val Met			
629	634	639	644	
cag gtc ctg gtg gcc agg tat gca gat gat	gac ctg atc ata gac ttt	2083		
Gln Val Leu Val Ala Arg Tyr Ala Asp Asp	Asp Leu Ile Ile Asp Phe			
645	650	655	660	
gac agc ttc atc agc tgt ttc ctg agg cta	aag acc atg ttc aca ttc	2131		
Asp Ser Phe Ile Ser Cys Phe Leu Arg Leu	Lys Thr Met Phe Thr Phe			
661	666	671	676	
ttt cta acc atg gac ccc aag aat act ggc	cat att tgc ttg agc ctg	2179		
Phe Leu Thr Met Asp Pro Lys Asn Thr Gly	His Ile Cys Leu Ser Leu			
677	682	687	692	
gaa cag tgg ctg cag atg acc atg tgg gga	tag aggcgctg taggagcctg	2230		
Glu Gln Trp Leu Gln Met Thr Met Trp Gly	*			
693	698	703		
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Pro Leu Cys His Cys Leu Asp His Cys Pro Cys Cys Phe Ser Gly Thr				
11 16 21 26				
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Thr Arg Thr Ser *				
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Met Thr Ser Phe Tyr Ser Thr Ser Ser Cys Pro Leu
1 5 10

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Gly Cys Thr Met Ala Pro Gly Ala Arg Asn Val Phe Val Ser Pro Ile
13 18 23 28

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Asp Val Gly Cys Gln Pro Val Ala Glu Ala Asn Ala Ala Ser Met Cys
29 34 39 44

ctc ttg gcc aac gtg gca cac gcc aac aga gtc cgt gtg ggg tgc act 312
Leu Leu Ala Asn Val Ala His Ala Asn Arg Val Arg Val Gly Ser Thr
45 50 55 60

ccc ctg ggc cgc ccc agc ctc tgt ctg ccc cca acc agt cac act gct 360
Pro Leu Gly Arg Pro Ser Leu Cys Leu Pro Pro Thr Ser His Thr Ala
61 66 71 76

tgt ccc ttg cca ggg acc tgt cac att ccc ggc aac atc gga atc tgt 408
Cys Pro Leu Pro Gly Thr Cys His Ile Pro Gly Asn Ile Gly Ile Cys
77 82 87 92

ggg gcc tac ggc aaa aac acc ctg aat ggc cat gag aag gag acc atg 456
Gly Ala Tyr Gly Lys Asn Thr Leu Asn Gly His Glu Lys Glu Thr Met
93 98 103 108

aag ttc ctg aat gac cgc ctg gcc aac tac ctg gag aag gtg cgc cag 504
Lys Phe Leu Asn Asp Arg Leu Ala Asn Tyr Leu Glu Lys Val Arg Gln
109 114 119 124

ctg gag cag gag aat gca gag ctg gag acc aca ctc ctc gag agg agc 552
Leu Glu Gln Glu Asn Ala Glu Leu Glu Thr Thr Leu Leu Glu Arg Ser
125 130 135 140

aag tgc cac gag tcc acc gtg tgc ccc gac tac cag tcc tac ttc cgt 600
Lys Cys His Glu Ser Thr Val Cys Pro Asp Tyr Gln Ser Tyr Phe Arg
141 146 151 156

aca atc gag gag ctc cag cag aag atc ctg tgc agc aag gct gag aat 648
Thr Ile Glu Glu Leu Gln Gln Lys Ile Leu Cys Ser Lys Ala Glu Asn
157 162 167 172

gcc agg ctg att gta caa att gac aac gcg aag ctg gct gct gat gac 696
Ala Arg Leu Ile Val Gln Ile Asp Asn Ala Lys Leu Ala Ala Asp Asp
173 178 183 188

ttt agg atc aag ctg gag agt gag cgc tcc ctt cac cag ctg gtg gag 744
Phe Arg Ile Lys Leu Glu Ser Glu Arg Ser Leu His Gln Leu Val Glu
189 194 199 204

gcg gac aag tgc ggg acg cag aag ctc ctg gat gac gcg acc ctg gcc 792
Ala Asp Lys Cys Gly Thr Gln Lys Leu Leu Asp Asp Ala Thr Leu Ala

205	210	215	220	
aag gcc gac ctg gag gcc cag cag gag tcc ctg aag gag gag cag ctc				840
Lys Ala Asp Leu Glu Ala Gln Gln Glu Ser Leu Lys Glu Glu Gln Leu				
221	226	231	236	
tcc ctc aag agc aac cac gag cag gaa gta aag att ctg agg agt cag				888
Ser Leu Lys Ser Asn His Glu Gln Glu Val Lys Ile Leu Arg Ser Gln				
237	242	247	252	
ctg ggg gag aag ttc cgg atc gag ctg gac att gag ccc acc att gac				936
Leu Gly Glu Lys Phe Arg Ile Glu Leu Asp Ile Glu Pro Thr Ile Asp				
253	258	263	268	
ctg aac agg gtg ttg ggg gag atg cgg gct cag tac gag gcc atg gtg				984
Leu Asn Arg Val Leu Gly Glu Met Arg Ala Gln Tyr Glu Ala Met Val				
269	274	279	284	
gag acc aac cac cag gat gtg gaa cag tgg ttc caa gcc cag tct gaa				1032
Glu Thr Asn His Gln Asp Val Glu Gln Trp Phe Gln Ala Gln Ser Glu				
285	290	295	300	
ggc atc agc ctg cag gcc atg tcc tgc tcc gag gag ctg cag tgc tgc				1080
Gly Ile Ser Leu Gln Ala Met Ser Cys Ser Glu Glu Leu Gln Cys Cys				
301	306	311	316	
cag tcg gag atc ctg gag ctg aga tgc acg gtg aat gcc ctg gag gtg				1128
Gln Ser Glu Ile Leu Glu Leu Arg Cys Thr Val Asn Ala Leu Glu Val				
317	322	327	332	
gag cgc caa gcc cag cac acc ttg aag gac tgt ctg cag aac tcc ctg				1176
Glu Arg Gln Ala Gln His Thr Leu Lys Asp Cys Leu Gln Asn Ser Leu				
333	338	343	348	
tgt gaa gcg gag gac cgc tac ggc aca gag ctg gcc cag atg cag agc				1224
Cys Glu Ala Glu Asp Arg Tyr Gly Thr Glu Leu Ala Gln Met Gln Ser				
349	354	359	364	
ctc att agc aac ttg gaa gag cag ttg tct gag atc cgg gcc gac ctg				1272
Leu Ile Ser Asn Leu Glu Glu Gln Leu Ser Glu Ile Arg Ala Asp Leu				
365	370	375	380	
gag cgg cag aac cag gag tac cag gtg ctg ctg gac gtg aag gcc cgg				1320
Glu Arg Gln Asn Gln Glu Tyr Gln Val Leu Leu Asp Val Lys Ala Arg				
381	386	391	396	
ttg gag aac gag att gcc aca tac cgg aac ctt act ccc ctg caa tcc				1368
Leu Glu Asn Glu Ile Ala Thr Tyr Arg Asn Leu Thr Pro Leu Gln Ser				
397	402	407	412	
ctg ttc cac gcc tgc ctc ctg tac ttc ttg tcc aag ctg tgg ccc tgt				1416
Leu Phe His Ala Cys Leu Leu Tyr Phe Leu Ser Lys Leu Trp Pro Cys				
413	418	423	428	
cac cgg tgg gtc tcc ctc tgg cca tgg agc cag cat ggg gag atg att				1464
His Arg Trp Val Ser Leu Trp Pro Trp Ser Gln His Gly Glu Met Ile				
429	434	439	444	

ctg aag gcc cga gtt agg aga ttg agg ctg gtt gca ctg ggg tca gga 1512
 Leu Lys Ala Arg Val Arg Arg Leu Arg Leu Val Ala Leu Gly Ser Gly
 445 450 455 460
 gtg ccc tca cct tgc cca gtc ttc ctt caa gac tag actc actgaggcat 1562
 Val Pro Ser Pro Cys Pro Val Phe Leu Gln Asp *
 461 466 471
 tttccctaaa tcaaccggta gcagatactt ccaaggagt gtcacctgcc tatgcctcta 1622
 agctgtatatt tttgttggtg ctaaaatggt gtaattatct tccatgaaag caattatttt 1682
 tcctgggtgct tcttcttggt acttttagtt ctattccagt gtttcagaat ctccaaaaat 1742
 gtaactgggt tccctgcatt aaatgggtcaa taaacctcct t 1783

<210> 360
 <211> 422
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (47)..(403)

<220>
 <221> misc_feature
 <222> (1)...(422)
 <223> n = a,t,c or g

<400> 360
 tgatctgctg cagtgcctga accagcttta ttcagcttct acagag atg tcc tgc 55
 Met Ser Cys
 1
 cag cag agc cag cag cag tgc cag cct cct ccc aaa tgt acc cct aaa 103
 Gln Gln Ser Gln Gln Gln Cys Gln Pro Pro Pro Lys Cys Thr Pro Lys
 4 9 14 19
 tgc cct ccc aag tgt act cct aag tgt cct ccc aag tgt ccc cca aaa 151
 Cys Pro Pro Lys Cys Thr Pro Lys Cys Pro Pro Lys Cys Pro Pro Lys
 20 25 30 35
 tgc cct ccc cag tat tca gcc cca tgc cca cct cca gtc tct tcc tgc 199
 Cys Pro Pro Gln Tyr Ser Ala Pro Cys Pro Pro Pro Val Ser Ser Cys
 36 41 46 51
 tgt ggt tcc agc tct ggg ggc tgc tgc agc tct gag ggt ggt ggc tgc 247
 Cys Gly Ser Ser Ser Gly Gly Cys Cys Ser Ser Glu Gly Gly Gly Cys
 52 57 62 67
 tgc ctg agc cac cac agg ccc cgc cag tcc ctc cga cgc cga cct cag 295
 Cys Leu Ser His His Arg Pro Arg Gln Ser Leu Arg Arg Arg Pro Gln

68	73	78	83	
agt tcc agc tgc tgt ggc agt ggc agt ggc cag cag tct ggg ggc tcc				343
Ser Ser Ser Cys Cys Gly Ser Gly Ser Gly Gln Gln Ser Gly Gly Ser				
84	89	94	99	
agc tgc tgc cac agc tct ggg ggc tct ggc tgc tgc cac agc tct gga				391
Ser Cys Cys His Ser Ser Gly Gly Ser Gly Cys Cys His Ser Ser Gly				
100	105	110	115	
ggc tgc tgc tga cctggggccat gaggagcan				422
Gly Cys Cys *				
116				

<210> 361
 <211> 1304
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (181)..(723)

<400> 361	
atttggccct cgaggccaag aattcggcac gagggcggcg cggacagcgt tcggggctgt	60
gtgccggcgc ctctggcagg gattggggaa tttttctgta aacacttcta agggcaatac	120
agccaaaaat ggtggcttgc ttctgtttct ctttttttcc ccacacatag cagtaccaat	180
atg aag tgg gta cag ttt tca aac cta cac gtt gat gtt cca aag gat	228
Met Lys Trp Val Gln Phe Ser Asn Leu His Val Asp Val Pro Lys Asp	
1 5 10 15	
ttg acc aaa cct gtg gta aca atc tct gat gaa cca gac ata tta tat	276
Leu Thr Lys Pro Val Val Thr Ile Ser Asp Glu Pro Asp Ile Leu Tyr	
17 22 27 32	
aag cgc ctc tcg gtt ttg gtg aaa ggt cac gat aag gct gta ttg gac	324
Lys Arg Leu Ser Val Leu Val Lys Gly His Asp Lys Ala Val Leu Asp	
33 38 43 48	
agt tat gaa tat ttt gct gtg ctt gct gct aaa gaa ctt ggt atc tct	372
Ser Tyr Glu Tyr Phe Ala Val Leu Ala Ala Lys Glu Leu Gly Ile Ser	
49 54 59 64	
att aaa gta cat gaa cct cca agg aaa ata gag cga ttt act ctt ctc	420
Ile Lys Val His Glu Pro Pro Arg Lys Ile Glu Arg Phe Thr Leu Leu	
65 70 75 80	
caa tca gtg cat att tac aag aag cac aga gtt cag tat gaa atg aga	468
Gln Ser Val His Ile Tyr Lys Lys His Arg Val Gln Tyr Glu Met Arg	
81 86 91 96	

aca ctt tac aga tgt tta gag tta gaa cat cta act gga agc aca gca	516
Thr Leu Tyr Arg Cys Leu Glu Leu Glu His Leu Thr Gly Ser Thr Ala	
97 102 107 112	
gat gtc tac ttg gaa tat att cag cga aac tta cct gaa ggg gtt gcc	564
Asp Val Tyr Leu Glu Tyr Ile Gln Arg Asn Leu Pro Glu Gly Val Ala	
113 118 123 128	
atg gaa gta aca aag ttt tgt ttc ttt att ttt tta gac aca att aga	612
Met Glu Val Thr Lys Phe Cys Phe Phe Ile Phe Leu Asp Thr Ile Arg	
129 134 139 144	
aca gtt acc aga aca cat caa gga gcc aat ctg gga aac act atc aga	660
Thr Val Thr Arg Thr His Gln Gly Ala Asn Leu Gly Asn Thr Ile Arg	
145 150 155 160	
aga aaa aga aga aag caa gtc ata aag cct cag gga ggc cat ttt tgc	708
Arg Lys Arg Arg Lys Gln Val Ile Lys Pro Gln Gly Gly His Phe Cys	
161 166 171 176	
cta aat ttg aaa tga ggggtgggcca gatgagtatg ttttaagtga gagtgcctcc	763
Leu Asn Leu Lys *	
177	
agctgagatg atttgagtct gtcctaactg ctccattgag ttctcgtgcc ctcatcagct	823
gagggcaggg aatggaactt taatggaaga accactttta tctattcttt ttattcattg	883
tttcagttct gatttcagca aacatgagca aaccactttg actgaaagca gaaagagtga	943
aaattctatt ttgttacgct actggtgttc aattattagt ttgtaccatt tttaatttat	1003
gtcagttgat gcatctgaaa ataagtgcct ggagtgttcg tacccttatt tttttttaag	1063
attcctagaa ggaatctttg gttaattcag attgagcagt taaagttttt gctatttacc	1123
tttgtgcagg ctggcatatg ctaatttggg ggtggtaacc aaccgatttt atctcatgta	1183
agcattacat tttgaagact gaatatactt cacagcagat caaacacatt tatggcatgc	1243
actgacctct tcttggagcc cagactttat agagttgcct accagggggt actgtaatgg	1303
a	1304

<210> 362
 <211> 414
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (53) .. (370)

<220>
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 <222> (1)...(414)
 <223> n = a,t,c or g

<400> 362
 ggacgtatct gttgctgcgt ctgaaccacac tgtttatcga aatcccacca ag atg 55
 Met
 1

tcc tgc cag cag aac caa cag cag tgc cag ccc cct ccc aag tgt cct 103
 Ser Cys Gln Gln Asn Gln Gln Gln Cys Gln Pro Pro Pro Lys Cys Pro
 2 7 12 17

atc ccc aag tat ccc cca aaa tgt ccc tca aag tgt gca tcc tca tgc 151
 Ile Pro Lys Tyr Pro Pro Lys Cys Pro Ser Lys Cys Ala Ser Ser Cys
 18 23 28 33

cca cct cca atc tct tcc tgc tgt ggc tcc agc tct ggg ggc tgc tgt 199
 Pro Pro Pro Ile Ser Ser Cys Cys Gly Ser Ser Ser Gly Gly Cys Cys
 34 39 44 49

agc tct ggg ggc tgt ggt tgc tgc agc tct gag gga ggt ggc tgc tgc 247
 Ser Ser Gly Gly Cys Gly Cys Cys Ser Ser Glu Gly Gly Gly Cys Cys
 50 55 60 65

ctg agc cac cac aga cac cat agg tcc cac tgc cac aga ccc aag agc 295
 Leu Ser His His Arg His His Arg Ser His Cys His Arg Pro Lys Ser
 66 71 76 81

tcc aat tgc tat ggc agt ggc agt ggc cag cag tct ggg ggt tct ggc 343
 Ser Asn Cys Tyr Gly Ser Gly Ser Gly Gln Gln Ser Gly Gly Ser Gly
 82 87 92 97

tgc tgc tct gga ggg ggc tgt tgc tga cctgg accaggagca gcaccaaagg 395
 Cys Cys Ser Gly Gly Gly Cys Cys *
 98 103

aattagtggg cgaaggacn 414

<210> 363
 <211> 2254
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (238)..(1278)

<400> 363
 aattccgggt cgacctacgc gtccgaagct ataggetacc cattcagctc ccctgtcaga 60
 gactcaagct ttgagaaagg ctagcaaaga gcaaggaaag agagaaaaca acaaagtggc 120

gaggccctca gagtgaaagc gtaaggttca gtcagcctgc tgcagctttg cagacctcag 180

ctgggcatct ccagactccc ctgaaggaag agccttcctc acccaaacc acaaaag 237
atg ctg aaa aag cct ctc tca gct gtg acc tgg ctc tgc att ttc atc 285
Met Leu Lys Lys Pro Leu Ser Ala Val Thr Trp Leu Cys Ile Phe Ile
1 5 10 15

gtg gcc ttt gtc agc cac cca gcg tgg ctg cag aag ctc tct aag cac 333
Val Ala Phe Val Ser His Pro Ala Trp Leu Gln Lys Leu Ser Lys His
17 22 27 32

aag aca cca gca cag cca cag ctc aaa gcg gcc aac tgc tgt gag gag 381
Lys Thr Pro Ala Gln Pro Gln Leu Lys Ala Ala Asn Cys Cys Glu Glu
33 38 43 48

gtg aag gag ctc aag gcc caa gtt gcc aac ctt agc agc ctg ctg agt 429
Val Lys Glu Leu Lys Ala Gln Val Ala Asn Leu Ser Ser Leu Leu Ser
49 54 59 64

gaa ctg aac aag aag cag gag agg gac tgg gtc agc gtg gtc atg cag 477
Glu Leu Asn Lys Lys Gln Glu Arg Asp Trp Val Ser Val Val Met Gln
65 70 75 80

gtg atg gag ctg gag agc aac agc aag cgc atg gag tgc cgg ctc aca 525
Val Met Glu Leu Glu Ser Asn Ser Lys Arg Met Glu Ser Arg Leu Thr
81 86 91 96

gat gct gag agc aag tac tcc gag atg aac aac caa att gac atc atg 573
Asp Ala Glu Ser Lys Tyr Ser Glu Met Asn Asn Gln Ile Asp Ile Met
97 102 107 112

cag ctg cag gca gca cag acg gtc act cag acc tcc gca gat gcc atc 621
Gln Leu Gln Ala Ala Gln Thr Val Thr Gln Thr Ser Ala Asp Ala Ile
113 118 123 128

tac gac tgc tct tcc ctc tac cag aag aac tac cgc atc tct gga gtg 669
Tyr Asp Cys Ser Ser Leu Tyr Gln Lys Asn Tyr Arg Ile Ser Gly Val
129 134 139 144

tat aag ctt cct cct gat gac ttc ctg ggc agc cct gaa ctg gag gtg 717
Tyr Lys Leu Pro Pro Asp Asp Phe Leu Gly Ser Pro Glu Leu Glu Val
145 150 155 160

ttc tgt gac atg gag act tca ggc gga ggc tgg acc atc atc cag aga 765
Phe Cys Asp Met Glu Thr Ser Gly Gly Gly Trp Thr Ile Ile Gln Arg
161 166 171 176

cga aaa agt ggc ctt gtc tcc ttc tac cgg gac tgg aag cag tac aag 813
Arg Lys Ser Gly Leu Val Ser Phe Tyr Arg Asp Trp Lys Gln Tyr Lys
177 182 187 192

cag ggc ttt ggc agc atc cgt ggg gac ttc tgg ctg ggg aac gaa cac 861
Gln Gly Phe Gly Ser Ile Arg Gly Asp Phe Trp Leu Gly Asn Glu His
193 198 203 208

atc cac cgg ctc tcc aga cag cca acc cgg ctg cgt gta gag atg gag 909
Ile His Arg Leu Ser Arg Gln Pro Thr Arg Leu Arg Val Glu Met Glu

209	214	219	224	
gac tgg gag ggc aac ctg cgc tac gct gag tat agc cac ttt gtt ttg				957
Asp Trp Glu Gly Asn Leu Arg Tyr Ala Glu Tyr Ser His Phe Val Leu				
225	230	235	240	
ggc aat gaa ctc aac agc tat cgc ctc ttc ctg ggg aac tac act ggc				1005
Gly Asn Glu Leu Asn Ser Tyr Arg Leu Phe Leu Gly Asn Tyr Thr Gly				
241	246	251	256	
aat gtg ggg aac gac gcc ctc cag tat cat aac aac aca gcc ttc agc				1053
Asn Val Gly Asn Asp Ala Leu Gln Tyr His Asn Asn Thr Ala Phe Ser				
257	262	267	272	
acc aag gac aag gac aat gac aac tgc ttg gac aag tgt gca cag ctc				1101
Thr Lys Asp Lys Asp Asn Asp Asn Cys Leu Asp Lys Cys Ala Gln Leu				
273	278	283	288	
cgc aaa ggt ggc tac tgg tac aac tgc tgc aca gac tcc aac ctc aat				1149
Arg Lys Gly Gly Tyr Trp Tyr Asn Cys Cys Thr Asp Ser Asn Leu Asn				
289	294	299	304	
gga gtg tac tac cgc ctg ggt gag cac aat aag cac ctg gat ggc atc				1197
Gly Val Tyr Tyr Arg Leu Gly Glu His Asn Lys His Leu Asp Gly Ile				
305	310	315	320	
acc tgg tat ggc tgg cat gga tct acc tac tcc ctc aaa cgg gtg gag				1245
Thr Trp Tyr Gly Trp His Gly Ser Thr Tyr Ser Leu Lys Arg Val Glu				
321	326	331	336	
atg aaa atc cgc cca gaa gac ttc aag cct taa aaggaggc tgccgtggag				1296
Met Lys Ile Arg Pro Glu Asp Phe Lys Pro *				
337	342	347		
cacggataca gaaactgaga cacgtggaga ctggatgagg gcagatgagg acaggaagag				1356
agtgttagaa agggtaggac tgagaaacag cctataatct ccaaagaaag aataagtctc				1416
caaggagcac aaaaaaatca tatgtaccaa ggatgttaca gtaaacagga tgaactattt				1476
aaaccactg ggtcctgcca catccttctc aaggtggtag actgagtggg gtctctctgc				1536
ccaagatccc tgacatagca gtagcttgtc ttttccacat gatttgtctg tgaaagaaaa				1596
taatttttgag atcgttttat ctattttctc tacggcttag gctatgtgag ggcaaacac				1656
aatcccttt gctaaaaaga accatattat tttgattctc aaaggatagg cctttgagtg				1716
ttagagaaag gagtgaagga ggcaggtggg aaatggtatt tctattttta aatccagtga				1776
aattatcttg agtctacaca ttatttttaa aacacaaaaa ttgttcggct ggaactgacc				1836
caggctggac ttgcggggag gaaactccag ggcactgcat ctggcgatca gactctgagc				1896
actgcccctg ctgccttggt tcatgtacag cactgaaagg aatgaagcac cagcaggagg				1956
tgacagagt ctctcatgga tgccggcaca aaactgcctt aaaatattca tagttaatac				2016

aggtatatct atttttatctt acttttgtaag aaacaagctc aaggagcttc ctttttaaatt 2076
 ttgtctgtag gaaatgggtg aaaactgaag gtagatgggtg ttatagttaa taataaatgc 2136
 tgtaaaataag catctcactt tgtaaaaata aaatattgtg gttttgtttt aaacattcaa 2196
 cgtttctttt ccttctacaa taaacacttt caaaatgtga aaaaaaaaaa aaaaaaaaaa 2254

<210> 364
 <211> 3655
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (50)..(1414)

<400> 364
 gcacgaggtt ttcttataac tgagctcagc caaggaaact cttgcacaa atg tac 55
 Met Tyr
 1

aat act gtt tgg aat atg gaa gac ctg gat tta gaa tat gcc aag aca 103
 Asn Thr Val Trp Asn Met Glu Asp Leu Asp Leu Glu Tyr Ala Lys Thr
 3 8 13 18

gat ata aat tgt ggc aca gac ttg atg ttt tat ata gaa atg gac cca 151
 Asp Ile Asn Cys Gly Thr Asp Leu Met Phe Tyr Ile Glu Met Asp Pro
 19 24 29 34

cca gca ctg cct cct aaa cca cca aaa cct act act gta gcc aac aac 199
 Pro Ala Leu Pro Pro Lys Pro Pro Lys Pro Thr Thr Val Ala Asn Asn
 35 40 45 50

ggg atg aat aac aat atg tcc tta caa gat gct gaa tgg tac tgg gga 247
 Gly Met Asn Asn Asn Met Ser Leu Gln Asp Ala Glu Trp Tyr Trp Gly
 51 56 61 66

gat atc tcg agg gaa gaa gtg aat gaa aaa ctt cga gat aca gca gac 295
 Asp Ile Ser Arg Glu Glu Val Asn Glu Lys Leu Arg Asp Thr Ala Asp
 67 72 77 82

ggg acc ttt ttg gta cga gat gcg tct act aaa atg cat ggt gat tat 343
 Gly Thr Phe Leu Val Arg Asp Ala Ser Thr Lys Met His Gly Asp Tyr
 83 88 93 98

act ctt aca cta agg aaa ggg gga aat aac aaa tta atc aaa ata ttt 391
 Thr Leu Thr Leu Arg Lys Gly Gly Asn Asn Lys Leu Ile Lys Ile Phe
 99 104 109 114

cat cga gat ggg aaa tat ggc ttc tct gac cca tta acc ttc agt tct 439
 His Arg Asp Gly Lys Tyr Gly Phe Ser Asp Pro Leu Thr Phe Ser Ser
 115 120 125 130

gtg gtt gaa tta ata aac cac tac cgg aat gaa tct cta gct cag tat	487
Val Val Glu Leu Ile Asn His Tyr Arg Asn Glu Ser Leu Ala Gln Tyr	
131 136 141 146	
aat ccc aaa ttg gat gtg aaa tta ctt tat cca gta tcc aaa tac caa	535
Asn Pro Lys Leu Asp Val Lys Leu Leu Tyr Pro Val Ser Lys Tyr Gln	
147 152 157 162	
cag gat caa gtt gtc aaa gaa gat aat att gaa gct gta ggg aaa aaa	583
Gln Asp Gln Val Val Lys Glu Asp Asn Ile Glu Ala Val Gly Lys Lys	
163 168 173 178	
tta cat gaa tat aac act cag ttt caa gaa aaa agt cga gaa tat gat	631
Leu His Glu Tyr Asn Thr Gln Phe Gln Glu Lys Ser Arg Glu Tyr Asp	
179 184 189 194	
aga tta tat gaa gaa tat acc cgc aca tcc cag gaa atc caa atg aaa	679
Arg Leu Tyr Glu Glu Tyr Thr Arg Thr Ser Gln Glu Ile Gln Met Lys	
195 200 205 210	
agg aca gct att gaa gca ttt aat gaa acc ata aaa ata ttt gaa gaa	727
Arg Thr Ala Ile Glu Ala Phe Asn Glu Thr Ile Lys Ile Phe Glu Glu	
211 216 221 226	
cag tgc cag acc caa gag cgg tac agc aaa gaa tac ata gaa aag ttt	775
Gln Cys Gln Thr Gln Glu Arg Tyr Ser Lys Glu Tyr Ile Glu Lys Phe	
227 232 237 242	
aaa cgt gaa ggc aat gag aaa gaa ata caa agg att atg cat aat tat	823
Lys Arg Glu Gly Asn Glu Lys Glu Ile Gln Arg Ile Met His Asn Tyr	
243 248 253 258	
gat aag ttg aag tct cga atc agt gaa att att gac agt aga aga aga	871
Asp Lys Leu Lys Ser Arg Ile Ser Glu Ile Ile Asp Ser Arg Arg Arg	
259 264 269 274	
ttg gaa gaa gac ttg aag aag cag gca gct gag tat cga gaa att gac	919
Leu Glu Glu Asp Leu Lys Lys Gln Ala Ala Glu Tyr Arg Glu Ile Asp	
275 280 285 290	
aaa cgt atg aac agc att aaa cca gac ctt atc cag ctg aga aag acg	967
Lys Arg Met Asn Ser Ile Lys Pro Asp Leu Ile Gln Leu Arg Lys Thr	
291 296 301 306	
aga gac caa tac ttg atg tgg ttg act caa aaa ggt gtt cgg caa aag	1015
Arg Asp Gln Tyr Leu Met Trp Leu Thr Gln Lys Gly Val Arg Gln Lys	
307 312 317 322	
aag ttg aac gag tgg ttg ggc aat gaa aac act gaa gac caa tat tca	1063
Lys Leu Asn Glu Trp Leu Gly Asn Glu Asn Thr Glu Asp Gln Tyr Ser	
323 328 333 338	
ctg gtg gaa gat gat gaa gat ttg ccc cat cat gat gag aag aca tgg	1111
Leu Val Glu Asp Asp Glu Asp Leu Pro His His Asp Glu Lys Thr Trp	
339 344 349 354	

aat gtt gga agc agc aac cga aac aaa gct gaa aac ctg ttg cga ggg	1159
Asn Val Gly Ser Ser Asn Arg Asn Lys Ala Glu Asn Leu Leu Arg Gly	
355 360 365 370	
aag cga gat ggc act ttt ctt gtc cgg gag agc agt aaa cag ggc tgc	1207
Lys Arg Asp Gly Thr Phe Leu Val Arg Glu Ser Ser Lys Gln Gly Cys	
371 376 381 386	
tat gcc tgc tct gta gtg gtg gac ggc gaa gta aag cat tgt gtc ata	1255
Tyr Ala Cys Ser Val Val Val Asp Gly Glu Val Lys His Cys Val Ile	
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Asn Lys Thr Ala Thr Gly Tyr Gly Phe Ala Glu Pro Tyr Asn Leu Tyr	
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Ser Ser Leu Lys Glu Leu Val Leu His Tyr Gln His Thr Ser Leu Val	
419 424 429 434	
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Gln His Asn Asp Ser Leu Asn Val Thr Leu Ala Tyr Pro Val Tyr Ala	
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Gln Gln Arg Arg *	
451	
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ccacctcaa atactttgtg agcagcgggt ccatcgcagt gaacgccgac tcttcgggtgc 540
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                               Met Leu Asp Leu Gly Ala Ala
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aag gca aac ttg gag aag gcc cag gcg gag ctg gtg ggg aca gct gac 641
Lys Ala Asn Leu Glu Lys Ala Gln Ala Glu Leu Val Gly Thr Ala Asp
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gag gcc acg cgg gca gag atc cag atc cga atc gag gcc aac gag gcc 689
Glu Ala Thr Arg Ala Glu Ile Gln Ile Arg Ile Glu Ala Asn Glu Ala
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ctg gtg aag gcc ctg gag tag gc gagccagccg ccaaggttga cctcagcttc 742
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201 206 211 216	
aag ccc cag gat gca gca gag gtt tca tca gag caa gaa aaa gaa caa	1024
Lys Pro Gln Asp Ala Ala Glu Val Ser Ser Glu Gln Glu Lys Glu Gln	
217 222 227 232	
gag act tta ata agc cag aaa agc atc cct gag cct ctc cca gca gca	1072
Glu Thr Leu Ile Ser Gln Lys Ser Ile Pro Glu Pro Leu Pro Ala Ala	
233 238 243 248	
gac atg aag aaa aaa ata gaa ggg tat cag gaa ttt tca gcg aag ccc	1120
Asp Met Lys Lys Lys Ile Glu Gly Tyr Gln Glu Phe Ser Ala Lys Pro	
249 254 259 264	
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Leu Ala Ser Arg Val Asp Pro Glu Lys Asp Asn Glu Thr Asp Gln Gly	
265 270 275 280	
tcc aac agt gag aag gtg gca gag gag gcg gga gag aag ggg ccc aca	1216
Ser Asn Ser Glu Lys Val Ala Glu Glu Ala Gly Glu Lys Gly Pro Thr	
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cct cca ctc cca agt gct cct ctg gcc cca gaa aaa gat tca gcc ttg	1264
Pro Pro Leu Pro Ser Ala Pro Leu Ala Pro Glu Lys Asp Ser Ala Leu	
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gtc cct ggg gcc agc aaa cag cca ctc acc tot cct agt gcc ctg gtg	1312
Val Pro Gly Ala Ser Lys Gln Pro Leu Thr Ser Pro Ser Ala Leu Val	
313 318 323 328	
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Asp Ser Lys Gln Glu Ser Lys Leu Cys Cys Phe Thr Glu Ser Pro Glu	
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Ser Glu Pro Gln Glu Ala Ser Phe Pro Ser Phe Pro Thr Thr Gln Ala	
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Thr Ala Gly Lys Pro Glu *	
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 ctgcaggag atg tgt aca aag aca atc cca gtc ctc tgg gga tgt ttc 168
 Met Cys Thr Lys Thr Ile Pro Val Leu Trp Gly Cys Phe
 1 5 10
 ctc ctg tgg aat ctc tat gtc tca tcc tct cag acc att tac cct gga 216
 Leu Leu Trp Asn Leu Tyr Val Ser Ser Ser Gln Thr Ile Tyr Pro Gly
 14 19 24 29
 atc aag gca agg att act cag agg gca ctt gac tat ggt gtt caa gct 264
 Ile Lys Ala Arg Ile Thr Gln Arg Ala Leu Asp Tyr Gly Val Gln Ala
 30 35 40 45
 gga atg aag atg att gag caa atg cta aaa gaa aag aaa ctc cca gat 312
 Gly Met Lys Met Ile Glu Gln Met Leu Lys Glu Lys Lys Leu Pro Asp
 46 51 56 61
 tta agc ggt tct gag tct ctt gaa ttt cta aaa gtt gat tat gta aac 360
 Leu Ser Gly Ser Glu Ser Leu Glu Phe Leu Lys Val Asp Tyr Val Asn
 62 67 72 77
 tac aat ttt tca aat ata aaa atc agt gcc ttt tca ttt cca aat acc 408
 Tyr Asn Phe Ser Asn Ile Lys Ile Ser Ala Phe Ser Phe Pro Asn Thr
 78 83 88 93
 tca ttg gct ttt gtg cct gga gtg gga atc aaa gcg cta acc aac cat 456
 Ser Leu Ala Phe Val Pro Gly Val Gly Ile Lys Ala Leu Thr Asn His
 94 99 104 109
 ggc act gcc aac atc agc aca gac tgg ggg ttc gag tct cca ctt ttt 504
 Gly Thr Ala Asn Ile Ser Thr Asp Trp Gly Phe Glu Ser Pro Leu Phe
 110 115 120 125
 gtt ctg tat aac tcc ttt gct gag ccc atg gag aaa ccc att tta aag 552
 Val Leu Tyr Asn Ser Phe Ala Glu Pro Met Glu Lys Pro Ile Leu Lys

126	131	136	141	
aac tta aat gaa atg ctc tgt ccc att att gca agt gaa gtc aaa gcg				600
Asn Leu Asn Glu Met Leu Cys Pro Ile Ile Ala Ser Glu Val Lys Ala				
142	147	152	157	
cta aat gcc aac ctc agc aca ctg gag gtt tta acc aag att gac aac				648
Leu Asn Ala Asn Leu Ser Thr Leu Glu Val Leu Thr Lys Ile Asp Asn				
158	163	168	173	
tac act ctg ctg gat tac tcc cta atc agt tct cca gaa att act gag				696
Tyr Thr Leu Leu Asp Tyr Ser Leu Ile Ser Ser Pro Glu Ile Thr Glu				
174	179	184	189	
aac tac ctt gac ctg aac ttg aag ggt gta ttc tac cca ctg gaa aac				744
Asn Tyr Leu Asp Leu Asn Leu Lys Gly Val Phe Tyr Pro Leu Glu Asn				
190	195	200	205	
ctc acc gac ccc ccc ttc tca cca gtt cct ttt gtg ctc cca gaa cgc				792
Leu Thr Asp Pro Pro Phe Ser Pro Val Pro Phe Val Leu Pro Glu Arg				
206	211	216	221	
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Ser Asn Ser Met Leu Tyr Ile Gly Ile Ala Glu Tyr Phe Phe Lys Ser				
222	227	232	237	
gcg tcc ttt gct cat ttc aca gct ggg gtt ttc aat gtc act ctc tcc				888
Ala Ser Phe Ala His Phe Thr Ala Gly Val Phe Asn Val Thr Leu Ser				
238	243	248	253	
acc gaa gag att tcc aac cat ttt gtt caa aac tct caa ggc ctt ggc				936
Thr Glu Glu Ile Ser Asn His Phe Val Gln Asn Ser Gln Gly Leu Gly				
254	259	264	269	
aac gtg ctc tcc cgg att gca gag atc tac atc ttg tcc cag ccc ttc				984
Asn Val Leu Ser Arg Ile Ala Glu Ile Tyr Ile Leu Ser Gln Pro Phe				
270	275	280	285	
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Met Val Arg Ile Met Ala Thr Glu Pro Pro Ile Ile Asn Leu Gln Pro				
286	291	296	301	
ggc aat ttc acc ctg gac atc cct gcc tcc atc atg atg ctc acc caa				1080
Gly Asn Phe Thr Leu Asp Ile Pro Ala Ser Ile Met Met Leu Thr Gln				
302	307	312	317	
ccc aag aac tcc aca gtt gaa acc atc gtt tcc atg gac ttc gtt gct				1128
Pro Lys Asn Ser Thr Val Glu Thr Ile Val Ser Met Asp Phe Val Ala				
318	323	328	333	
agt acc agt gtt ggc ctg gtt att ttg gga caa aga ctg gtc tgc tcc				1176
Ser Thr Ser Val Gly Leu Val Ile Leu Gly Gln Arg Leu Val Cys Ser				
334	339	344	349	
ttg tct ctg aac aga ttc cgc ctt gct ttg cca gag tcc aat cgc agc				1224
Leu Ser Leu Asn Arg Phe Arg Leu Ala Leu Pro Glu Ser Asn Arg Ser				
350	355	360	365	

aac att gag gtc ttg agg ttt gaa aat att cta tcg tcc att ctt cac	1272
Asn Ile Glu Val Leu Arg Phe Glu Asn Ile Leu Ser Ser Ile Leu His	
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Phe Gly Val Leu Pro Leu Ala Asn Ala Lys Leu Gln Gln Gly Phe Pro	
382 387 392 397	
ctg ccc aat cca cac aaa ttc tta ttc gtc aat tca gat att gaa gtt	1368
Leu Pro Asn Pro His Lys Phe Leu Phe Val Asn Ser Asp Ile Glu Val	
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Ser Lys Gln Gln Pro Ser Phe His Val Trp Glu Gly Leu Asn Leu Ile	
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 Gln Leu Leu Lys Asp Pro Gln Val Leu Phe Ala Gly Tyr Lys Val Pro
 30 35 40 45
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 His Pro Leu Glu His Lys Ile Ile Ile Arg Val Gln Thr Thr Pro Asp
 46 51 56 61
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 Tyr Ser Pro Gln Glu Ala Phe Thr Asn Ala Ile Thr Asp Leu Ile Ser
 62 67 72 77
 gag ctg tcc ctg ctg gag gag cgc ttc cgg acg tgc ctg ctt ccc ctt 889
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 Arg Leu Leu Pro *
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<400> 369

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ttcctccact aagagcggaa a  atg aac aaa tcc cag gaa caa gtg tca ttc      291
                        Met Asn Lys Ser Gln Glu Gln Val Ser Phe
                        1                      5

aag gat gta tgt gtg gac ttc act cag gaa gag tgg tat ctg ctg gac      339
Lys Asp Val Cys Val Asp Phe Thr Gln Glu Glu Trp Tyr Leu Leu Asp
 11                      16                      21                      26

cct gct cag aag att cta tac aga gat gtg atc ctg gaa aat tat agc      387
Pro Ala Gln Lys Ile Leu Tyr Arg Asp Val Ile Leu Glu Asn Tyr Ser
 27                      32                      37                      42

aat ctt gtc tca gta ggg tat tgc att act aaa cca gaa gtg atc ttt      435
Asn Leu Val Ser Val Gly Tyr Cys Ile Thr Lys Pro Glu Val Ile Phe
 43                      48                      53                      58

aag atc gag caa gga gaa gag ccc tgg ata tta gaa aaa gga ttc cca      483
Lys Ile Glu Gln Gly Glu Glu Pro Trp Ile Leu Glu Lys Gly Phe Pro
 59                      64                      69                      74

agc cag tgc caa cca gaa agg gaa tgg gaa gtt gat gac gtg tta gag      531
Ser Gln Cys Gln Pro Glu Arg Glu Trp Glu Val Asp Asp Val Leu Glu
 75                      80                      85                      90

agc agc cag gaa cat gaa gat gac cca ttt tgg gag ctt cta ttc ccc      579
Ser Ser Gln Glu His Glu Asp Asp Pro Phe Trp Glu Leu Leu Phe Pro
 91                      96                      101                      106

aac aac aaa cag taa gtgtagaaaa tggggataga ggaagcaaac tttcaatttg      634
Asn Asn Lys Gln *
107

gggcaagacc ctgttcttta agaattaccc tataaatttg tgcccatgtg aatgatttgg      694

gaattttggg gttaattttt gtaaagactt tccgaaagtc ctggtggttt atgttta      751

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<210> 370
 <211> 1902
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (981)..(1880)

<400> 370

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taagggcaaa gtgagttaat gtgtagacaa aggcgagggga caagagagag ttaacatcta      120
gacagtggaa aaagccatgg tgtgtggttt ctgggaacca ccaacacttg caggtttagc      180
tttttcccag ggttgactac aagaaagaaa accatgtttt tgcaagatta aaatgtggtt      240
gagtgtgcct aaattaacca tccccatttt tatcatattt ccaccatcac ttcagggttt      300
taagagtcag tgctcacctg ggcggagctg gtagtacatt ttgcttctta gaaagctaag      360
tcctgggttc cgtctgattt taggttccag gaacttcctg agaacacccg atcgagagg      420
gtaattttct ggagtttggt ttgcagggat agctgggagt atggccaccc tgctccacga      480
tgcggtaatg aatccagcag aagtggtgaa gcagcgcttg cagatgtaca actcgagca      540
ccggtcagca atcagctgca tccggacggt gtggaggacc gaggggttgg gggccttcta      600
ccggagctac accacgcagc tgaccatgaa catccccctc cagtccatcc acttcatcac      660
ctatgagttc ctgcaggagc aggtcaaccc ccaccggacc tacaacccgc attcccacat      720
catctcaggc gggctggccg gggccctcgc cgcggccgcc acgacccccc tggacgtctg      780
taaaaccctt ctgaacactc aggagaacgt ggcctctctg ctggccaaca tcagcggccg      840
gctggtggtg cctatgggcc ctctgctccc caatgcctta gagagaggag gggacggcac      900
ggccgctcac cggaaggctg tgtgcgggga catccgagag gtctgggagc tggaccggct      960
gctgccttgt gacatccggg      atg gcg cct tca tta cta tgc cct ttc act      1010
                        Met Ala Pro Ser Leu Leu Cys Pro Phe Thr
                        1                      5

gct atg cac aaa acc gtg ggg agg gcc tcc tgc gcc ccg ccg agc tgg      1058
Ala Met His Lys Thr Val Gly Arg Ala Ser Cys Ala Pro Pro Ser Trp
  11                16                21                26

cgg atg gag ctg cgc agc ggg agc gtg ggc agc cag gcg gtg gcg cgg      1106
Arg Met Glu Leu Arg Ser Gly Ser Val Gly Ser Gln Ala Val Ala Arg
  27                32                37                42

agg atg gat ggg gac agc cga gat ggc ggc ggc ggc aag gac gcc acc      1154
Arg Met Asp Gly Asp Ser Arg Asp Gly Gly Gly Gly Lys Asp Ala Thr

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43	48	53	58	
ggg tcg gag gac tac gag aac ctg ccg act agc gcc tcc gtg tcc acc				1202
Gly Ser Glu Asp Tyr Glu Asn Leu Pro Thr Ser Ala Ser Val Ser Thr				
59	64	69	74	
cac atg aca gca gga gcg atg gcc ggg atc ctg gag cac tcg gtc atg				1250
His Met Thr Ala Gly Ala Met Ala Gly Ile Leu Glu His Ser Val Met				
75	80	85	90	
tac ccg gtg gac tcg gtg aag aca cga atg cag agt ttg agt cca gat				1298
Tyr Pro Val Asp Ser Val Lys Thr Arg Met Gln Ser Leu Ser Pro Asp				
91	96	101	106	
ccc aaa gcc cag tac aca agt gtc tac gga gcc ctc aag aaa atc atg				1346
Pro Lys Ala Gln Tyr Thr Ser Val Tyr Gly Ala Leu Lys Lys Ile Met				
107	112	117	122	
cgg acc gaa ggc ttc tgg agg ccc ttg cga ggc gtc aac gtc atg atc				1394
Arg Thr Glu Gly Phe Trp Arg Pro Leu Arg Gly Val Asn Val Met Ile				
123	128	133	138	
atg ggt gca ggg cca gcc cat gcc atg tat ttt gcc tgc tat gaa aac				1442
Met Gly Ala Gly Pro Ala His Ala Met Tyr Phe Ala Cys Tyr Glu Asn				
139	144	149	154	
atg aaa agg act tta aat gac gtt ttc cac cac caa gga aac agc cac				1490
Met Lys Arg Thr Leu Asn Asp Val Phe His His Gln Gly Asn Ser His				
155	160	165	170	
cta gcc aac ggg ata gct ggg agt atg gcc acc ctg ctc cac gat gcg				1538
Leu Ala Asn Gly Ile Ala Gly Ser Met Ala Thr Leu Leu His Asp Ala				
171	176	181	186	
gta atg aat cca gca gaa gtg gtg aag cag cgc ttg cag atg tac aac				1586
Val Met Asn Pro Ala Glu Val Val Lys Gln Arg Leu Gln Met Tyr Asn				
187	192	197	202	
tcg cag cac cgg tca gca atc agc tgc atc cgg acg gtg tgg agg acc				1634
Ser Gln His Arg Ser Ala Ile Ser Cys Ile Arg Thr Val Trp Arg Thr				
203	208	213	218	
gag ggg ttg ggg gcc ttc tac cgg agc tac acc acg cag ctg acc atg				1682
Glu Gly Leu Gly Ala Phe Tyr Arg Ser Tyr Thr Thr Gln Leu Thr Met				
219	224	229	234	
aac atc ccc ttc cag tcc atc cac ttc atc acc tat gag ttc ctg cag				1730
Asn Ile Pro Phe Gln Ser Ile His Phe Ile Thr Tyr Glu Phe Leu Gln				
235	240	245	250	
gag cag gtc aac ccc cac cgg acc tac aac ccg cag tcc cac atc atc				1778
Glu Gln Val Asn Pro His Arg Thr Tyr Asn Pro Gln Ser His Ile Ile				
251	256	261	266	
tca ggc ggg ctg gcc ggg gcc ctc gcc gcg gcc gcg aat tcg gat cct				1826
Ser Gly Gly Leu Ala Gly Ala Leu Ala Ala Ala Asn Ser Asp Pro				
267	272	277	282	

<210> 372
 <211> 608
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (49)..(468)

<400> 372

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                                   Met Ser Ser
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tta ccc gtg cca tac aaa ctg cct gtg tct ttg tct gtt ggt tcc tgc      105
Leu Pro Val Pro Tyr Lys Leu Pro Val Ser Leu Ser Val Gly Ser Cys
  4                               9                14                19

gtg ata atc aaa ggg aca cca atc cac tct ttt atc aat gac cca cag      153
Val Ile Ile Lys Gly Thr Pro Ile His Ser Phe Ile Asn Asp Pro Gln
  20                               25                30                35

ctg cag gtg gat ttc tac act gac atg gat gag gat tca gat att gcc      201
Leu Gln Val Asp Phe Tyr Thr Asp Met Asp Glu Asp Ser Asp Ile Ala
  36                               41                46                51

ttc cgt ttc cga gtg cac ttt ggc aat cat gtg gtc atg aac agg cgt      249
Phe Arg Phe Arg Val His Phe Gly Asn His Val Val Met Asn Arg Arg
  52                               57                62                67

gag ttt ggg ata tgg atg ttg gag gag aca aca gac tac gtg ccc ttt      297
Glu Phe Gly Ile Trp Met Leu Glu Glu Thr Thr Asp Tyr Val Pro Phe
  68                               73                78                83

gag gat ggc aaa caa ttt gag ctg tgc atc tac gta cat tac aat gag      345
Glu Asp Gly Lys Gln Phe Glu Leu Cys Ile Tyr Val His Tyr Asn Glu
  84                               89                94                99

tat gag ata aag gtc aat ggc ata cgc att tac ggc ttt gtc cat cga      393
Tyr Glu Ile Lys Val Asn Gly Ile Arg Ile Tyr Gly Phe Val His Arg
 100                               105                110                115

atc ccg cca tca ttt gtg aag atg gtg caa gtg tcg aga gat atc tcc      441
Ile Pro Pro Ser Phe Val Lys Met Val Gln Val Ser Arg Asp Ile Ser
 116                               121                126                131

ctg acc tca gtg tgt gtc tgc aat tga gggag atgatcacac tcctcattgt      493
Leu Thr Ser Val Cys Val Cys Asn  *
 132                               137

tgaggaatcc ctctttctac ctgaccatgg gattcccaga acctgctaac agaataatcc      553

ctgctcacat tttcccctac actttgtcat taaaacagca cgaaaactca aaaaa      608

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<210> 373
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 <212> DNA
 <213> Homo sapiens

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 <222> (40)..(1179)

<400> 373

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				1	
ctc agt gac ctg ggc aag aga gag ccg gcc gcc gcc gcg gac gag cgg	102				
Leu Ser Asp Leu Gly Lys Arg Glu Pro Ala Ala Ala Ala Asp Glu Arg					
6 11 16 21					
ggc acg cag cag cgc cgg gcc tgc gcc aac gcc acc tgg aac agc atc	150				
Gly Thr Gln Gln Arg Arg Ala Cys Ala Asn Ala Thr Trp Asn Ser Ile					
22 27 32 37					
cac aac ggg gtg atc gcc gtc ttc cag cgc aag ggg ctg ccc gac cag	198				
His Asn Gly Val Ile Ala Val Phe Gln Arg Lys Gly Leu Pro Asp Gln					
38 43 48 53					
gag ctg ttc agc ctg aac gag ggc gtc cgg cag ctg ttg aag aca gag	246				
Glu Leu Phe Ser Leu Asn Glu Gly Val Arg Gln Leu Leu Lys Thr Glu					
54 59 64 69					
ctg ggg tcc ttc ttc acg gag tac ctg cag aac cag ctg ctg aca aaa	294				
Leu Gly Ser Phe Phe Thr Glu Tyr Leu Gln Asn Gln Leu Leu Thr Lys					
70 75 80 85					
ggc atg gtg atc ctt cgg gac aag att cgc ttc tat gag gga cag aag	342				
Gly Met Val Ile Leu Arg Asp Lys Ile Arg Phe Tyr Glu Gly Gln Lys					
86 91 96 101					
ctg ctg gac tca ctg gca gag acc tgg gac ttc ttc ttc agt gac gtg	390				
Leu Leu Asp Ser Leu Ala Glu Thr Trp Asp Phe Phe Phe Ser Asp Val					
102 107 112 117					
ctg ccc atg ctg cag gcc atc ttc tac ccg gtg cag ggc aag gag cca	438				
Leu Pro Met Leu Gln Ala Ile Phe Tyr Pro Val Gln Gly Lys Glu Pro					
118 123 128 133					
tcg gtg cgc cag ctg gcc ctg ctg cac ttc cgg aat gcc atc acc ctc	486				
Ser Val Arg Gln Leu Ala Leu Leu His Phe Arg Asn Ala Ile Thr Leu					
134 139 144 149					
agt gtg aag cta gag gat gcg ctg gcc cgg gcc cat gcc cgt gtg ccc	534				
Ser Val Lys Leu Glu Asp Ala Leu Ala Arg Ala His Ala Arg Val Pro					
150 155 160 165					

cct gcc atc gtg cag atg ctg ctg gtg ctg cag ggg gta cat gag tcc	582
Pro Ala Ile Val Gln Met Leu Leu Val Leu Gln Gly Val His Glu Ser	
166 171 176 181	
agg ggc gtg act gag gac tac ctg cgc ctg gag acg ctg gtc cag aag	630
Arg Gly Val Thr Glu Asp Tyr Leu Arg Leu Glu Thr Leu Val Gln Lys	
182 187 192 197	
gtg gtg tgc cca tac ctg ggc acc tac ggc ctc cac tcc agc gag ggg	678
Val Val Ser Pro Tyr Leu Gly Thr Tyr Gly Leu His Ser Ser Glu Gly	
198 203 208 213	
ccc ttc acc cat tcc tgc atc ctg gaa aag cgc ctc ctc cgc cgc tcc	726
Pro Phe Thr His Ser Cys Ile Leu Glu Lys Arg Leu Leu Arg Arg Ser	
214 219 224 229	
cgc tgc ggg gac gtg ctg gcc aag aac cct gtg gtg cgc tcc aag agc	774
Arg Ser Gly Asp Val Leu Ala Lys Asn Pro Val Val Arg Ser Lys Ser	
230 235 240 245	
tac aac acg cct ctg ctg aac ccc gtg cag gag cac gag gcg gag ggc	822
Tyr Asn Thr Pro Leu Leu Asn Pro Val Gln Glu His Glu Ala Glu Gly	
246 251 256 261	
gcg gcg gcc ggc ggt acc agc atc cgc agg cac tct gtg tgc gag atg	870
Ala Ala Ala Gly Gly Thr Ser Ile Arg Arg His Ser Val Ser Glu Met	
262 267 272 277	
acg tcc tgc ccc gag cct cag ggc ttc tcc gac ccg ccc ggc cag ggc	918
Thr Ser Cys Pro Glu Pro Gln Gly Phe Ser Asp Pro Pro Gly Gln Gly	
278 283 288 293	
ccc acc ggg acc ttc agg tcc tcc ccg gcg ccc cac tca ggg ccc tgc	966
Pro Thr Gly Thr Phe Arg Ser Ser Pro Ala Pro His Ser Gly Pro Cys	
294 299 304 309	
ccc agc aga ctg tac ccc acg acc cag ccc cct gag cag ggc ttg gat	1014
Pro Ser Arg Leu Tyr Pro Thr Thr Gln Pro Pro Glu Gln Gly Leu Asp	
310 315 320 325	
ccc acc cgc agc tcc ctg ccc cgc tcc agc ccg gag aac ctg gtg gac	1062
Pro Thr Arg Ser Ser Leu Pro Arg Ser Ser Pro Glu Asn Leu Val Asp	
326 331 336 341	
cag atc ctg gag tcc gtg gac tgc gat tct gaa ggg att ttc att gac	1110
Gln Ile Leu Glu Ser Val Asp Ser Asp Ser Glu Gly Ile Phe Ile Asp	
342 347 352 357	
ttt ggc cgg ggc cgg ggc tct ggc atg tcc gac ttg gag ggc tct ggg	1158
Phe Gly Arg Gly Arg Gly Ser Gly Met Ser Asp Leu Glu Gly Ser Gly	
358 363 368 373	
ggc cgg cag agt gtc gtg tga gg cctcacagct ggccttgagt ttttactgac	1211
Gly Arg Gln Ser Val Val *	
374 379	
acgtccctgt gtgcgggggt gtccatgtgg cgtgtgtgtg agtgagactt ttttactgcg	1271

tcccgccccg ccagccctat cggcctcgtc actggccttg gtcactttgt atttctgtct 1331
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 ggcgtttacc cagggggcgg gccagagacg ggggtcggcc gctcgctccc acgctcctcc 1451
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 ccacgccggg ccccaaagt accagactcc agcacacctg tctcctcctg cctgggggtgg 1571
 ccatggggat ggaagggggg ggaataaac ctgtcaacct ggaaaaaaaa aaaa 1625

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 <212> DNA
 <213> Homo sapiens

<220>
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 gctgctgctc cgcggtggag tcaccgcacc gctcccgga tc atg gtg ttc tac 174
 Met Val Phe Tyr
 1
 ttc acc agc agc agc gtt aat tca tct gcc tac act att tac atg gga 222
 Phe Thr Ser Ser Ser Val Asn Ser Ser Ala Tyr Thr Ile Tyr Met Gly
 5 10 15 20
 aaa gat aaa tat gaa aat gaa gat ctg atc aag cat ggc tgg cct gaa 270
 Lys Asp Lys Tyr Glu Asn Glu Asp Leu Ile Lys His Gly Trp Pro Glu
 21 26 31 36
 gat atc tgg ttt cat gtg gac aaa ctc tct tcg gct cat gta tac ctt 318
 Asp Ile Trp Phe His Val Asp Lys Leu Ser Ser Ala His Val Tyr Leu
 37 42 47 52
 cga tta cat aag gga gag aat ata gaa gac atc cca aag gaa gtg ctg 366
 Arg Leu His Lys Gly Glu Asn Ile Glu Asp Ile Pro Lys Glu Val Leu
 53 58 63 68
 atg gac tgt gcc cac ctt gtg aag gcc aat agc att caa ggc tgc aag 414
 Met Asp Cys Ala His Leu Val Lys Ala Asn Ser Ile Gln Gly Cys Lys
 69 74 79 84
 atg aac aac gtt aat gtg gta tat acg ccg tgg tct aac ctg aag aaa 462
 Met Asn Asn Val Asn Val Val Tyr Thr Pro Trp Ser Asn Leu Lys Lys
 85 90 95 100

aca gct gac atg gat gtg ggg cag ata ggc ttt cac agg cag aag gat	510
Thr Ala Asp Met Asp Val Gly Gln Ile Gly Phe His Arg Gln Lys Asp	
101 106 111 116	
gta aaa att gtg aca gtg gag aag aaa gta aat gag atc ctg aac cga	558
Val Lys Ile Val Thr Val Glu Lys Lys Val Asn Glu Ile Leu Asn Arg	
117 122 127 132	
tta gaa aag acc aaa gtc gag cgg ttc tca gac cta gca gca gag aaa	606
Leu Glu Lys Thr Lys Val Glu Arg Phe Ser Asp Leu Ala Ala Glu Lys	
133 138 143 148	
gaa tgc aga gat cgt gaa gag agg aat gag aaa aaa gcc caa att cag	654
Glu Cys Arg Asp Arg Glu Glu Arg Asn Glu Lys Lys Ala Gln Ile Gln	
149 154 159 164	
gaa atg aaa aag aga gaa aaa gaa gaa atg aag aag aag agg gaa atg	702
Glu Met Lys Lys Arg Glu Lys Glu Glu Met Lys Lys Lys Arg Glu Met	
165 170 175 180	
gat gaa ctt agg agc tat tca tca cta atg aaa gtt gaa aat atg tct	750
Asp Glu Leu Arg Ser Tyr Ser Ser Leu Met Lys Val Glu Asn Met Ser	
181 186 191 196	
tca aat cag gat ggc aat gat tca gat gaa ttc atg taa aaggagaaaa	799
Ser Asn Gln Asp Gly Asn Asp Ser Asp Glu Phe Met *	
197 202 207	
ggagaaaagg acctttgaaa gatgtgaatg tagagacaat tgcagacctt ttggtttcat	859
ctgtgttctg aaatataaaa tacaaccaa attctacctt catcctaccc agaaattatt	919
gattttcaag ttttaaaaaa attgtacctt ttttgctgac agaaaaggat cagatatgta	979
taaaatagtt gaacttgaca gcatataact taaagtgaaa atgtttttgc cagaacatgt	1039
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<210> 375
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (163)..(423)

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ctaaagggaa taagcttgcg gccgccgcga gtctggtatc ctgagcttcg tgagttgagc	120

gctgctgctc cgcggtggag tcaccgcacc gctccccgga tc atg gtg ttc tac 174
Met Val Phe Tyr
1

ttc acc agc agc agc gtt aat tca tct gcc tac act att tac atg gga 222
Phe Thr Ser Ser Ser Val Asn Ser Ser Ala Tyr Thr Ile Tyr Met Gly
5 10 15 20

aaa gat aaa tat gaa aat gaa gat ctg atc aag cat ggc tgg cct gaa 270
Lys Asp Lys Tyr Glu Asn Glu Asp Leu Ile Lys His Gly Trp Pro Glu
21 26 31 36

gat atc tgg ttt cat gtg gac aaa ctc tct tcg gct cat gta tac ctt 318
Asp Ile Trp Phe His Val Asp Lys Leu Ser Ser Ala His Val Tyr Leu
37 42 47 52

cga tta cat aag gga gag aat ata gaa gac atc cca aag gaa gtg ctg 366
Arg Leu His Lys Gly Glu Asn Ile Glu Asp Ile Pro Lys Glu Val Leu
53 58 63 68

atg gac tgt gcc cac ctt gtg aag gcc aat agc att caa gga gct att 414
Met Asp Cys Ala His Leu Val Lys Ala Asn Ser Ile Gln Gly Ala Ile
69 74 79 84

cat cac taa tgaaagt tgaaaatatg tcttcaaatc aggatggcca tgattcatat 470
His His *
85

gaattcatgt aaaaggagaa gaggagaaaa ggacctttga 510

<210> 376
<211> 2430
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (959)..(1345)

<400> 376

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ctcacactag tacgtggccc ctcggtgggt tgtcctcgag gtcgaaggtc cagatgtcca 180
ggggctgccc tggactccag agtgggtgcgg ctgagcaggc tgtggtcttg ggtgcttggg 240
cacctcccggt ctctccctgc tcagagttct tctctcctgg gcagccagaa aggatcagaa 300
ccggtcacat gcagagcggc ctcccgatc ccacagcagc tccgttctct aatctgggtc 360
ttcagatgcg gctgtgtctc ccggcacctt gctggaatgt ggtgcatccc tcggagtcca 420

gcagccctta ggcagagctg ggtgccgagc ttgagtccag gagggcctca gacacctgcg 480

atcttgacgc ctgttgccct ggacagtggg tgtgctgtgg gtggaggatg gcgccctgcc 540

tccacggaag catccccagc ttgccctca gtcacacgaa gcgtctgtcc ccagcctggg 600

gcatttctga gtggcctcca cttggcctct tcctttttct ggagcaagta tttgaactcc 660

tgcaggcgcc agagatctcc ttacctgttt cccgctaccc ttctccagcc aggtttctgc 720

cctcagccag attgtcctgc agtgacttgc ttttggccat ggagtagtgg ctgctcagtg 780

cctgagattg ttttagcagc agaagggacc gggccccct gctgctggca acacagacgc 840

ttgcttacag ttctctggtc ctggacacct gaggtctcgg cctccccagg acggcccttc 900

cagattctca ggaccacctt gccctccctg ccctgtctcc taggtgaccc tggcaaag 958

atg aga gtg cac att tgc tcc tgc ctg aag gtc cag gag cag atg gcc 1006

Met Arg Val His Ile Ser Ser Cys Leu Lys Val Gln Glu Gln Met Ala

1 5 10 15

aac tgc ccc aag ttc gtc ccc gtg gtg ccc aca tca cag cct atc ccc 1054

Asn Cys Pro Lys Phe Val Pro Val Val Pro Thr Ser Gln Pro Ile Pro

17 22 27 32

agc aac atc ccc aac agg tcc acc ttc gcc tgc ccg tac tgt ggt gcc 1102

Ser Asn Ile Pro Asn Arg Ser Thr Phe Ala Cys Pro Tyr Cys Gly Ala

33 38 43 48

cgc aac ctg gac cag cag gag ctg gtg aag cac tgt gtg gaa agc cac 1150

Arg Asn Leu Asp Gln Gln Glu Leu Val Lys His Cys Val Glu Ser His

49 54 59 64

cgc agc gac ccc aac cgc gtg gtg tgc ccc atc tgc tgc gca atg ccc 1198

Arg Ser Asp Pro Asn Arg Val Val Cys Pro Ile Cys Ser Ala Met Pro

65 70 75 80

tgg ggg gac ccc agc tac aag agc gcc aac ttc ctg cag cac ctg ctt 1246

Trp Gly Asp Pro Ser Tyr Lys Ser Ala Asn Phe Leu Gln His Leu Leu

81 86 91 96

cac cga cac aag ttc tcc tac gac acc ttt gtg gac tac agt att gac 1294

His Arg His Lys Phe Ser Tyr Asp Thr Phe Val Asp Tyr Ser Ile Asp

97 102 107 112

gag gag gcc gcc ttc cag gct gct ctg gcc ctg tct ctc tct gag aac 1342

Glu Glu Ala Ala Phe Gln Ala Ala Leu Ala Leu Ser Leu Ser Glu Asn

113 118 123 128

tga aggg aagcgcagcc acccgctgc gtctggggtc agggatgtcc ccgctcctgt 1399

*

129

gtcgcacctg gcacctgtc gggagcgac ctcaccggac tgagctcaca ggaggagcct 1459

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Arg Tyr Thr Arg Lys Ala Val Pro Gln Ser Leu Glu Leu Lys Gly Ile
4 9 14 19
aca aaa cat gct ctt aac cat cat ccc cct cca gag aag ctg gag gaa 212

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Ile	Ser	Pro	Thr	Ser	Asp	Ser	His	Glu	Lys	Asp	Thr	Ser	Ser	Gln	Ser		
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Lys	Ser	Asp	Ile	Thr	Arg	Glu	Ser	Ser	Phe	Thr	Ser	Ala	Asp	Thr	Gly		
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Asn	Ser	Leu	Ser	Ala	Phe	Pro	Ser	Tyr	Thr	Gly	Ala	Gly	Ile	Ser	Thr		
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Glu	Gly	Ser	Ser	Asp	Phe	Ser	Trp	Gly	Tyr	Gly	Glu	Leu	Asp	Gln	Asn		
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Gln	Gln	Trp	Thr	Ala	Ser	Phe	Pro	His	Leu	Arg	Ile	Leu	Gly	Arg	Gln		
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Ile	Ile	Thr	Pro	Ser	Glu	Gly	Tyr	Arg	Leu	Tyr	Pro	Arg	Ser	Pro	Ser		
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Ala	His	Lys	Ala	Ser	Ser	Ile	Ala	Lys	Ser	Ser	Ser	Phe	Cys	Ser	Met		
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Ile Ala Pro Phe Tyr Cys Met Lys Glu Asp Val Leu Ala Tyr Val Phe				
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Asp Ser Val Trp Cys Lys Val Val Ser Cys Met Glu Gln Leu Thr Arg				
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Ser His Trp Glu Gly Phe Ala Ser Asp Asp Glu Ser Asn Val Ala Val				
292	297	302	307	
acc aga ccc gat tca gaa agt tcc tgt gtg ctg agt gaa cta cat cct				1076
Thr Arg Pro Asp Ser Glu Ser Ser Cys Val Leu Ser Glu Leu His Pro				
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Leu Val Leu Pro Arg Val Pro Gln Ser Lys Val Leu Tyr Ile Thr Ser				
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Asn Pro Met Ser Leu Cys Gln Ala Ser Arg His Gln Pro Asn Val Asn				
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Asp Leu Leu Val His Gly Met Pro Leu Gln Pro Arg Asn Leu Ser Leu				
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atg gac aag ctc cta gat ctt gat gac aag cta ctt atg agg cct ggg				1268
Met Asp Lys Leu Leu Asp Leu Asp Asp Lys Leu Leu Met Arg Pro Gly				
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Ser Ser Thr Ile Leu Ser Thr Arg Asn Trp Pro Asn Arg Ala Val Glu				
388	393	398	403	
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Phe Ser Thr Ser Ser Leu Ser Tyr Thr Val Gln Ser Thr Arg Arg Arg				
404	409	414	419	
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Asn Pro Pro Pro Arg Thr Leu His Pro Ile Ser Thr Ser His Ser Cys				
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Ala Glu Thr Pro Arg Ser Val Glu Glu Ile Leu Arg Gly Ala Arg Val				
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Pro Val Ala Pro Asp Ser Leu Ser Ser Pro Ser Pro Thr Pro Leu Ser				
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Arg Asn Asn Leu Leu Pro Pro Ile Gly Thr Ala Glu Val Glu His Val				
468	473	478	483	

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gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt gag ggc cgg	153
Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys Glu Gly Pro	
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agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg ctt gta cag	201

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gac	ctg	gga	ggg	ggc	ttg	ggg	tgg	ccc	ctg	gcc	ctg	cct	ctt	ggc	ctc	297
Asp	Leu	Gly	Gly	Gly	Leu	Gly	Trp	Pro	Leu	Ala	Leu	Pro	Leu	Gly	Leu	
67					72					77					82	
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Tyr	Ala	Val	Gln	Leu	Thr	Ile	Ser	Trp	Thr	Val	Leu	Val	Leu	Phe	Phe	
83					88					93					98	
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Thr	Val	His	Asn	Pro	Gly	Leu	Ala	Leu	Leu	His	Leu	Leu	Leu	Leu	Tyr	
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Gly	Leu	Val	Val	Ser	Thr	Ala	Leu	Ile	Trp	His	Pro	Ile	Asn	Lys	Leu	
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Ala	Leu	Thr	Tyr	His	Leu	Trp	Arg	Asp	Ser	Leu	Cys	Pro	Val	His	Gln	
147					152					157					162	
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Pro	Gln	Pro	Thr	Glu	Lys	Ser	Asp	*								
163					168											
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 Val Gln Asn Phe Arg Phe Phe Ala Ser Ser Ser Leu His His Thr Ser
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 Glu Cys Thr Gln Met Asp His Leu Gly Cys Met His Tyr Thr Val Arg
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 gcc ccg ggg gga gtc gct ggt ctg atc agc ccc tgg aat ttg cca ctc 438
 Ala Pro Gly Gly Val Ala Gly Leu Ile Ser Pro Trp Asn Leu Pro Leu
 39 44 49 54
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 Tyr Leu Leu Thr Trp Lys Ile Ala Pro Ala Met Ala Ala Gly Asn Thr
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 Val Ile Ala Lys Pro Ser Glu Leu Thr Ser Val Thr Ala Trp Met Leu
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 Cys Lys Leu Leu Asp Lys Ala Gly Val Pro Pro Gly Val Val Asn Ile
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 Val Phe Gly Thr Gly Pro Arg Val Gly Glu Ala Leu Val Ser His Pro
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 119 124 129 134
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 Ile Thr Gln Leu Ser Ala Pro His Cys Lys Lys Leu Ser Leu Glu Leu
 135 140 145 150
 ggg ggc aag aat cct gcc atc atc ttt gag gac gcc aac ctg gat gag 774
 Gly Gly Lys Asn Pro Ala Ile Ile Phe Glu Asp Ala Asn Leu Asp Glu
 151 156 161 166
 tgc att ccg gca acc gtc agg tcc agc ttt gcc aac cag ggt gaa atc 822
 Cys Ile Pro Ala Thr Val Arg Ser Ser Phe Ala Asn Gln Gly Glu Ile
 167 172 177 182
 tgt ctc tgt acc agc agg atc ttt gtc cag aag agc atc tat agt gaa 870
 Cys Leu Cys Thr Ser Arg Ile Phe Val Gln Lys Ser Ile Tyr Ser Glu

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Phe Leu Lys Arg Phe Val Glu Ala Thr Arg Lys Trp Lys Val Gly Ile				
199	204	209	214	
ccc tct gat cca ctg gtg agc ata ggt gct ctg ata agt aaa gca cat				966
Pro Ser Asp Pro Leu Val Ser Ile Gly Ala Leu Ile Ser Lys Ala His				
215	220	225	230	
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Leu Glu Lys Val Arg Ser Tyr Val Lys Arg Ala Leu Ala Glu Gly Ala				
231	236	241	246	
caa att tgg tgc ggt gag gga gtg gat aag ttg agc ctc cct gcc agg				1062
Gln Ile Trp Cys Gly Glu Gly Val Asp Lys Leu Ser Leu Pro Ala Arg				
247	252	257	262	
aac cag gca ggc tac ttt atg ctt ccc acg gtg ata aca gac att aag				1110
Asn Gln Ala Gly Tyr Phe Met Leu Pro Thr Val Ile Thr Asp Ile Lys				
263	268	273	278	
gat gaa tcc tgc tgc atg acg gaa gag ata ttt ggt cca gtg acg tgt				1158
Asp Glu Ser Cys Cys Met Thr Glu Glu Ile Phe Gly Pro Val Thr Cys				
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gtc gtc ccc ttt gat agt gaa gag gag gtg att gaa aga gcc aac aac				1206
Val Val Pro Phe Asp Ser Glu Glu Glu Val Ile Glu Arg Ala Asn Asn				
295	300	305	310	
gtt aag tat ggg ctg gcg gct acc gtg tgg tcc agc aat gtg ggg cgc				1254
Val Lys Tyr Gly Leu Ala Ala Thr Val Trp Ser Ser Asn Val Gly Arg				
311	316	321	326	
gtc cac cgg gtg gct aag aag ctg cag tct ggc ttg gtc tgg acc aac				1302
Val His Arg Val Ala Lys Lys Leu Gln Ser Gly Leu Val Trp Thr Asn				
327	332	337	342	
tgc tgg ctc atc agg gag ctg aac ctt cct ttc ggg ggg atg aag agt				1350
Cys Trp Leu Ile Arg Glu Leu Asn Leu Pro Phe Gly Gly Met Lys Ser				
343	348	353	358	
tct gga ata ggt aga gag gga gcc aag gac tct tac gac ttc ttc act				1398
Ser Gly Ile Gly Arg Glu Gly Ala Lys Asp Ser Tyr Asp Phe Phe Thr				
359	364	369	374	
gag atc aaa acc atc acc gtt aaa cac tga t ctttgctaatt ggtggagcca				1449
Glu Ile Lys Thr Ile Thr Val Lys His *				
375	380			
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gcc tca tct aca cca aag gat cac agc gcc tcg cca gca acg gaa caa	96
Ala Ser Ser Thr Pro Lys Asp His Ser Ala Ser Pro Ala Thr Glu Gln	
17 22 27 32	
agc tgg atg ggg aat gac ttt gat gag ttg aca gaa tta ggc ttc aga	144
Ser Trp Met Gly Asn Asp Phe Asp Glu Leu Thr Glu Leu Gly Phe Arg	
33 38 43 48	
aaa tcg gta atg aca aac ttc tcc cag cta aag gag gat gtt cga acc	192
Lys Ser Val Met Thr Asn Phe Ser Gln Leu Lys Glu Asp Val Arg Thr	
49 54 59 64	
cat cac aaa gaa gct aaa aac cta gaa aaa aga tta gac aaa tgg cta	240
His His Lys Glu Ala Lys Asn Leu Glu Lys Arg Leu Asp Lys Trp Leu	
65 70 75 80	
act aga ata aac agc ata gag gag acc tta aat gac ctg atg gag ctg	288
Thr Arg Ile Asn Ser Ile Glu Glu Thr Leu Asn Asp Leu Met Glu Leu	
81 86 91 96	
aaa acc atg gca cga gaa cta cgt gac aca tgc aca agc ttc agt agc	336
Lys Thr Met Ala Arg Glu Leu Arg Asp Thr Cys Thr Ser Phe Ser Ser	
97 102 107 112	
cga ttc gat caa gtg gaa gaa ggg gaa ata caa act acc atc aga gaa	384
Arg Phe Asp Gln Val Glu Glu Gly Glu Ile Gln Thr Thr Ile Arg Glu	
113 118 123 128	
tat tat gaa cac ctc tac gca aat aaa cta gaa aat cta gaa gaa atg	432
Tyr Tyr Glu His Leu Tyr Ala Asn Lys Leu Glu Asn Leu Glu Glu Met	
129 134 139 144	
gat aaa ttc ctg gac aca tac act ctc cca aga cta aac cag gaa gaa	480
Asp Lys Phe Leu Asp Thr Tyr Thr Leu Pro Arg Leu Asn Gln Glu Glu	
145 150 155 160	
gtt gaa tcc ctg aat aga cca ata aca ggt tct gaa att gag gca ata	528
Val Glu Ser Leu Asn Arg Pro Ile Thr Gly Ser Glu Ile Glu Ala Ile	
161 166 171 176	
att aat agc cta cca acc aaa aaa att cca ggg cca gac aga ttc aca	576

Ile	Asn	Ser	Leu	Pro	Thr	Lys	Lys	Ile	Pro	Gly	Pro	Asp	Arg	Phe	Thr	
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gcc	aaa	ttc	tac	cag	agg	tac	aaa	gag	gag	ctg	agt	aac	ctg	atc	cac	624
Ala	Lys	Phe	Tyr	Gln	Arg	Tyr	Lys	Glu	Glu	Leu	Ser	Asn	Leu	Ile	His	
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tac	ctg	gga	ctg	agc	cat	cac	ctg	ctg	gca	ctg	aat	ttt	atc	att	gtt	672
Tyr	Leu	Gly	Leu	Ser	His	His	Leu	Leu	Ala	Leu	Asn	Phe	Ile	Ile	Val	
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tct	ttt	ggc	aaa	aaa	agc	gcg	tgg	tct	tct	gcc	caa	gtg	aag	gtg	acc	720
Ser	Phe	Gly	Lys	Lys	Ser	Ala	Trp	Ser	Ser	Ala	Gln	Val	Lys	Val	Thr	
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gac	aca	gac	ttt	gat	ggc	gtg	gaa	gtc	aga	gtg	ttt	gaa	ggc	cct	ccg	768
Asp	Thr	Asp	Phe	Asp	Gly	Val	Glu	Val	Arg	Val	Phe	Glu	Gly	Pro	Pro	
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aag	ccc	gaa	gag	cca	ctg	aaa	cgc	agc	gtc	gtt	tat	atc	cac	gga	gga	816
Lys	Pro	Glu	Glu	Pro	Leu	Lys	Arg	Ser	Val	Val	Tyr	Ile	His	Gly	Gly	
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ggc	tgg	gcc	ttg	gca	agt	gca	aaa	atc	agg	tat	tat	gat	gag	ctg	tgt	864
Gly	Trp	Ala	Leu	Ala	Ser	Ala	Lys	Ile	Arg	Tyr	Tyr	Asp	Glu	Leu	Cys	
273					278					283					288	
aca	gca	atg	gct	gag	gaa	ttg	aat	gct	gtc	att	gtt	tcc	att	gaa	tac	912
Thr	Ala	Met	Ala	Glu	Glu	Leu	Asn	Ala	Val	Ile	Val	Ser	Ile	Glu	Tyr	
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agg	cta	gtt	cca	aag	gtt	tat	ttt	cct	gag	caa	att	cat	gat	gtt	gta	960
Arg	Leu	Val	Pro	Lys	Val	Tyr	Phe	Pro	Glu	Gln	Ile	His	Asp	Val	Val	
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cgg	gcc	aca	aag	tat	ttc	ctg	aag	cca	gaa	gtc	tta	cag	aag	tat	atg	1008
Arg	Ala	Thr	Lys	Tyr	Phe	Leu	Lys	Pro	Glu	Val	Leu	Gln	Lys	Tyr	Met	
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gtt	gat	cca	ggc	aga	att	tgc	att	tct	ggc	gac	agt	gct	ggc	gga	aat	1056
Val	Asp	Pro	Gly	Arg	Ile	Cys	Ile	Ser	Gly	Asp	Ser	Ala	Gly	Gly	Asn	
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ctg	gct	gct	gcc	ctt	gga	caa	cag	ttt	act	caa	gat	gcc	agc	cta	aaa	1104
Leu	Ala	Ala	Ala	Leu	Gly	Gln	Gln	Phe	Thr	Gln	Asp	Ala	Ser	Leu	Lys	
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aat	aag	ctc	aaa	cta	caa	gct	tta	att	tat	cca	gtt	ctt	caa	gct	tta	1152
Asn	Lys	Leu	Lys	Leu	Gln	Ala	Leu	Ile	Tyr	Pro	Val	Leu	Gln	Ala	Leu	
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gat	ttt	aac	aca	cca	tct	tat	cag	caa	aat	gtg	aac	acc	cca	atc	ctg	1200
Asp	Phe	Asn	Thr	Pro	Ser	Tyr	Gln	Gln	Asn	Val	Asn	Thr	Pro	Ile	Leu	
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Pro	Arg	Tyr	Val	Met	Val	Lys	Tyr	Trp	Val	Asp	Tyr	Phe	Lys	Gly	Asn	

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tat gac ttt gtg cag gca atg atc gtt aac aat cac act tca ctt gat				1296
Tyr Asp Phe Val Gln Ala Met Ile Val Asn Asn His Thr Ser Leu Asp				
417	422	427	432	
gtg gaa gag gct gct gct gtc agg gcc cgt cta aac tgg aca tcc ctc				1344
Val Glu Glu Ala Ala Val Arg Ala Arg Leu Asn Trp Thr Ser Leu				
433	438	443	448	
ttg cct gca tcc ttc aca aag aac tac aag cct gtt gta cag acc aca				1392
Leu Pro Ala Ser Phe Thr Lys Asn Tyr Lys Pro Val Val Gln Thr Thr				
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ggc aat gcc agg att gtc cag gag ctt cct cag ttg ctg gat gcc cgc				1440
Gly Asn Ala Arg Ile Val Gln Glu Leu Pro Gln Leu Leu Asp Ala Arg				
465	470	475	480	
tcc gcc cca ctc att gca gac cag gca gtg ctg cag ctc ctc cca aag				1488
Ser Ala Pro Leu Ile Ala Asp Gln Ala Val Leu Gln Leu Leu Pro Lys				
481	486	491	496	
acc tac att ctg acg tgt gag cat gat gtc ctc aga gac gat ggc atc				1536
Thr Tyr Ile Leu Thr Cys Glu His Asp Val Leu Arg Asp Asp Gly Ile				
497	502	507	512	
atg tat gcc aag cgt ttg gag agt gcc ggt gtg gag gtg acc ctg gat				1584
Met Tyr Ala Lys Arg Leu Glu Ser Ala Gly Val Glu Val Thr Leu Asp				
513	518	523	528	
cac ttt gag gat ggc ttt cac gga tgt atg att ttc act agc tgg ccc				1632
His Phe Glu Asp Gly Phe His Gly Cys Met Ile Phe Thr Ser Trp Pro				
529	534	539	544	
acc aac ttc tca gtg gga atc cgg act agg aat agt tac atc aag tgg				1680
Thr Asn Phe Ser Val Gly Ile Arg Thr Arg Asn Ser Tyr Ile Lys Trp				
545	550	555	560	
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Leu Asp Gln Asn Leu *				
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2232

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Met
1

agg ctc ctc cgc aga cgc cac atg ccc ctg cgc ctg gcc atg gtg ggc 405
Arg Leu Leu Arg Arg Arg His Met Pro Leu Arg Leu Ala Met Val Gly
2 7 12 17

tgc gcc ttt gtg ctc ttc ctc ttc ctc ctg cat agg gat gtg agc agc 453
Cys Ala Phe Val Leu Phe Leu Phe Leu Leu His Arg Asp Val Ser Ser
18 23 28 33

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Arg Glu Glu Ala Thr Glu Lys Pro Trp Leu Lys Ser Leu Val Ser Arg
34 39 44 49

aag gat cac gtc ctg gac ctc atg ctg gag gcc atg aac aac ctt aga 549
Lys Asp His Val Leu Asp Leu Met Leu Glu Ala Met Asn Asn Leu Arg
50 55 60 65

gat tca atg ccc aag ctc caa atc agg gct cca gaa gcc cag cag act 597
Asp Ser Met Pro Lys Leu Gln Ile Arg Ala Pro Glu Ala Gln Gln Thr
66 71 76 81

ctg ttc tcc ata aat cag tcc tgc ctc cct ggg ttc tat acc cca gct 645
Leu Phe Ser Ile Asn Gln Ser Cys Leu Pro Gly Phe Tyr Thr Pro Ala
82 87 92 97

gaa ctg aag ccc ttc tgg gaa cgg cca cca cag gac ccc aat gcc cct 693
Glu Leu Lys Pro Phe Trp Glu Arg Pro Pro Gln Asp Pro Asn Ala Pro
98 103 108 113

ggg gca gat gga aaa gca ttt cag aag agc aag tgg acc ccc ctg gag	741
Gly Ala Asp Gly Lys Ala Phe Gln Lys Ser Lys Trp Thr Pro Leu Glu	
114 119 124 129	
acc cag gaa aag gaa gaa ggc tat aag aag cac tgt ttc aat gcc ttt	789
Thr Gln Glu Lys Glu Glu Gly Tyr Lys Lys His Cys Phe Asn Ala Phe	
130 135 140 145	
gcc agc gac cgg atc tcc ctg cag agg tcc ctg ggg cca gac acc cga	837
Ala Ser Asp Arg Ile Ser Leu Gln Arg Ser Leu Gly Pro Asp Thr Arg	
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Pro Pro Glu Cys Val Asp Gln Lys Phe Arg Arg Cys Pro Pro Leu Ala	
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Thr Thr Ser Val Ile Ile Val Phe His Asn Glu Ala Trp Ser Thr Leu	
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Leu Arg Thr Val Tyr Ser Val Leu His Thr Thr Pro Ala Ile Leu Leu	
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Lys Glu Ile Ile Leu Val Asp Asp Ala Ser Thr Glu Glu His Leu Lys	
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Ser Val Ala Gln Ala Glu Val Leu Thr Phe Leu Asp Ala His Cys Glu	
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Cys Phe His Gly Trp Leu Glu Pro Leu Leu Ala Arg Ile Ala Glu Asp	
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Phe Glu Phe Ala Lys Pro Val Gln Arg Gly Arg Val His Ser Arg Gly	
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Asn Phe Asp Trp Ser Leu Thr Phe Gly Trp Glu Thr Leu Pro Pro His	
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Gly Thr Tyr Asp Asn Gln Met Glu Ile Trp Gly Gly Glu Asn Val Glu	
370 375 380 385	
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Cys Ser Val Val Gly His Val Phe Arg Thr Lys Ser Pro His Thr Phe	
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Pro Lys Gly Thr Ser Val Ile Ala Arg Asn Gln Val Arg Leu Ala Glu	
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Val Trp Met Asp Ser Tyr Lys Lys Ile Phe Tyr Arg Arg Asn Leu Gln	
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Ala Ala Lys Met Ala Gln Glu Lys Ser Phe Gly Asp Ile Ser Glu Arg	
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466 471 476 481	
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His Asn Val Tyr Pro Glu Met Phe Val Pro Asp Leu Thr Pro Thr Phe	
482 487 492 497	
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Tyr Gly Ala Ile Lys Asn Leu Gly Thr Asn Gln Cys Leu Asp Val Gly	
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Leu Gly Gly Asn Gln Tyr Phe Glu Tyr Thr Thr Gln Arg Asp Leu Arg	
530 535 540 545	
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His Asn Ile Ala Lys Gln Leu Cys Leu His Val Ser Lys Gly Ala Leu	
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Gln Gln Ala Gln Glu Glu Leu Ala Glu Met Lys Arg Tyr Ser Glu Ser	
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Ser Ser Lys Leu Glu Glu Asp Lys Asp Lys Lys Ile Asn Glu Met Ser	
237 242 247 252	
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Lys Glu Val Thr Lys Leu Lys Glu Ala Leu Asn Ser Leu Ser Gln Leu	
253 258 263 268	
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269 274 279 284	
ctg cag cag caa gtc aaa cag ctc cag aac cag ctg gcg gaa tgc aag	1392
Leu Gln Gln Gln Val Lys Gln Leu Gln Asn Gln Leu Ala Glu Cys Lys	
285 290 295 300	
aaa caa cac cag gag gtc ata tca gtt tac aga atg cat ctt ctg tat	1440
Lys Gln His Gln Glu Val Ile Ser Val Tyr Arg Met His Leu Leu Tyr	
301 306 311 316	
gct gtg cag ggc cag atg gat gaa gat gtc cag aaa gta ctg aag caa	1488
Ala Val Gln Gly Gln Met Asp Glu Asp Val Gln Lys Val Leu Lys Gln	
317 322 327 332	
atc ctt acc atg tgt aaa aac cag tct caa aag aag taa agtggattcc	1537
Ile Leu Thr Met Cys Lys Asn Gln Ser Gln Lys Lys *	
333 338 343	
ttggcaggac actgcccctt gtcattctgtc tttgtgttag atccagagtt gtcggcagcc	1597
gctgccattg ttctcattcg tggatatgcac tgtggcctag cgtagcttct tccctttcca	1657
aaggtttctg aggacttctc ccaggagaag actgcccgcc tcagaactgc ttagagactt	1717
caaaccagca gaggtgaaag tccctgtcat ccccttcagat tccagagctg ggatcagcca	1777
tgcccagagg tctggtcctg atgctggcag gggggccccc tccctccatcc ctgactggct	1837
gagtggcttt atcaccaccg agtgatgtgc tgaggcctcc tgcagtgaat gctccttcca	1897
ttcctgtact cgggcagtgc cattcagcac aggagagctc tttttgcctt tggctttcaa	1957
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ttaaaaccct tcatcatgat atcctgtgga tttaaaaact ctaattccat gttttcttcc	2077

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aattgttgac atactgcaaa ttttctatgc aaacttgccct cctgctgtta tctgtgaagc	2257
tcaggaaatc caaacatttg tgtttcaaca agggacagta aactgtgtgt ttacagccaa	2317
aagaaatgcc tcatagttct taacctcaac tttttagtaa gtattttttt ctctgtaata	2377
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gctgccacca acacccttag aactttcagc catgggtgtct tcagaattgt agcgcatttc	2617
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gcccataaat gatctctaga aggactgtta gtaccaatct gtttttcaac tttgaagcta	2737
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gctttaaaagc ttggtgttac ttttcttaag ttgtttaatt atagttaagc aatttcaaaa	3097
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atgcctgacg aggtgtagcc ttttatcttg tttccggatg catatttatt acgagtactc	3277
tggttaaata ttgaaaagtt atatgctgta gtttttagta ttttgtcttt gtaatttaca	3337
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166 171 176 181	
tggt gag agc ctg cac aat gtg gat gga gac agc tgc ttt tgt gac tct	989
Trp Glu Ser Leu His Asn Val Asp Gly Asp Ser Cys Phe Cys Asp Ser	
182 187 192 197	
gac ttt cac ctg agt cat tcc ctg ggc aag ggg cct gga gca gaa ggt	1037
Asp Phe His Leu Ser His Ser Leu Gly Lys Gly Pro Gly Ala Glu Gly	
198 203 208 213	
ggg agt ggc tcc cca gaa aag cag ctg cag gta gac cag gac tac ctg	1085
Gly Ser Gly Ser Pro Glu Lys Gln Leu Gln Val Asp Gln Asp Tyr Leu	
214 219 224 229	
att gct ctg tcc ctg cag cag caa cag cca cga ggc ccg ctg ggg ctt	1133
Ile Ala Leu Ser Leu Gln Gln Gln Gln Pro Arg Gly Pro Leu Gly Leu	
230 235 240 245	
acc gac ttg gag ctg gcc cag cag ctt cag caa gag gag tat caa cag	1181
Thr Asp Leu Glu Leu Ala Gln Gln Leu Gln Gln Glu Glu Tyr Gln Gln	
246 251 256 261	
cag cag gca gcg cag cca gtg cgg atg cgg acg cgg gtc ctg tca ctg	1229
Gln Gln Ala Ala Gln Pro Val Arg Met Arg Thr Arg Val Leu Ser Leu	
262 267 272 277	
cag ggg aga gga gcc aca tct gga cgc cca gcc ggg gag cgt cgg cag	1277
Gln Gly Arg Gly Ala Thr Ser Gly Arg Pro Ala Gly Glu Arg Arg Gln	
278 283 288 293	
agg ccg aag cac gag tca gac tgc att ctg ctg tag ctct gccccagtgc	1327
Arg Pro Lys His Glu Ser Asp Cys Ile Leu Leu *	
294 299 304	
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cacacgtatg tacagactga ggctctgggg tgaggtccct atccagaatg catctcttct	1627
gcttcccatc cctgctgcct ggatgctcct gatcacctag gcaggcctgt ctccagtgtg	1687
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aaaacttctg gccgggcaaa aaaaaaa	1774

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agc gta gct gag ggg gtg cgg cta agt cca gag cct ggc agg gag gga	96
Ser Val Ala Glu Gly Val Arg Leu Ser Pro Glu Pro Gly Arg Glu Gly	
17 22 27 32	
gta agg gac tta gca ggg gcg gag gag ttc ggc ggc gga gag gag ggg	144
Val Arg Asp Leu Ala Gly Ala Glu Glu Phe Gly Gly Gly Glu Glu Gly	
33 38 43 48	
aca ggg ctg aca ggg ata aag gag ata ggg gat gga gag gaa gga agt	192
Thr Gly Leu Thr Gly Ile Lys Glu Ile Gly Asp Gly Glu Glu Gly Ser	
49 54 59 64	
gga caa agg cca gag gaa ata ccg atg gac cta acg gta gtg aag cag	240
Gly Gln Arg Pro Glu Glu Ile Pro Met Asp Leu Thr Val Val Lys Gln	
65 70 75 80	
gaa att ata gac tgg cca ggt aca gaa ggc agg ttg gct ggc cag tgg	288
Glu Ile Ile Asp Trp Pro Gly Thr Glu Gly Arg Leu Ala Gly Gln Trp	
81 86 91 96	
gta gaa cag gag gtg gag gat agg cct gag gtg aag gat gag aac gca	336
Val Glu Gln Glu Val Glu Asp Arg Pro Glu Val Lys Asp Glu Asn Ala	
97 102 107 112	
ggc gta ttg gag gtg aag cag gag acg gat agt agt tta gtg gta aaa	384
Gly Val Leu Glu Val Lys Gln Glu Thr Asp Ser Ser Leu Val Val Lys	
113 118 123 128	
gaa gcg aag gtg ggt gaa cca gag gta aag gaa gag aag gta aag gaa	432
Glu Ala Lys Val Gly Glu Pro Glu Val Lys Glu Glu Lys Val Lys Glu	
129 134 139 144	
gag gta atg gac tgg tca gaa gtg aag gaa gag aag gat aac ttg gag	480
Glu Val Met Asp Trp Ser Glu Val Lys Glu Glu Lys Asp Asn Leu Glu	
145 150 155 160	
ata aaa cag gag gag aag ttt gtt ggt caa tgc ata aaa gag gaa ttg	528
Ile Lys Gln Glu Glu Lys Phe Val Gly Gln Cys Ile Lys Glu Glu Leu	
161 166 171 176	
atg cat gga gag tgt gta aaa gaa gag aag gat ttc ctg aag aaa gaa	576
Met His Gly Glu Cys Val Lys Glu Glu Lys Asp Phe Leu Lys Lys Glu	
177 182 187 192	
atc gtg gat gat aca aag gtg aaa gaa gag cct ccg ata aat cac ccg	624

Ile Val Asp Asp Thr Lys Val Lys Glu Glu Pro Pro Ile Asn His Pro	
193 198 203 208	
gtg ggc tgc aag cgg aaa ctg gcc atg tca agg tgt gag act tgt ggt	672
Val Gly Cys Lys Arg Lys Leu Ala Met Ser Arg Cys Glu Thr Cys Gly	
209 214 219 224	
aca gaa gaa gca aag tac aga tgt cca cgt tgt atg cga tat tcc tgc	720
Thr Glu Glu Ala Lys Tyr Arg Cys Pro Arg Cys Met Arg Tyr Ser Cys	
225 230 235 240	
agt ttg ccc tgt gta aag aaa cac aaa gca gaa ctg aca tgt aat gga	768
Ser Leu Pro Cys Val Lys Lys His Lys Ala Glu Leu Thr Cys Asn Gly	
241 246 251 256	
gtt cga gat aaa act gca tac att tca ata caa cag ttt act gaa atg	816
Val Arg Asp Lys Thr Ala Tyr Ile Ser Ile Gln Gln Phe Thr Glu Met	
257 262 267 272	
aat ctc cta agt gat tat cga ttt ttg gaa gat gtg gca aga aca gcg	864
Asn Leu Leu Ser Asp Tyr Arg Phe Leu Glu Asp Val Ala Arg Thr Ala	
273 278 283 288	
gac cat att tct aga gat gct ttt ttg aag aga cca ata agc aat aaa	912
Asp His Ile Ser Arg Asp Ala Phe Leu Lys Arg Pro Ile Ser Asn Lys	
289 294 299 304	
tat atg tac ttt atg aaa aat cgt gcc cgg agg caa ggt att aac tta	960
Tyr Met Tyr Phe Met Lys Asn Arg Ala Arg Arg Gln Gly Ile Asn Leu	
305 310 315 320	
aaa ctt cta ccc aat gga ttc acc aag agg aag gag aat tca acc ttt	1008
Lys Leu Leu Pro Asn Gly Phe Thr Lys Arg Lys Glu Asn Ser Thr Phe	
321 326 331 336	
ttt gat aag aaa aaa caa cag ttt tgt tgg cat gtg aag ctc cag ttt	1056
Phe Asp Lys Lys Lys Gln Gln Phe Cys Trp His Val Lys Leu Gln Phe	
337 342 347 352	
cct caa agt caa gct gag tac ata gaa aaa aga gta cca gat gat aaa	1104
Pro Gln Ser Gln Ala Glu Tyr Ile Glu Lys Arg Val Pro Asp Asp Lys	
353 358 363 368	
act att aat gaa atc cta aaa cct tac att gat cct gaa aag tct gat	1152
Thr Ile Asn Glu Ile Leu Lys Pro Tyr Ile Asp Pro Glu Lys Ser Asp	
369 374 379 384	
cct gta att cgt caa agg ttg aaa gcc tac att cgc tct cag act ggg	1200
Pro Val Ile Arg Gln Arg Leu Lys Ala Tyr Ile Arg Ser Gln Thr Gly	
385 390 395 400	
gtt cag att tta atg aag att gaa tat atg cag caa aat tta gta aga	1248
Val Gln Ile Leu Met Lys Ile Glu Tyr Met Gln Gln Asn Leu Val Arg	
401 406 411 416	
tat tat gaa cta gat cct tat aaa agt ctc cta gac aat ttg agg aac	1296
Tyr Tyr Glu Leu Asp Pro Tyr Lys Ser Leu Leu Asp Asn Leu Arg Asn	

417	422	427	432	
aaa gtg atc att gag tat cca aca tta cat	gtg gta ttg aaa gga tcc	1344		
Lys Val Ile Ile Glu Tyr Pro Thr Leu His	Val Val Leu Lys Gly Ser			
433	438	443	448	
aat aat gac atg aaa gtt ctt cac caa gtg	aag agt gaa tct acc aag	1392		
Asn Asn Asp Met Lys Val Leu His Gln Val	Lys Ser Glu Ser Thr Lys			
449	454	459	464	
aac gtt ggc aat gaa aat tga gc attttttctg	gaagaagaaa gtgaaaactt	1445		
Asn Val Gly Asn Glu Asn *				
465	470			
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gaccttctctg gtgctagagc gaagcagcgc gcaactggtgg	ctggccgcgc gggcgcgcag 180
tggtgagacg ggctacgtgc cgccagccta cctgcgcgc	ctgcaggtct aactgctgtc 240
ccctgcccc ccgaaggcct ggagcaggat gtccctccagg	ccattgaccg ggccatcgag 300
gctgtacaca acacagcc atg cgg gat ggt ggc aag	tac agc ctg gaa cag 351
Met Arg Asp Gly Gly Lys Tyr Ser Leu Glu Gln	

cgt gga gtc ctc cag aag ctg atc cac cac cgg aaa gag acc ctg tca	399
Arg Gly Val Leu Gln Lys Leu Ile His His Arg Lys Glu Thr Leu Ser	
12 17 22 27	
cgc aga ggc cct tca gcc tcc agt gtt gca gtt atg acc tca tca acc	447
Arg Arg Gly Pro Ser Ala Ser Ser Val Ala Val Met Thr Ser Ser Thr	
28 33 38 43	
agt gac cac cac ttg gat gct gct gca gcc agg cag ccc aat ggg gtg	495
Ser Asp His His Leu Asp Ala Ala Ala Arg Gln Pro Asn Gly Val	
44 49 54 59	
tgt cga gct ggg ttc gag cgg cag cac agc cta ccc agt tct gag cat	543
Cys Arg Ala Gly Phe Glu Arg Gln His Ser Leu Pro Ser Ser Glu His	
60 65 70 75	
ctt ggg gca gat gga ggc ctc tac cag atc cca ctt cca tct tcc cag	591
Leu Gly Ala Asp Gly Gly Leu Tyr Gln Ile Pro Leu Pro Ser Ser Gln	
76 81 86 91	
atc cca cca cag cct cgc cga gca gca ccc acc aca ccg ccc cca cca	639
Ile Pro Pro Gln Pro Arg Arg Ala Ala Pro Thr Thr Pro Pro Pro	
92 97 102 107	
gtg aag cgc cga gac cgc gag gcc ctg atg gcc tct ggg agt ggt ggc	687
Val Lys Arg Arg Asp Arg Glu Ala Leu Met Ala Ser Gly Ser Gly Gly	
108 113 118 123	
cac aac acc atg ccc tcc ggg ggt aac tct gtg tcc agc ggc tcc tca	735
His Asn Thr Met Pro Ser Gly Gly Asn Ser Val Ser Ser Gly Ser Ser	
124 129 134 139	
gtc agc agc acc tcc ctg gac acg ctc tat acc agc tcc agc cca tct	783
Val Ser Ser Thr Ser Leu Asp Thr Leu Tyr Thr Ser Ser Ser Pro Ser	
140 145 150 155	
gaa cca ggc tcc agc tgc tca ccc aca ccc cca cct gtg ccc cgc cga	831
Glu Pro Gly Ser Ser Cys Ser Pro Thr Pro Pro Pro Val Pro Arg Arg	
156 161 166 171	
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Gly Thr His Thr Thr Val Ser Gln Val Gln Pro Pro Pro Ser Lys Ala	
172 177 182 187	
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Ser Ala Pro Glu Pro Pro Ala Glu Glu Glu Val Ala Thr Gly Thr Thr	
188 193 198 203	
tca gcc tct gat gac ctg gaa gcc ctg ggt aca ctg agc ctg ggg acc	975
Ser Ala Ser Asp Asp Leu Glu Ala Leu Gly Thr Leu Ser Leu Gly Thr	
204 209 214 219	
aca gag gag aag gca gca gct gag gcg gct gtg ccc agg acc att ggg	1023
Thr Glu Glu Lys Ala Ala Ala Glu Ala Ala Val Pro Arg Thr Ile Gly	
220 225 230 235	

gcc gag ctg atg gag ctg gtg cgg aga aac act ggc ctg agc cac gaa	1071
Ala Glu Leu Met Glu Leu Val Arg Arg Asn Thr Gly Leu Ser His Glu	
236 241 246 251	
tta tgc cgg gtg gcc atc ggc atc ata gtg ggt cac atc cag gcc tcg	1119
Leu Cys Arg Val Ala Ile Gly Ile Ile Val Gly His Ile Gln Ala Ser	
252 257 262 267	
gtg ccg gcc agc tca cca gtc atg gag cag gtc ctc ctc tca ctc gta	1167
Val Pro Ala Ser Ser Pro Val Met Glu Gln Val Leu Leu Ser Leu Val	
268 273 278 283	
gag ggc aag gac ctc agc atg gcc ctg ccc tca ggg cag gtc tgc cac	1215
Glu Gly Lys Asp Leu Ser Met Ala Leu Pro Ser Gly Gln Val Cys His	
284 289 294 299	
gac cag cag agg ctg gag gtg atc ttt gca gac ctg gct cgc cgg aag	1263
Asp Gln Gln Arg Leu Glu Val Ile Phe Ala Asp Leu Ala Arg Arg Lys	
300 305 310 315	
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Asp Asp Ala Gln Gln Arg Ser Trp Ala Leu Tyr Glu Asp Glu Gly Val	
316 321 326 331	
atc cgc tgc tac cta gag gag ctg ctg cat att ctg act gat gca gac	1359
Ile Arg Cys Tyr Leu Glu Glu Leu Leu His Ile Leu Thr Asp Ala Asp	
332 337 342 347	
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Pro Glu Val Cys Lys Lys Met Cys Lys Arg Asn Glu Phe Glu Ser Val	
348 353 358 363	
ctg gcc ttg gtg gcc tat tac caa atg gaa cac cga gca tca ctg cgg	1455
Leu Ala Leu Val Ala Tyr Tyr Gln Met Glu His Arg Ala Ser Leu Arg	
364 369 374 379	
ctg ctg ctc ctc aag tgc ttt ggc gcc atg tgc agc ctg gat gca gcc	1503
Leu Leu Leu Leu Lys Cys Phe Gly Ala Met Cys Ser Leu Asp Ala Ala	
380 385 390 395	
atc atc tcc acg ctt gtg tca tcc gtg ctg cct gta gag ctg gcg agg	1551
Ile Ile Ser Thr Leu Val Ser Ser Val Leu Pro Val Glu Leu Ala Arg	
396 401 406 411	
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Asp Met Gln Thr Asp Thr Gln Asp His Gln Lys Leu Cys Tyr Ser Ala	
412 417 422 427	
ctc atc ctg gcc atg gtc ttc tcc atg gga gag gca gtg ccc tat gca	1647
Leu Ile Leu Ala Met Val Phe Ser Met Gly Glu Ala Val Pro Tyr Ala	
428 433 438 443	
cac tat gag cac ctg ggc acg cct ttc gcc cag ttc cta ctg aac atc	1695
His Tyr Glu His Leu Gly Thr Pro Phe Ala Gln Phe Leu Leu Asn Ile	
444 449 454 459	

gtc gag gat ggg ctg ccc ttg gac acc aca gag cag ctg ccg gac ctc	1743
Val Glu Asp Gly Leu Pro Leu Asp Thr Thr Glu Gln Leu Pro Asp Leu	
460 465 470 475	
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Cys Val Asn Leu Leu Leu Ala Leu Asn Leu His Leu Pro Ala Ala Asp	
476 481 486 491	
cag aat gtc atc atg gct gcc ctg agc aaa cac gcc aat gtc aag atc	1839
Gln Asn Val Ile Met Ala Ala Leu Ser Lys His Ala Asn Val Lys Ile	
492 497 502 507	
ttc tcc gag aag ctg ttg ttg ctc ctg aac aga ggg gat gac cct gtg	1887
Phe Ser Glu Lys Leu Leu Leu Leu Leu Asn Arg Gly Asp Asp Pro Val	
508 513 518 523	
cgc atc ttc aaa cat gag cca cag cca cca cac tct gtc ctc aag ttc	1935
Arg Ile Phe Lys His Glu Pro Gln Pro Pro His Ser Val Leu Lys Phe	
524 529 534 539	
ctg cag gac gtg ttt ggc agc ccg gcc aca gct gcc atc ttc tac cac	1983
Leu Gln Asp Val Phe Gly Ser Pro Ala Thr Ala Ala Ile Phe Tyr His	
540 545 550 555	
aca gac atg atg gct ctc att gac atc act gtg cgg cac atc gca gac	2031
Thr Asp Met Met Ala Leu Ile Asp Ile Thr Val Arg His Ile Ala Asp	
556 561 566 571	
ctg tca cca gga gac aag ctg cgc atg gag tac ctc tcc ctg atg cat	2079
Leu Ser Pro Gly Asp Lys Leu Arg Met Glu Tyr Leu Ser Leu Met His	
572 577 582 587	
gct ata gtc cgc acc aca ccc tac ctg cag cac cgc cac cgg cta ccc	2127
Ala Ile Val Arg Thr Thr Pro Tyr Leu Gln His Arg His Arg Leu Pro	
588 593 598 603	
gac ctg cag gcc ata ctg cga cgc atc ctg aat gag gag gag acc tca	2175
Asp Leu Gln Ala Ile Leu Arg Arg Ile Leu Asn Glu Glu Glu Thr Ser	
604 609 614 619	
ccc cag tgc cag atg gac cgc atg att gtc cga gag atg tgc aag gaa	2223
Pro Gln Cys Gln Met Asp Arg Met Ile Val Arg Glu Met Cys Lys Glu	
620 625 630 635	
ttc ctg gtg ctg ggg gag gct ccc agc tag c accttgctgt cctcccttcc	2274
Phe Leu Val Leu Gly Glu Ala Pro Ser *	
636 641	
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 Met Leu Lys Ser Met
 1
 gtt ctg tgg tta gga gaa cag gta caa agc ttg cag ttg cag cag caa 163
 Val Leu Trp Leu Gly Glu Gln Val Gln Ser Leu Gln Leu Gln Gln
 6 11 16 21
 ttg cgt cat cat ttt aat cac att cat att tgc gta act aac tca gaa 211
 Leu Arg His His Phe Asn His Ile His Ile Cys Val Thr Asn Ser Glu
 22 27 32 37
 tat aac caa agt gag tat ccg tgg gac ctt gtg aaa gcc cat ttg caa 259
 Tyr Asn Gln Ser Glu Tyr Pro Trp Asp Leu Val Lys Ala His Leu Gln
 38 43 48 53
 gga gct ttc aca tcc aac atc acc ttt gat att agt gaa tta caa aac 307
 Gly Ala Phe Thr Ser Asn Ile Thr Phe Asp Ile Ser Glu Leu Gln Asn
 54 59 64 69
 aaa att ctt gat tta aat agg cac act caa gaa ttt cag cct tct tta 355
 Lys Ile Leu Asp Leu Asn Arg His Thr Gln Glu Phe Gln Pro Ser Leu
 70 75 80 85
 gaa gac tgg act gaa ttc cag gaa ggc ctg gag agc ctc aac cct tgg 403
 Glu Asp Trp Thr Glu Phe Gln Glu Gly Leu Glu Ser Leu Asn Pro Trp
 86 91 96 101

28	33	38	43	
gac atg ctg gtt cat gat ttt gat gat gaa cga aca tta gaa gag gaa				435
Asp Met Leu Val His Asp Phe Asp Asp Glu Arg Thr Leu Glu Glu				
44	49	54	59	
gaa atg atg gaa gga gaa aca aac ttc agc tct gaa ata gaa gat ctt				483
Glu Met Met Glu Gly Glu Thr Asn Phe Ser Ser Glu Ile Glu Asp Leu				
60	65	70	75	
gca agg gaa ggc gac atg cca att cat gaa ctt ctc agc ctt tat ggt				531
Ala Arg Glu Gly Asp Met Pro Ile His Glu Leu Leu Ser Leu Tyr Gly				
76	81	86	91	
tat ggt agt act gtt cga cta cct gaa gaa gat gag gaa gag gaa gaa				579
Tyr Gly Ser Thr Val Arg Leu Pro Glu Glu Asp Glu Glu Glu Glu				
92	97	102	107	
gag gaa gaa gaa ggt gaa gat gat gaa gat gct gat aat gat gac aac				627
Glu Glu Glu Glu Gly Glu Asp Asp Glu Asp Ala Asp Asn Asp Asp Asn				
108	113	118	123	
agt ggc tgt agt ggg gaa aat aaa gag gag aat ata aag gat tca tca				675
Ser Gly Cys Ser Gly Glu Asn Lys Glu Glu Asn Ile Lys Asp Ser Ser				
124	129	134	139	
ggg cag gag gat gaa act cag tct tcc aat gat gat cca tca caa tct				723
Gly Gln Glu Asp Glu Thr Gln Ser Ser Asn Asp Asp Pro Ser Gln Ser				
140	145	150	155	
gtt gct tct caa gat gcc cag gaa ata atc cgc cca cgt cga tgt aaa				771
Val Ala Ser Gln Asp Ala Gln Glu Ile Ile Arg Pro Arg Arg Cys Lys				
156	161	166	171	
tat ttt gat aca aat agt gaa gta gaa gaa gaa tct gaa gaa gat gaa				819
Tyr Phe Asp Thr Asn Ser Glu Val Glu Glu Glu Ser Glu Glu Asp Glu				
172	177	182	187	
gat tat att cca tca gaa gac tgg aaa aag gag att atg gtg ggc tcc				867
Asp Tyr Ile Pro Ser Glu Asp Trp Lys Lys Glu Ile Met Val Gly Ser				
188	193	198	203	
atg ttt caa gca gaa att cca gtt ggc att tgt aga tac aaa gaa aat				915
Met Phe Gln Ala Glu Ile Pro Val Gly Ile Cys Arg Tyr Lys Glu Asn				
204	209	214	219	
gaa aaa gta tat gaa aat gat gat cag ctc ctg tgg gac cct gag tac				963
Glu Lys Val Tyr Glu Asn Asp Asp Gln Leu Leu Trp Asp Pro Glu Tyr				
220	225	230	235	
tta cca gaa gat aaa gtg att ata ttt ctt aaa gat gca tct aga aga				1011
Leu Pro Glu Asp Lys Val Ile Ile Phe Leu Lys Asp Ala Ser Arg Arg				
236	241	246	251	
aca ggt gat gag aag ggt gta gaa gca att cct gaa gga tct cac ata				1059
Thr Gly Asp Glu Lys Gly Val Glu Ala Ile Pro Glu Gly Ser His Ile				
252	257	262	267	

aaa gac aat gaa cag gct tta tat gaa ttg gtt aaa tgc aat ttt gat	1107
Lys Asp Asn Glu Gln Ala Leu Tyr Glu Leu Val Lys Cys Asn Phe Asp	
268 273 278 283	
aca gaa gaa gca ttg aga aga tta aga ttt aat gta aaa gca gct aga	1155
Thr Glu Glu Ala Leu Arg Arg Leu Arg Phe Asn Val Lys Ala Ala Arg	
284 289 294 299	
gag gaa tta tct gtt tgg aca gag gaa gag tgt aga aat ttt gaa caa	1203
Glu Glu Leu Ser Val Trp Thr Glu Glu Glu Cys Arg Asn Phe Glu Gln	
300 305 310 315	
ggg ctg aag gcc tat gga aag gat ttt cat ttg att cag gct aat aaa	1251
Gly Leu Lys Ala Tyr Gly Lys Asp Phe His Leu Ile Gln Ala Asn Lys	
316 321 326 331	
gtc cga aca agg tca gtt ggt gaa tgt gta gca ttc tat tac atg tgg	1299
Val Arg Thr Arg Ser Val Gly Glu Cys Val Ala Phe Tyr Tyr Met Trp	
332 337 342 347	
aaa aaa tct gaa cgt tat gat ttc ttt gct cag caa aca cga ttt gga	1347
Lys Lys Ser Glu Arg Tyr Asp Phe Phe Ala Gln Gln Thr Arg Phe Gly	
348 353 358 363	
aag aag aaa tat aat ctt cat cct ggt gta acg gat tac atg gat cgt	1395
Lys Lys Lys Tyr Asn Leu His Pro Gly Val Thr Asp Tyr Met Asp Arg	
364 369 374 379	
ctt cta gac gaa agt gaa agt gct gca tct agt cga gca caa tcc cct	1443
Leu Leu Asp Glu Ser Glu Ser Ala Ala Ser Ser Arg Ala Gln Ser Pro	
380 385 390 395	
ccc cca act gca tca aac agt agt aac agc cag tct gag aaa gaa gat	1491
Pro Pro Thr Ala Ser Asn Ser Ser Asn Ser Gln Ser Glu Lys Glu Asp	
396 401 406 411	
ggc act gta agc act gct aat caa aat ggt aag caa cca gag aaa cat	1539
Gly Thr Val Ser Thr Ala Asn Gln Asn Gly Lys Gln Pro Glu Lys His	
412 417 422 427	
ttc tct ttc ttc ata ata agg gac act ttc ttg cag tga cttgggaaat	1588
Phe Ser Phe Phe Ile Ile Arg Asp Thr Phe Leu Gln *	
428 433 438	
tccgtttggg tttctattaa acttccagag cagaaagtaa aaaatgataa cacatgagac	1648
aaacataaca tcagcataca tatatactaa cagaatacaa agtgattgga catcactaaa	1708
aagtaatttt aataaagcct actgtcaaca gtgactattt cttgtaagaa atttgttctt	1768
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<400> 388

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ccgcccccg ccgtccccc gccgcgatgc cctcccttcg gggccccggc ggcccgcgcc 120
cctgctaggc tgcggcggca tggcccgcgc gcccggcgcg acctctgcgg attgcatcgg 180
tgtgtggcgg cggggcatgc ccagagcacc gggcacggcc ttca atg ggc gag gac 236
                                     Met Gly Glu Asp

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1

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acg gac acg cgg aaa att aac cac agc ttc ctg cgg gac cac agc tat 284
Thr Asp Thr Arg Lys Ile Asn His Ser Phe Leu Arg Asp His Ser Tyr
5 10 15 20

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gtg act gaa gct gac atc atc tct acc gtt gag ttc aac cac acg gga 332
Val Thr Glu Ala Asp Ile Ile Ser Thr Val Glu Phe Asn His Thr Gly
21 26 31 36

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gag ctg ctg gcc aca ggt gac aag ggc ggc cgg gtc gtc atc ttc cag 380
Glu Leu Leu Ala Thr Gly Asp Lys Gly Gly Arg Val Val Ile Phe Gln
37 42 47 52

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cgg gaa cca gag agt aaa aat gcg ccc cac agc cag ggc gaa tac gac 428
Arg Glu Pro Glu Ser Lys Asn Ala Pro His Ser Gln Gly Glu Tyr Asp
53 58 63 68

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gtg tac agc act ttc cag agc cac gag ccg gag ttt gac tat ctc aag 476
Val Tyr Ser Thr Phe Gln Ser His Glu Pro Glu Phe Asp Tyr Leu Lys
69 74 79 84

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agc ctg gag ata gag gag aag atc aac aag atc aag tgg ctc cca cag 524
Ser Leu Glu Ile Glu Glu Lys Ile Asn Lys Ile Lys Trp Leu Pro Gln
85 90 95 100

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cag aac gcc gcc cac tca ctc ctg tcc acc aac gat aaa act atc aaa 572
Gln Asn Ala Ala His Ser Leu Leu Ser Thr Asn Asp Lys Thr Ile Lys
101 106 111 116

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tta tgg aag att acc gaa cga gat aaa agg ccc gaa gga tac aac ctg 620
Leu Trp Lys Ile Thr Glu Arg Asp Lys Arg Pro Glu Gly Tyr Asn Leu
117 122 127 132

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aag gat gaa gag ggg aaa ctt aag gac ctg tcc acg gtg acg tca ctg 668
Lys Asp Glu Glu Gly Lys Leu Lys Asp Leu Ser Thr Val Thr Ser Leu
133 138 143 148

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cag gtg cca gtg ctg aag ccc atg gat ctg atg gtg gag gtg agc cct 716
Gln Val Pro Val Leu Lys Pro Met Asp Leu Met Val Glu Val Ser Pro

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149	154	159	164	
cgg agg atc ttt gcc aat ggc cac acc tac cac atc aac tcc atc tcc				764
Arg Arg Ile Phe Ala Asn Gly His Thr Tyr		His Ile Asn Ser Ile Ser		
165	170	175	180	
gtc aac agt gac tgc gag acc tac atg tcg gcg gat gac ctg cgc atc				812
Val Asn Ser Asp Cys Glu Thr Tyr Met Ser		Ala Asp Asp Leu Arg Ile		
181	186	191	196	
aac ctc tgg cac ctg gcc atc acc gac agg agc ttc aac atc gtg gac				860
Asn Leu Trp His Leu Ala Ile Thr Asp Arg Ser Phe Asn Ile Val Asp				
197	202	207	212	
atc aag ccg gcc aac atg gag gac ctt acg gag gtg atc aca gca tct				908
Ile Lys Pro Ala Asn Met Glu Asp Leu Thr		Glu Val Ile Thr Ala Ser		
213	218	223	228	
gag ttc cat ccg cac cac tgc aac ctc ttc gtc tac agc agc agc aag				956
Glu Phe His Pro His His Cys Asn Leu Phe Val Tyr Ser Ser Ser Lys				
229	234	239	244	
ggc tcc ctg cgg ctc tgc gac atg cgg gca gct gcc ctg tgt gac aag				1004
Gly Ser Leu Arg Leu Cys Asp Met Arg Ala Ala Leu Cys Asp Lys				
245	250	255	260	
cat tcc aag ctc ttt gaa gag cct gag gac ccc agt aac cgc tca ttc				1052
His Ser Lys Leu Phe Glu Glu Pro Glu Asp Pro Ser Asn Arg Ser Phe				
261	266	271	276	
ttc tcg gaa atc atc tcc tcc gtg tcc gac gtg aag ttc agc cac agc				1100
Phe Ser Glu Ile Ile Ser Ser Val Ser Asp Val Lys Phe Ser His Ser				
277	282	287	292	
ggc cgc tac atg ctc acc cgg gac tac ctt aca gtc aag gtc tgg gac				1148
Gly Arg Tyr Met Leu Thr Arg Asp Tyr Leu Thr Val Lys Val Trp Asp				
293	298	303	308	
ctg aac atg gag gca aga ccc ata gag acc tac cag gtc cat gac tac				1196
Leu Asn Met Glu Ala Arg Pro Ile Glu Thr Tyr Gln Val His Asp Tyr				
309	314	319	324	
ctt cgg agc aag ctc tgt tcc ctg tac gag aac gac tgc att ttc gac				1244
Leu Arg Ser Lys Leu Cys Ser Leu Tyr Glu Asn Asp Cys Ile Phe Asp				
325	330	335	340	
aag ttt gaa tgt gcc tgg aac ggg agc gac agc gtc atc atg acc ggg				1292
Lys Phe Glu Cys Ala Trp Asn Gly Ser Asp Ser Val Ile Met Thr Gly				
341	346	351	356	
acc tac aac aac ttc ttc cgc atg ttc gat cgg aac acc aag cgg gac				1340
Thr Tyr Asn Asn Phe Phe Arg Met Phe Asp Arg Asn Thr Lys Arg Asp				
357	362	367	372	
gtg acc ctg gag gcc tcg agg gaa agc agc aag ccc cgg gct gtg ctc				1388
Val Thr Leu Glu Ala Ser Arg Glu Ser Ser Lys Pro Arg Ala Val Leu				
373	378	383	388	

aag cca cgg cgc gtg tgc gtg ggg ggc aag cgc cgg cgt gat gac atc	1436
Lys Pro Arg Arg Val Cys Val Gly Gly Lys Arg Arg Arg Asp Asp Ile	
389 394 399 404	
agt gtg gac agc ttg gac ttc acc aag aag atc ctg cac acg gcc tgg	1484
Ser Val Asp Ser Leu Asp Phe Thr Lys Lys Ile Leu His Thr Ala Trp	
405 410 415 420	
cac ccg gct gag aac atc att gcc att gcc gcc acc aac aac ctg tac	1532
His Pro Ala Glu Asn Ile Ile Ala Ile Ala Ala Thr Asn Asn Leu Tyr	
421 426 431 436	
atc ttc cag gac aag gta aac tct gac atg cac tag gtat gtgcagatcc	1582
Ile Phe Gln Asp Lys Val Asn Ser Asp Met His *	
437 442 447	
cgccccctgc caccagcct catgcaagtc atccccgaca tgaccttcac gaccgcaatg	1642
caaggagggg aagaaagtca cagcactgat gaggacagct gcagaggtgg cagtgtgtgg	1702
acacaggaag tttgggcccc ctccctgccc cagctttcct aggccagaat tgtgtttggc	1762
agtaattgtc tgtttaaaaa aataaaaagg agaggaagcg ttcaccgcca caaatcataa	1822
aatggacatg actgtggagt cttacagttc agggttcttt cattcacgtc ccttcctgtc	1882
tcggtctgcg gtctttacca catcaatagg actttttatg cgtccggggt aatttttcac	1942
tccagtgtgt cctgttgacg ggaccggagc tgatgggagc tgcttctccc ccatgcctca	2002
ctgggtcccag atcagggctc cagggacaga tgatgagtct caaacgagcc agccaggggt	2062
tcttttggtt ataaatgggg caattcgccc tgtctcagag ctgatgacct caccgttggt	2122
ttttggatgg tgaattcatg ctgagaatth gcagatgcaa gctcctctcc taggtcttct	2182
gaatgtcttg aaacatccca ggtcccaggt ctggtgagggt ttcccagagag gagcggagtg	2242
gggtttgtct tctgtgtgcc tgtgtcctca tctgattcac ctgccatttg ctgagcctct	2302
gctgtgtacc aggcgtgggtg ctcagcccta gaggcagttg acttaccctc tgcagccctc	2362
cctgccgcct cacccttcag cattcaactgg gcaccttccc ggagcggaca ctgactccca	2422
tgcacgattt tttggaatct tcctcctgac tgtgaggtgg gtgttcattc atttcctcca	2482
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 <213> Homo sapiens

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 <222> (132)..(557)

<400> 389

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ccaataaagc cagtgaagaaa ggagcttacc aaaggcagtg tacgaagaag gttcctggga	120
gactgtcaga a atg agt ttt tca ctg aac ttc acc ctg ccg gcg aac aca	170
Met Ser Phe Ser Leu Asn Phe Thr Leu Pro Ala Asn Thr	
1 5 10	
acg tcc tct cct gtc aca ggt ggg aaa gaa acg gac tgt ggg ccc tct	218
Thr Ser Ser Pro Val Thr Gly Gly Lys Glu Thr Asp Cys Gly Pro Ser	
14 19 24 29	
ctt gga tta gcg gcg ggc ata cca ttg ctg gtg gcc aca gcc ctg ctg	266
Leu Gly Leu Ala Ala Gly Ile Pro Leu Leu Val Ala Thr Ala Leu Leu	
30 35 40 45	
gtg gct tta cta ttt act ttg att cac cga aga aga agc agc att gag	314
Val Ala Leu Leu Phe Thr Leu Ile His Arg Arg Arg Ser Ser Ile Glu	
46 51 56 61	
gcc atg gag gaa agt gac aga cca tgt gaa att tca gaa att gat gac	362
Ala Met Glu Glu Ser Asp Arg Pro Cys Glu Ile Ser Glu Ile Asp Asp	
62 67 72 77	
aat ccc aag ata tct gag aat cct agg aga tca ccc aca cat gag aag	410
Asn Pro Lys Ile Ser Glu Asn Pro Arg Arg Ser Pro Thr His Glu Lys	
78 83 88 93	
aat acg atg gga gca caa gag gcc cac ata tat gtg aag act gta gca	458
Asn Thr Met Gly Ala Gln Glu Ala His Ile Tyr Val Lys Thr Val Ala	
94 99 104 109	
gga agc gag gaa cct gtg cat gac cgt tac cgt cct act ata gaa atg	506
Gly Ser Glu Glu Pro Val His Asp Arg Tyr Arg Pro Thr Ile Glu Met	
110 115 120 125	
gaa aga agg agg gga ttg tgg tgg ctt gtg ccc aga ctg agc ctg gaa	554
Glu Arg Arg Arg Gly Leu Trp Trp Leu Val Pro Arg Leu Ser Leu Glu	
126 131 136 141	
tga tgca gctcagtcaa ggagcagcag acctggcact ggaacagggt tgaaaaccca	611
*	
142	
gggttttgta cttggagagg aaagatgcca agctgcttct taatcaatcc aaatttcatt	671
tacagctctg gaacactttg gggctgattt gtctcttttag gggacatccc caacatgggt	731
aattccaact ctcagatctt gtgctttagt tagtacatgt gactcaccag atggggctct	791
tagatcctat tctgtctccc agtgggaatt tgcttttctt tgtcattttg ggaaaggggc	851

ttgggttctg agtgtcttgc cttctcatct ttttttttca tctcttttt ctcaaaaaag 911
 ccatcagatc tgactttcat ggaagtgttg ctgaggtcag cctggtgcaa gttgggatac 971
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 gtaggaacca tgtggagcca cacattccct gaccacaggg aagcacctgg ctcaatcatg 1091
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 aaagatgatt ctaggtgttg ctggtagtat gtgaatcttc caatctaggt gtgacgtgt 1511
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 ggtggtgtta catttaacct taaagatgtt aatgttgatg gaaattcatg tttcatatta 1631
 aaacaacact ttgtctttac aatgaaacat tttgcttaat ttttaaagta agacattatg 1691
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 aagttacaac ttcttttatt ttatttttta aaggcttcag attaaacaag agcccttaag 1811
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 aaaggagagg ctacttcaag tgggtgttggc ccattgagcc tattgggcaa actataacca 1931
 ggttgcccta ttttgggtgg attactccag gagaggccac cctccagctt tctcttatcc 1991
 cagtaactcc tcttccatt ttccaatcca tcccagcca ttttttttt tcttctgtac 2051
 tcttcttttg ccttcaatat gagtttcatt tctctgtgt ctttgggcag ac 2103

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 <222> (458) .. (901)

<400> 390
 gctggcccat ggctgagacc tctctcccag agctgggggg agaggacaaa gccacgcctt 60

<210> 391
 <211> 583
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (105)..(518)

<400> 391

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taggtgaccc tcggctgctg cagggatctg cagcgactgc agcc atg ggg gcg cac      116
                               Met Gly Ala His
                               1

ctg gtc cgg cgc tac ctg ggc gat gcc tcg gtg gag ccc gac ccc ctg      164
Leu Val Arg Arg Tyr Leu Gly Asp Ala Ser Val Glu Pro Asp Pro Leu
   5                10                15                20

cag atg cca acc ttc ccg cca gac tac ggc ttc ccc gaa cgc aag gag      212
Gln Met Pro Thr Phe Pro Pro Asp Tyr Gly Phe Pro Glu Arg Lys Glu
  21                26                31                36

cgc gag atg gtg gcc aca cag cag gag atg atg gac gcg cag ctg agg      260
Arg Glu Met Val Ala Thr Gln Gln Glu Met Met Asp Ala Gln Leu Arg
  37                42                47                52

ctc cag ctg cgg gac tac tgc gcc cac cac ctc atc cgg ctg ctc aag      308
Leu Gln Leu Arg Asp Tyr Cys Ala His His Leu Ile Arg Leu Leu Lys
  53                58                63                68

tgc aag cgt gac agc ttc ccc aac ttc ctg gcc tgc aag cag gag cgg      356
Cys Lys Arg Asp Ser Phe Pro Asn Phe Leu Ala Cys Lys Gln Glu Arg
  69                74                79                84

cac gac tgg gac tac tgc gag cac cgc gac tat gtg atg cgc atg aag      404
His Asp Trp Asp Tyr Cys Glu His Arg Asp Tyr Val Met Arg Met Lys
  85                90                95                100

gag ttt gag cgg gag cgg agg ctg ctc cag cgg aag aag cgg cgg gag      452
Glu Phe Glu Arg Glu Arg Arg Leu Leu Gln Arg Lys Lys Arg Arg Glu
 101                106                111                116

aag aag gcg gca gag ttg gcc aaa ggc cag gga ccc ggg gaa gtg gac      500
Lys Lys Ala Ala Glu Leu Ala Lys Gly Gln Gly Pro Gly Glu Val Asp
 117                122                127                132

ccc aag gtg gcc ctg tag ggggtg cccccccac cctatggacc agtcaaataa      554
Pro Lys Val Ala Leu *
 133                138

aagccttcag gccctcaaa aaaaaaaaaa      583
  
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 <213> Homo sapiens

<220>
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 <222> (105)..(470)

<400> 392

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taggtgaccc tcggctgctg cagggatctg cagcgactgc agcc atg ggg gcg cac      116
                               Met Gly Ala His
                               1

ctg gtc cgg cgc tac ctg ggc gat gcc tcg gtg gag ccc gac ccc ctg      164
Leu Val Arg Arg Tyr Leu Gly Asp Ala Ser Val Glu Pro Asp Pro Leu
   5                10                15                20

cag atg cca acc ttc ccg cca gac tac ggc ttc ccc gaa cgc aag gag      212
Gln Met Pro Thr Phe Pro Pro Asp Tyr Gly Phe Pro Glu Arg Lys Glu
  21                26                31                36

cgc gag atg gtg gcc aca cag cag gag atg atg gac gcg ctg ctc aag      260
Arg Glu Met Val Ala Thr Gln Gln Glu Met Met Asp Ala Leu Leu Lys
  37                42                47                52

tgc aag cgt gac agc ttc ccc aac ttc ctg gcc tgc aag cag gag cgg      308
Cys Lys Arg Asp Ser Phe Pro Asn Phe Leu Ala Cys Lys Gln Glu Arg
  53                58                63                68

cac gac tgg gac tac tgc gag cac cgc gac tat gtg atg cgc atg aag      356
His Asp Trp Asp Tyr Cys Glu His Arg Asp Tyr Val Met Arg Met Lys
  69                74                79                84

gag ttt gag cgg gag cgg agg ctg ctc cag cgg aag aag cgg cgg gag      404
Glu Phe Glu Arg Glu Arg Arg Leu Leu Gln Arg Lys Lys Arg Arg Glu
  85                90                95                100

aag aag gcg gca gag ttg gcc aaa ggc cag gga ccc ggg gaa gtg gac      452
Lys Lys Ala Ala Glu Leu Ala Lys Gly Gln Gly Pro Gly Glu Val Asp
 101                106                111                116

ccc aag gtg gcc ctg tag ggggtg cccccccac cctatggacc agtcaaataa      506
Pro Lys Val Ala Leu *
 117                122

aagccttcag gcccctcaaa aaaaaaaaaa      535
  
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 <211> 3897

<212> DNA
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<220>
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<400> 393

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taagggaagc cgtg atg agg gcc gtg ttg acg tgg aga gat aaa gcc gag	110
Met Arg Ala Val Leu Thr Trp Arg Asp Lys Ala Glu	
1 5 10	
cac tgt ata aat gac atc gca ttt aag cct gat gga act caa ctg att	158
His Cys Ile Asn Asp Ile Ala Phe Lys Pro Asp Gly Thr Gln Leu Ile	
13 18 23 28	
ttg gct gcc gga agc aga tta ctg gtt tat gac acc tct gat ggc acc	206
Leu Ala Ala Gly Ser Arg Leu Leu Val Tyr Asp Thr Ser Asp Gly Thr	
29 34 39 44	
tta ctt cag ccc ctc aag gga cac aaa gac act gtg tac tgt gtg gca	254
Leu Leu Gln Pro Leu Lys Gly His Lys Asp Thr Val Tyr Cys Val Ala	
45 50 55 60	
tat gcg aag gat ggc aag cgc ttt gct tct gga tca gct gac aaa agc	302
Tyr Ala Lys Asp Gly Lys Arg Phe Ala Ser Gly Ser Ala Asp Lys Ser	
61 66 71 76	
gtt att atc tgg aca tca aaa ctg gaa ggc att ctg aag tac acg cac	350
Val Ile Ile Trp Thr Ser Lys Leu Glu Gly Ile Leu Lys Tyr Thr His	
77 82 87 92	
aat gat gct ata caa tgt gtc tcc tac aat cct att act cat caa ctg	398
Asn Asp Ala Ile Gln Cys Val Ser Tyr Asn Pro Ile Thr His Gln Leu	
93 98 103 108	
gca tct tgt tcc tcc agt gac ttt ggg ttg tgg tct cct gaa cag aag	446
Ala Ser Cys Ser Ser Ser Asp Phe Gly Leu Trp Ser Pro Glu Gln Lys	
109 114 119 124	
tct gtc tcc aaa cac aaa tca agc agc aag atc atc tgc tgc agc tgg	494
Ser Val Ser Lys His Lys Ser Ser Ser Lys Ile Ile Cys Cys Ser Trp	
125 130 135 140	
aca aat gat ggt cag tac ctg gcg ctg ggg atg ttc aat ggg atc atc	542
Thr Asn Asp Gly Gln Tyr Leu Ala Leu Gly Met Phe Asn Gly Ile Ile	
141 146 151 156	
agc ata cgg aac aaa aat ggc gag gag aaa gta aag atc gag cgg ccg	590
Ser Ile Arg Asn Lys Asn Gly Glu Glu Lys Val Lys Ile Glu Arg Pro	
157 162 167 172	
ggg ggc tcc ctc tcg cca ata tgg tcc atc tgc tgg aac cct tca agc	638
Gly Gly Ser Leu Ser Pro Ile Trp Ser Ile Cys Trp Asn Pro Ser Ser	
173 178 183 188	

cga tgg gag agt ttc tgg atg aac aga gag aat gag gat gcc gag gat	686
Arg Trp Glu Ser Phe Trp Met Asn Arg Glu Asn Glu Asp Ala Glu Asp	
189 194 199 204	
gtc att gtc aac aga tat att cag gaa atc cct tcc act ctg aag tca	734
Val Ile Val Asn Arg Tyr Ile Gln Glu Ile Pro Ser Thr Leu Lys Ser	
205 210 215 220	
gca gtg tac agt agt cag ggt agt gag gca gag gag gaa gaa cca gag	782
Ala Val Tyr Ser Ser Gln Gly Ser Glu Ala Glu Glu Glu Glu Pro Glu	
221 226 231 236	
gaa gag gac gac agt ccc agg gac gac aac tta gag gaa cgt aat gac	830
Glu Glu Asp Asp Ser Pro Arg Asp Asp Asn Leu Glu Glu Arg Asn Asp	
237 242 247 252	
atc ctg gct gtg gct gac tgg gga cag aaa gtt tcc ttc tac cag ctg	878
Ile Leu Ala Val Ala Asp Trp Gly Gln Lys Val Ser Phe Tyr Gln Leu	
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agt gga aaa cag att gga aag gat cgg gca ctg aac ttt gac ccc tgc	926
Ser Gly Lys Gln Ile Gly Lys Asp Arg Ala Leu Asn Phe Asp Pro Cys	
269 274 279 284	
tgc atc agc tac ttt act aaa ggc gag tac att ttg ctg ggg ggt tca	974
Cys Ile Ser Tyr Phe Thr Lys Gly Glu Tyr Ile Leu Leu Gly Gly Ser	
285 290 295 300	
gac aag caa gta tct ctt ttc acc aag gat gga gtg cgg ctt ggg act	1022
Asp Lys Gln Val Ser Leu Phe Thr Lys Asp Gly Val Arg Leu Gly Thr	
301 306 311 316	
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Val Gly Glu Gln Asn Ser Trp Val Trp Thr Cys Gln Ala Lys Pro Asp	
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Ser Asn Tyr Val Val Val Gly Cys Gln Asp Gly Thr Ile Ser Phe Tyr	
333 338 343 348	
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Gln Leu Ile Phe Ser Thr Val His Gly Leu Tyr Lys Asp Arg Tyr Ala	
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Tyr Arg Asp Ser Met Thr Asp Val Ile Val Gln His Leu Ile Thr Glu	
365 370 375 380	
cag aaa gtt cgg att aaa tgc aaa gag ctt gtc aag aag att gcc atc	1262
Gln Lys Val Arg Ile Lys Cys Lys Glu Leu Val Lys Lys Ile Ala Ile	
381 386 391 396	
tac aga aat cga ttg gct atc caa ctg cca gag aaa atc ctc atc tat	1310
Tyr Arg Asn Arg Leu Ala Ile Gln Leu Pro Glu Lys Ile Leu Ile Tyr	
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Glu Leu Tyr Ser Glu Asp Leu Ser Asp Met His Tyr Arg Val Lys Glu	
413 418 423 428	
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Lys Ile Ile Lys Lys Phe Glu Cys Asn Leu Leu Val Val Cys Ala Asn	
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cac atc atc ctg tgc cag gag aaa cgg ctg cag tgc ctg tcc ttc agc	1454
His Ile Ile Leu Cys Gln Glu Lys Arg Leu Gln Cys Leu Ser Phe Ser	
445 450 455 460	
gga gtg aag gag cgg gag tgg cag atg gag tct ctc att cgt tac atc	1502
Gly Val Lys Glu Arg Glu Trp Gln Met Glu Ser Leu Ile Arg Tyr Ile	
461 466 471 476	
aag gtg atc ggt ggc cct cct gga aga gaa ggc ctc tta gtg ggg ctg	1550
Lys Val Ile Gly Gly Pro Pro Gly Arg Glu Gly Leu Leu Val Gly Leu	
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Lys Asn Gly Gln Ile Leu Lys Ile Phe Val Asp Asn Leu Phe Ala Ile	
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Val Leu Leu Lys Gln Ala Thr Ala Val Arg Cys Leu Asp Met Ser Ala	
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Ser Arg Lys Lys Leu Ala Val Val Asp Glu Asn Asp Thr Cys Leu Val	
525 530 535 540	
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Tyr Asp Ile Asp Thr Lys Glu Leu Leu Phe Gln Glu Pro Asn Ala Asn	
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agt gta gct tgg aac acc cag tgt gag gac atg ctc tgc ttc tcg gga	1790
Ser Val Ala Trp Asn Thr Gln Cys Glu Asp Met Leu Cys Phe Ser Gly	
557 562 567 572	
gga ggc tac ctc aac atc aaa gcc agc acc ttc cct gtg cac cgg cag	1838
Gly Gly Tyr Leu Asn Ile Lys Ala Ser Thr Phe Pro Val His Arg Gln	
573 578 583 588	
aag ctg cag ggc ttt gtg gtc ggc tac aat ggc tcc aag atc ttc tgc	1886
Lys Leu Gln Gly Phe Val Val Gly Tyr Asn Gly Ser Lys Ile Phe Cys	
589 594 599 604	
ctc cat gtc ttc tcc att tct gcc gtg gag gtg ccg cag tcc gct ccc	1934
Leu His Val Phe Ser Ile Ser Ala Val Glu Val Pro Gln Ser Ala Pro	
605 610 615 620	
atg tac cag tac ctg gat agg aaa ctg ttc aag gaa gcc tac cag att	1982
Met Tyr Gln Tyr Leu Asp Arg Lys Leu Phe Lys Glu Ala Tyr Gln Ile	
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gct tgc ttg ggt gtc aca gac act gat tgg cgt gaa ctg gcc atg gaa	2030

Ala Cys Leu Gly Val Thr Asp Thr Asp Trp Arg Glu Leu Ala Met Glu	
637 642 647 652	
gcg cta gaa ggt tta gat ttt gaa aca gca aag aag gcc ttc atc aga	2078
Ala Leu Glu Gly Leu Asp Phe Glu Thr Ala Lys Lys Ala Phe Ile Arg	
653 658 663 668	
gta caa gac ctc cga tat tta gag ctc atc agc agc att gag gag agg	2126
Val Gln Asp Leu Arg Tyr Leu Glu Leu Ile Ser Ser Ile Glu Glu Arg	
669 674 679 684	
aag aag cgg gga gag acc aac aat gac ctg ttt ctg gca gat gtg ttt	2174
Lys Lys Arg Gly Glu Thr Asn Asn Asp Leu Phe Leu Ala Asp Val Phe	
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Ser Tyr Gln Gly Lys Phe His Glu Ala Ala Lys Leu Tyr Lys Arg Ser	
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Gly His Glu Asn Leu Ala Leu Glu Met Tyr Thr Asp Leu Cys Met Phe	
717 722 727 732	
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Glu Tyr Ala Lys Asp Phe Leu Gly Ser Gly Asp Pro Lys Glu Thr Lys	
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atg cta atc acc aaa cag gct gac tgg gcc aga aat atc aag gag ccc	2366
Met Leu Ile Thr Lys Gln Ala Asp Trp Ala Arg Asn Ile Lys Glu Pro	
749 754 759 764	
aaa gcc gcc gtg gag atg tac atc tca gca gga gag cac gtc aag gcc	2414
Lys Ala Ala Val Glu Met Tyr Ile Ser Ala Gly Glu His Val Lys Ala	
765 770 775 780	
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Ile Glu Ile Cys Gly Asp His Gly Trp Val Asp Met Leu Ile Asp Ile	
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Ala Arg Lys Leu Asp Lys Ala Glu Arg Glu Pro Leu Leu Leu Cys Ala	
797 802 807 812	
acc tac ctc aag aag ctg gac agc cct ggc tat gct gct gag acc tac	2558
Thr Tyr Leu Lys Lys Leu Asp Ser Pro Gly Tyr Ala Ala Glu Thr Tyr	
813 818 823 828	
ctg aag atg ggt gac ctc aag tcc ctg gtg cag ctg cac gtg gag acc	2606
Leu Lys Met Gly Asp Leu Lys Ser Leu Val Gln Leu His Val Glu Thr	
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Gln Arg Trp Asp Glu Ala Phe Ala Leu Gly Glu Lys His Pro Glu Phe	
845 850 855 860	
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Lys Asp Asp Ile Tyr Met Pro Tyr Ala Gln Trp Leu Ala Glu Asn Asp	

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Arg Phe Glu Glu Ala Gln Lys Ala Phe His Lys Ala Gly Arg Gln Arg				
877	882	887	892	
gaa gcg gtc cag gtg ctg gag cag ctc aca aac aat gcc gtg gcg gag				2798
Glu Ala Val Gln Val Leu Glu Gln Leu Thr Asn Asn Ala Val Ala Glu				
893	898	903	908	
agc agg ttt aat gat gct gcc tat tat tac tgg atg ctg tcc atg cag				2846
Ser Arg Phe Asn Asp Ala Ala Tyr Tyr Tyr Trp Met Leu Ser Met Gln				
909	914	919	924	
tgc ctc gat ata gct caa gat cct gcc cag aag gac aca atg ctt ggc				2894
Cys Leu Asp Ile Ala Gln Asp Pro Ala Gln Lys Asp Thr Met Leu Gly				
925	930	935	940	
aag ttc tac cac ttc cag cgt ttg gca gag ctg tac cat ggt tac cat				2942
Lys Phe Tyr His Phe Gln Arg Leu Ala Glu Leu Tyr His Gly Tyr His				
941	946	951	956	
gcc atc cat cgc cac acg gaa gat ccg ttc agt gtc cat cgt cct gaa				2990
Ala Ile His Arg His Thr Glu Asp Pro Phe Ser Val His Arg Pro Glu				
957	962	967	972	
act ctt ttc aac atc tcc agg ttc ctg ctg cac agc ctg ccc aag gac				3038
Thr Leu Phe Asn Ile Ser Arg Phe Leu Leu His Ser Leu Pro Lys Asp				
973	978	983	988	
acc ccc tcg ggc atc tct aaa gtg aaa ata ctc ttc acc ttg gcc aag				3086
Thr Pro Ser Gly Ile Ser Lys Val Lys Ile Leu Phe Thr Leu Ala Lys				
989	994	999	1004	
cag agc aag gcc ctc ggt gcc tac agg ctg gcc cgg cac gcc tat gac				3134
Gln Ser Lys Ala Leu Gly Ala Tyr Arg Leu Ala Arg His Ala Tyr Asp				
1005	1010	1015	1020	
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Lys Leu Arg Gly Leu Tyr Ile Pro Ala Arg Phe Gln Lys Ser Ile Glu				
1021	1026	1031	1036	
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Leu Gly Thr Leu Thr Ile Arg Ala Lys Pro Phe His Asp Ser Glu Glu				
1037	1042	1047	1052	
ttg gtg ccc ttg tgc tac cgc tgc tcc acc aac aac ccg ctg ctc aac				3278
Leu Val Pro Leu Cys Tyr Arg Cys Ser Thr Asn Asn Pro Leu Leu Asn				
1053	1058	1063	1068	
aac ctg ggc aac gtc tgc atc aac tgc cgc cag ccc ttc atc ttc tcc				3326
Asn Leu Gly Asn Val Cys Ile Asn Cys Arg Gln Pro Phe Ile Phe Ser				
1069	1074	1079	1084	
gcc tct tcc tac gac gtg cta cac ctg gtt gag ttc tac ctg gag gaa				3374
Ala Ser Ser Tyr Asp Val Leu His Leu Val Glu Phe Tyr Leu Glu Glu				
1085	1090	1095	1100	

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Gly Ile Thr Asp Glu Glu Ala Ile Ser Leu Ile Asp Leu Glu Val Leu	
1101 1106 1111 1116	
aga ccc aag cgg gat gac aga cag cta gag att gca aac aac agc tcc	3470
Arg Pro Lys Arg Asp Asp Arg Gln Leu Glu Ile Ala Asn Asn Ser Ser	
1117 1122 1127 1132	
cag att ctg cgg cta gtg gag acc aag gac tcc atc gga gat gag gac	3518
Gln Ile Leu Arg Leu Val Glu Thr Lys Asp Ser Ile Gly Asp Glu Asp	
1133 1138 1143 1148	
ccg ttc aca gct aag ctg agc ttt gag caa ggt ggc tca gag ttc gtg	3566
Pro Phe Thr Ala Lys Leu Ser Phe Glu Gln Gly Gly Ser Glu Phe Val	
1149 1154 1159 1164	
cca gtg gtg gtg agc cgg ctg gtg ctg cgc tcc atg agc cgc cgg gat	3614
Pro Val Val Val Ser Arg Leu Val Leu Arg Ser Met Ser Arg Arg Asp	
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Val Leu Ile Lys Arg Trp Pro Pro Pro Leu Arg Trp Gln Tyr Phe Arg	
1181 1186 1191 1196	
tca ctg ctg cct gac gcc tcc att acc atg tgc ccc tcc tgc ttc cag	3710
Ser Leu Leu Pro Asp Ala Ser Ile Thr Met Cys Pro Ser Cys Phe Gln	
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Met Phe His Ser Glu Asp Tyr Glu Leu Leu Val Leu Gln His Gly Cys	
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Cys Pro Tyr Cys Arg Arg Cys Lys Asp Asp Pro Gly Pro *	
1229 1234 1239	
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Met Asn Pro Arg Gly Leu Phe Gln Asp
1 5

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Phe Asn Pro Ser Lys Val Leu Ile Tyr Thr Cys Leu Leu Leu Phe Ser	
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ggg ctg ctg ccc ctc cgc ctg gac ggc atc atc caa tgg agc tac tgg	209
Gly Leu Leu Pro Leu Arg Leu Asp Gly Ile Ile Gln Trp Ser Tyr Trp	
26 31 36 41	
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Ala Val Phe Ala Pro Ile Trp Leu Arg Lys Leu Leu Val Val Ala Gly	
42 47 52 57	
gcc tcc gtg ggc gcg ggc gtt tgg gcc cgc aac cct cgc tac cgc acc	305
Ala Ser Val Gly Ala Gly Val Trp Ala Arg Asn Pro Arg Tyr Arg Thr	
58 63 68 73	
gag gga gag gcc tgt gtg gag atc aaa gcc atg ctg atc gct gtg ggc	353
Glu Gly Glu Ala Cys Val Glu Ile Lys Ala Met Leu Ile Ala Val Gly	
74 79 84 89	
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Ile His Leu Leu Leu Leu Met Phe Glu Val Leu Val Cys Asp Arg Val	
90 95 100 105	
gag agg ggc acc cac ttc tgg ctg ctg gtc ttc atg cct ctc ttc ttc	449
Glu Arg Gly Thr His Phe Trp Leu Leu Val Phe Met Pro Leu Phe Phe	
106 111 116 121	
gtg tcc ccc gtg tcc gtg gct gcc tgc gtc tgg ggc ttt cga cac gat	497
Val Ser Pro Val Ser Val Ala Ala Cys Val Trp Gly Phe Arg His Asp	
122 127 132 137	
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Arg Ser Leu Glu Leu Glu Ile Leu Cys Ser Val Asn Ile Leu Gln Phe	
138 143 148 153	
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Ile Phe Ile Ala Leu Lys Leu Asp Arg Ile Ile His Trp Pro Trp Leu	
154 159 164 169	
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Val Val Phe Val Pro Leu Trp Ile Leu Met Ser Phe Leu Cys Leu Val	
170 175 180 185	
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Val Leu Tyr Tyr Ile Val Trp Ser Leu Leu Phe Leu Arg Ser Leu Asp	
186 191 196 201	
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Val Val Ala Glu Gln Arg Arg Thr His Val Thr Met Ala Ile Ser Trp	
202 207 212 217	
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Ile Thr Ile Val Val Pro Leu Leu Thr Phe Glu Val Leu Leu Val His	

218	223	228	233	
aga ttg gat ggc cac aat aca ttc tcc tac gtc tcc ata ttt gtc ccc				833
Arg Leu Asp Gly His Asn Thr Phe Ser Tyr Val Ser Ile Phe Val Pro				
234	239	244	249	
ctt tgg ctt tcc tta cta act tta atg gcc aca aca ttt agg cga aag				881
Leu Trp Leu Ser Leu Leu Thr Leu Met Ala Thr Thr Phe Arg Arg Lys				
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Gly Gly Asn His Trp Trp Phe Gly Ile Arg Arg Asp Phe Cys Gln Phe				
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ctg ctt gaa att ttc cca ttt tta aga gaa tat ggg aac att tca tat				977
Leu Leu Glu Ile Phe Pro Phe Leu Arg Glu Tyr Gly Asn Ile Ser Tyr				
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gat ctc cat cac gaa gat agt gaa gat gct gaa gaa aca tca gtt cca				1025
Asp Leu His His Glu Asp Ser Glu Asp Ala Glu Glu Thr Ser Val Pro				
298	303	308	313	
gaa gct ccg aaa att gct cca ata ttt gga aag aag gcc aga gta gtt				1073
Glu Ala Pro Lys Ile Ala Pro Ile Phe Gly Lys Lys Ala Arg Val Val				
314	319	324	329	
ata acc cag agc cct ggg aaa tac gtt ccc ccc cct ccc aag tta aat				1121
Ile Thr Gln Ser Pro Gly Lys Tyr Val Pro Pro Pro Pro Lys Leu Asn				
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Ile Asp Met Pro Asp *				
346	351			
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		1				5										
act	gga	ctt	cag	gga	ata	acc	ttg	tgt	tat	agt	tgt	ttt	ccc	tcc	ttc	98
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tgc	aag	atg	aaa	agc	agg	atg	tgc	atg	gct	atc	agc	att	tgt	cag	acg	146
Cys	Lys	Met	Lys	Ser	Arg	Met	Cys	Met	Ala	Ile	Ser	Ile	Cys	Gln	Thr	
27					32					37					42	
ctt	tcc	atg	ttg	agt	ttt	gtg	gtc	tgt	gct	ttc	agg	tac	agg	cat	atg	194
Leu	Ser	Met	Leu	Ser	Phe	Val	Val	Cys	Ala	Phe	Arg	Tyr	Arg	His	Met	
43					48					53					58	
ttc	aaa	agg	ggg	tgg	cca	atg	ggg	aca	tgt	tgt	ttg	ttt	ctg	ccc	aca	242
Phe	Lys	Arg	Gly	Trp	Pro	Met	Gly	Thr	Cys	Cys	Leu	Phe	Leu	Pro	Thr	
59					64					69					74	
gct	gcc	cca	gtg	ctc	agc	tgt	gaa	gct	gca	aca	cag	act	gaa	agg	aga	290
Ala	Ala	Pro	Val	Leu	Ser	Cys	Glu	Ala	Ala	Thr	Gln	Thr	Glu	Arg	Arg	
75					80					85					90	
ctg	gat	ctg	gct	gca	gtg	act	ctg	agg	aga	ggc	ttg	aga	tct	aga	gct	338
Leu	Asp	Leu	Ala	Ala	Val	Thr	Leu	Arg	Arg	Gly	Leu	Arg	Ser	Arg	Ala	
91					96					101					106	
tgc	cga	tgc	aga	ccg	cgg	tct	ttg	ata	gat	tac	aaa	tcc	tac	atg	gac	386
Ser	Arg	Cys	Arg	Pro	Arg	Ser	Leu	Ile	Asp	Tyr	Lys	Ser	Tyr	Met	Asp	
107					112					117					122	
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Thr	Lys	Leu	Leu	Val	Ala	Arg	Phe	Leu	Glu	Gln	Ser	Ser	Cys	Thr	Met	
123					128					133					138	
acc	cca	gac	atc	cat	gaa	ctt	gta	gaa	aac	att	aaa	tct	gtt	ttg	aaa	482
Thr	Pro	Asp	Ile	His	Glu	Leu	Val	Glu	Asn	Ile	Lys	Ser	Val	Leu	Lys	
139					144					149					154	
tct	gat	gag	gag	cac	atg	gag	gaa	gcc	atc	aca	agt	gcc	agt	ttt	cta	530
Ser	Asp	Glu	Glu	His	Met	Glu	Glu	Ala	Ile	Thr	Ser	Ala	Ser	Phe	Leu	
155					160					165					170	
gaa	cag	ata	atg	gcc	cca	ttg	cag	ccc	agc	aca	tcc	agg	gcc	cac	aag	578

Glu Gln Ile Met Ala Pro Leu Gln Pro Ser Thr Ser Arg Ala His Lys	
171 176 181 186	
ctg ccc ttg cgg aga cag cct ggc ctg ctg cac ctc cag agc tgc ggc	626
Leu Pro Leu Arg Arg Gln Pro Gly Leu Leu His Leu Gln Ser Cys Gly	
187 192 197 202	
gac ctt cac acc atc aca cca gcg ggg agg ccc cga gcc gag agg agg	674
Asp Leu His Thr Ile Thr Pro Ala Gly Arg Pro Arg Ala Glu Arg Arg	
203 208 213 218	
ccc cgg cga gtg gag gct gag cgg tca cac agc ctc att ggg gtc atc	722
Pro Arg Arg Val Glu Ala Glu Arg Ser His Ser Leu Ile Gly Val Ile	
219 224 229 234	
cga gag act gtc ctg tga accctg gaagacagaa ggtcactcca aggggaagga	776
Arg Glu Thr Val Leu *	
235 240	
tccctctcct ctctgtcatg tcttgatgg gagctgtggc ccacctcaaa aaaaaaggag	836
cactctggac acgtgttccc acctgttggg tcccggtgtc gctgactgag ggcattcagg	896
agtaaagcga caggctcggc caggcccgtc tgggtttggg atgcactgag ttggagggtta	956
tgaaagcttt gatcctcttc ttcctctgct gggcctcgca gcattcccaa gggtcacatg	1016
ccctggcatg ggcagaaact gggctaataa ttctttgccc acttcacccc tcgtgtctct	1076
ctttgttgct aagttctttc cctcttgga ggacagatct gccgggctgc tatttatagt	1136
tgcccttggc ctttctactgc tctgcgattt ggcaggaaat aaggcgatta accctatgtg	1196
tccacaagcc tcaagccttg tttcagggtca ccctcaaata acactctctt taggcaaaac	1256
aggaaacttc ttaagtgaca aattttaatg ccagacattt aaggagagga ttattgttga	1316
ttccatttac tcatgcttgc aaaactagag acccctaagg cagaactgag aataaacatg	1376
tttacttttg gccactgggc ttgatgtgta aaaaaaa	1413

<210> 396
 <211> 1711
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (338) .. (1051)

<400> 396	
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tgaggacgtt tgggacaaag gtatagtcaa agtgatcaga gcattacatt catctgacaa	120

gtcttgctc	tcttcagccc	cttcctctct	taattgacta	cttcacctc	gctccttgga	180				
acatcctttc	attggtcagc	cacatttttc	ctgcttgggc	catccatccc	catctatttg	240				
tcatacccca	tgaaacttaa	cctcattatg	gtttgcattc	tggattctcc	tctccaccat	300				
ctggcctttac	cttgggggtg	gtgtcgtaca	tgacaca	atg	acg	tgt	ttc	ggg	cca	355
				Met	Thr	Cys	Phe	Gly	Pro	
				1						

tat	cct	att	gga	act	gga	ctt	cag	gga	ata	acc	ttg	tgt	tgt	ttt	ccc	403
Tyr	Pro	Ile	Gly	Thr	Gly	Leu	Gln	Gly	Ile	Thr	Leu	Cys	Cys	Phe	Pro	
7					12					17					22	

tcc ttc tgc aag atg aaa agc agg atg tgc atg gct atc agc att tgt 451
Ser Phe Cys Lys Met Lys Ser Arg Met Cys Met Ala Ile Ser Ile Cys
23 28 33 38

cag atg ctt tcc atg ttg agt ttt gtg gtc tgt gct ttc agg tac agg 499
Gln Met Leu Ser Met Leu Ser Phe Val Val Cys Ala Phe Arg Tyr Arg
39 44 49 54

cat atg ttc aaa agg ggc tgg cca atg ggt aca tgt tgt ttg ttt ctg 547
His Met Phe Lys Arg Gly Trp Pro Met Gly Thr Cys Cys Leu Phe Leu
55 60 65 70

ccc aca gct gcc cca gtg ctc agc tgt gaa gct gca aca cag act gaa 595
Pro Thr Ala Ala Pro Val Leu Ser Cys Glu Ala Ala Thr Gln Thr Glu
71 76 81 86

agg aga ctg gat ctg gct gca gtg act ctg agg aga ggc ttg aga tct 643
Arg Arg Leu Asp Leu Ala Ala Val Thr Leu Arg Arg Gly Leu Arg Ser
87 92 97 102

aga gct tcg cga tgc aga ccg cgg tct ttg ata gat tac aaa tcc tac 691
Arg Ala Ser Arg Cys Arg Pro Arg Ser Leu Ile Asp Tyr Lys Ser Tyr
103 108 113 118

atg	gac	acc	aag	ctg	ctg	gtg	gcg	agg	ttc	ctg	gag	cag	tcc	tct	tgt	739
Met	Asp	Thr	Lys	Leu	Leu	Val	Ala	Arg	Phe	Leu	Glu	Gln	Ser	Ser	Cys	
119					124					129					134	

acc atg acc cca gac atc cat gaa ctt gta gaa aac att aaa tct gtt 787
Thr Met Thr Pro Asp Ile His Glu Leu Val Glu Asn Ile Lys Ser Val
135 140 145 150

ttg	aaa	tct	gat	gag	gag	cac	atg	gag	gaa	gcc	atc	aca	agt	gcc	agt	835
Leu	Lys	Ser	Asp	Glu	Glu	His	Met	Glu	Glu	Ala	Ile	Thr	Ser	Ala	Ser	
151					156					161					166	

ttt	cta	gaa	cag	ata	atg	gcc	cca	ttg	cag	ccc	agc	aca	tcc	agg	gcc	883
Phe	Leu	Glu	Gln	Ile	Met	Ala	Pro	Leu	Gln	Pro	Ser	Thr	Ser	Arg	Ala	
167					172					177					182	

cac aag ctg ccc tcg cgg aga cag cct ggc ctg ctg cac ctc cag agc 931
 His Lys Leu Pro Ser Arg Arg Gln Pro Gly Leu Leu His Leu Gln Ser

183	188	193	198	
tgc ggc gac ctt cac acc ttc aca cca gcg ggg agg ccc cga gcc gag				979
Cys Gly Asp Leu His Thr Phe Thr Pro Ala Gly Arg Pro Arg Ala Glu				
199	204	209	214	
agg agg ccc cgg cga gtg gag gct gag cgg cca cac agc ctc att ggg				1027
Arg Arg Pro Arg Arg Val Glu Ala Glu Arg Pro His Ser Leu Ile Gly				
215	220	225	230	
gtc atc cga gag act gtc ctg tga accctggaag acagaaggcc actccaagg				1081
Val Ile Arg Glu Thr Val Leu *				
231	236			
gaaggatccc tctcctctct gccatttctt ggctgggagc tgtggtccac ctcaaaaaa				1141
aggagcactc tggaggacac gttttcccac ctgttggtct ccgtgtctgc tgactgaggg				1201
cattcaggag taaatgcaca ggctcggtcca ggcccgtctg ggtttgggat gcactgagtt				1261
ggaggttatg aaagctttga tcctcttctt cctctgctgg gcctcgcagc attccaagg				1321
gtcacatgcc ctggcatggg cagaaactgg gctaattgatt ctttgccac ttcaccctc				1381
gtgtctctct ttgttgctaa gttctttccc tcttggaagg acagatctgc cgggctgcta				1441
tttatagttg cctttggcct ttcactgctc tgcgatttgg caggaaataa ggcgattaac				1501
cctatgtgtc cacaagcctc aagccttggt tcaggtcacc ctcaaatac actctcttta				1561
ggcaaaacag gaaacttctt aagtgacaaa ttttaatgcc agacatttaa ggagaggatt				1621
attgttgatt ccatttactc atgcttgcaa aactagagac ccctaaggca gaactgagaa				1681
taaacatggt tactttgggc caaaaaaaaa				1711

<210> 397
 <211> 453
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (90) .. (407)

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gcagtgtttt gccttcaccc caagtgacc atg aga ggt gcc acg cga gtc tca	113
Met Arg Gly Ala Thr Arg Val Ser	
1 5	
atc atg ctc ctc cta gta act gtg tct gac tgt gct gtg atc aca ggg	161
Ile Met Leu Leu Leu Val Thr Val Ser Asp Cys Ala Val Ile Thr Gly	

9	14	19	24	
gcc tgt gag cgg gat gtc cag tgt ggg gca ggc acc tgc tgt gcc atc				209
Ala Cys Glu Arg Asp Val Gln Cys Gly Ala Gly Thr Cys Cys Ala Ile				
25	30	35	40	
agc ctg tgg ctt cga ggg ctg cgg atg tgc acc ccg ctg ggg cgg gaa				257
Ser Leu Trp Leu Arg Gly Leu Arg Met Cys Thr Pro Leu Gly Arg Glu				
41	46	51	56	
ggc gag gag tgc cac ccc ggc agc cac aag atc ccc ttc ttc agg aaa				305
Gly Glu Glu Cys His Pro Gly Ser His Lys Ile Pro Phe Phe Arg Lys				
57	62	67	72	
cgc aag cac cac acc tgt cct tgc ttg ccc aac ctg ctg tgc tcc agg				353
Arg Lys His His Thr Cys Pro Cys Leu Pro Asn Leu Leu Cys Ser Arg				
73	78	83	88	
ttc ccg gac ggc agg tac cgc tgc tcc atg gac ttg aag aac atc aat				401
Phe Pro Asp Gly Arg Tyr Arg Cys Ser Met Asp Leu Lys Asn Ile Asn				
89	94	99	104	
ttt tag gcgcttgccct ggtctcagga taccacccat tcttttctg agcaca				453
Phe *				
105				

<210> 398
 <211> 1735
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (473)..(1201)

<400> 398	
cccggtcgac cccacgcgtc cggcggcgct cggctcggct cgggcatttc cgcctctttg	60
ttttaaaactc cggacgggct tttttctcct cctcttgggg gggaccacaga gggagcggcg	120
ccccctcccc cctcgggcgc ggaccccgcg tgcgccttgc tcgcccgcag ccccgagacc	180
gcaggcgtca caatgtagca gggaccccgag gcgtcgtgct cagaaaatgg aaaaagagcc	240
agggccggaa ggagggtgca gaagcgagtc cgcgtgcgga gccaggaggc agcgtcgcgt	300
gggagtgcctg gcctgaagcc tccatgcccc ggcagaggga cggacacgcg gacgtctagc	360
ggaggctccc gtgtcctcag tatgcatcag gtctcccgaa cctcacagcc ccgcaggag	420
gaggagaagg ggaggatttg actttggaag tctctgtgac cagaagccaa ag atg	475
	Met
	1

ttg acc agg aag atc aag ctg tgg gac atc aac gcc cac atc acc tgc	523
Leu Thr Arg Lys Ile Lys Leu Trp Asp Ile Asn Ala His Ile Thr Cys	
2 7 12 17	
cgc ctg tgc agc ggg tac ctc atc gac gcc acc acg gtg acc gag tgt	571
Arg Leu Cys Ser Gly Tyr Leu Ile Asp Ala Thr Thr Val Thr Glu Cys	
18 23 28 33	
ctg cac acc ttc tgc agg agc tgc ctg gtg aag tac ctg gag gag aac	619
Leu His Thr Phe Cys Arg Ser Cys Leu Val Lys Tyr Leu Glu Glu Asn	
34 39 44 49	
atc acc tgc ccc acc tgc agg att gtg atc cac cag agc cac ccc ctg	667
Ile Thr Cys Pro Thr Cys Arg Ile Val Ile His Gln Ser His Pro Leu	
50 55 60 65	
cag tac atc ggt cat gac aga acc atg caa gat att gtt tac aaa ttg	715
Gln Tyr Ile Gly His Asp Arg Thr Met Gln Asp Ile Val Tyr Lys Leu	
66 71 76 81	
gta cca ggc ctc caa gaa gcg gaa atg aga aag cag agg gag ttc tat	763
Val Pro Gly Leu Gln Glu Ala Glu Met Arg Lys Gln Arg Glu Phe Tyr	
82 87 92 97	
cac aaa ttg ggc atg gag gtg ccg gga gac atc aag ggg gag acc tgc	811
His Lys Leu Gly Met Glu Val Pro Gly Asp Ile Lys Gly Glu Thr Cys	
98 103 108 113	
tct gca aaa cag cac tta gat tcc cat cgg aat ggt gaa acc aaa gca	859
Ser Ala Lys Gln His Leu Asp Ser His Arg Asn Gly Glu Thr Lys Ala	
114 119 124 129	
gac gac agt tca aac aaa gag gcc gcg gag gag aag ccg gag gag gac	907
Asp Asp Ser Ser Asn Lys Glu Ala Ala Glu Glu Lys Pro Glu Glu Asp	
130 135 140 145	
aac gac tac cac cgc agc gac gag cag gtg agc atc tgc ctg gag tgt	955
Asn Asp Tyr His Arg Ser Asp Glu Gln Val Ser Ile Cys Leu Glu Cys	
146 151 156 161	
aac agc agc aaa ctg cgc ggg ctg aag cgg aag tgg atc cgc tgc tca	1003
Asn Ser Ser Lys Leu Arg Gly Leu Lys Arg Lys Trp Ile Arg Cys Ser	
162 167 172 177	
gcc cag gcg acc gtc ttg cat ctg aag aag ttc atc gcc aaa aaa ctc	1051
Ala Gln Ala Thr Val Leu His Leu Lys Lys Phe Ile Ala Lys Lys Leu	
178 183 188 193	
aac ctt tca tcc ttt aac gag ctg gac att tta tgc aac gag gag atc	1099
Asn Leu Ser Ser Phe Asn Glu Leu Asp Ile Leu Cys Asn Glu Glu Ile	
194 199 204 209	
ctg ggc aag gac cac aca ctc aag ttc gtg gtt gtc act agg tgg aga	1147
Leu Gly Lys Asp His Thr Leu Lys Phe Val Val Val Thr Arg Trp Arg	
210 215 220 225	

ttc aag aag gcg ccg ctc ctg ctg cac tac aga ccc aag atg gac ttg 1195
 Phe Lys Lys Ala Pro Leu Leu Leu His Tyr Arg Pro Lys Met Asp Leu
 226 231 236 241
 ctg tga atggtgccac acagcgccca cagactgggc cctcgacccc ttgggtgctc 1251
 Leu *
 242
 cgggccgccg cgcttaagaa cattgcctct ggggtgcatg tggaccagac ttctgaatag 1311
 agaataattta taacttttgt atgagagaga attcacactc aacaagacac taccagcacc 1371
 acgtttacag aggatgaaaa cacttcacag tctcccagag ccgatcgtcc tctccccgc 1431
 cccaccccggt gcttcagcct tgcagggaga gtgatgctcc aggcaacacg gttctgagtc 1491
 accttctgac acgagctccc tctgcttgct ttccaggtct tgaaaatctg aattcacttc 1551
 agtttagttt atgaatttta ggtttcatga taagcctcaa ttgtagttgg acttttattg 1611
 aatccttcct aagttattga aaaaatgtct tttcatgggtg aatgacaata tttatgttgc 1671
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 aaaa 1735

<210> 399
 <211> 1185
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (6) .. (1139)

<400> 399
 gcggt atg ccg cac gag gtg gta cgc gat gag aac agc agc gtc tac 47
 Met Pro His Glu Val Val Arg Asp Glu Asn Ser Ser Val Tyr
 1 5 10
 gcc gag gtc tcc cgg ctg ctc ctc gcc acc ggc cac tgg aag agg ctg 95
 Ala Glu Val Ser Arg Leu Leu Leu Ala Thr Gly His Trp Lys Arg Leu
 15 20 25 30
 cgg cga gac aac ccc aga ttc aac ctg atg ctg gga gag agg aat cgg 143
 Arg Arg Asp Asn Pro Arg Phe Asn Leu Met Leu Gly Glu Arg Asn Arg
 31 36 41 46
 ctg ccc ttc ggg aga ctg ggt cac gag ccc ggg ctg gta cag ttg gtg 191
 Leu Pro Phe Gly Arg Leu Gly His Glu Pro Gly Leu Val Gln Leu Val
 47 52 57 62
 aat tac tac agg ggt gct gac aaa ctg tgt cgc aaa gct tct tta gtg 239
 Asn Tyr Tyr Arg Gly Ala Asp Lys Leu Cys Arg Lys Ala Ser Leu Val

63	68	73	78	
aag cta atc aag aca agc cct gaa ctg gct gag tcc tgc aca tgg ttc				287
Lys Leu Ile Lys Thr Ser Pro Glu Leu Ala Glu Ser Cys Thr Trp Phe				
79	84	89	94	
cct gaa tct tat gtg att tat cca acc aat ctc aag act cca gtt gct				335
Pro Glu Ser Tyr Val Ile Tyr Pro Thr Asn Leu Lys Thr Pro Val Ala				
95	100	105	110	
cca gca cag aat gga att cag cca cca atc agt aac tca agg aca gat				383
Pro Ala Gln Asn Gly Ile Gln Pro Pro Ile Ser Asn Ser Arg Thr Asp				
111	116	121	126	
gaa aga gaa ttc ttt ctc gcc tct tat aac aga aag aaa gag gat gga				431
Glu Arg Glu Phe Phe Leu Ala Ser Tyr Asn Arg Lys Lys Glu Asp Gly				
127	132	137	142	
gag ggc aac gtt tgg att gca aag tca tca gcc ggt gcc aaa ggt gaa				479
Glu Gly Asn Val Trp Ile Ala Lys Ser Ser Ala Gly Ala Lys Gly Glu				
143	148	153	158	
ggc att ctc atc tcc tca gag gct tca gag ctt ctc gat ttc ata gac				527
Gly Ile Leu Ile Ser Ser Glu Ala Ser Glu Leu Leu Asp Phe Ile Asp				
159	164	169	174	
aac cag ggc caa gtg cac gtg atc cag aaa tat ctt gag cac cct ctg				575
Asn Gln Gly Gln Val His Val Ile Gln Lys Tyr Leu Glu His Pro Leu				
175	180	185	190	
ctg ctt gag cca ggt cat cgc aag ttt gac atc cga agc tgg gtc ttg				623
Leu Leu Glu Pro Gly His Arg Lys Phe Asp Ile Arg Ser Trp Val Leu				
191	196	201	206	
gtg gat cat cag tat aat atc tac ctc tat aga gag ggt gtg ctt cgg				671
Val Asp His Gln Tyr Asn Ile Tyr Leu Tyr Arg Glu Gly Val Leu Arg				
207	212	217	222	
act gct tca gaa cca tat cat gtt gat aat ttc caa gac aaa acc tgc				719
Thr Ala Ser Glu Pro Tyr His Val Asp Asn Phe Gln Asp Lys Thr Cys				
223	228	233	238	
cat ttg acc aat cac tgc att caa aaa gag tat tca aag aac tac ggg				767
His Leu Thr Asn His Cys Ile Gln Lys Glu Tyr Ser Lys Asn Tyr Gly				
239	244	249	254	
aag tat gaa gaa gga aat gaa atg ttc ttc aag gag ttc aat cag tac				815
Lys Tyr Glu Glu Gly Asn Glu Met Phe Phe Lys Glu Phe Asn Gln Tyr				
255	260	265	270	
cta aca agt gct ttg aac att acc cta gaa agt agt atc tta cta caa				863
Leu Thr Ser Ala Leu Asn Ile Thr Leu Glu Ser Ser Ile Leu Leu Gln				
271	276	281	286	
atc aaa cat ata ata agg aac tgc ctc ctg agc gtg gag cct gcc att				911
Ile Lys His Ile Ile Arg Asn Cys Leu Leu Ser Val Glu Pro Ala Ile				
287	292	297	302	

agc acc aag cac ctc cct tac cag agc ttc cag ctc ttc ggc ttt gac	959
Ser Thr Lys His Leu Pro Tyr Gln Ser Phe Gln Leu Phe Gly Phe Asp	
303 308 313 318	
ttc atg gtc gac gag gag ctg aag gtg tgg ctc att gag gtc aac ggt	1007
Phe Met Val Asp Glu Glu Leu Lys Val Trp Leu Ile Glu Val Asn Gly	
319 324 329 334	
gcc cct gca tgt gct cag aag ctc tat gca gaa ctg tgc caa ggc atc	1055
Ala Pro Ala Cys Ala Gln Lys Leu Tyr Ala Glu Leu Cys Gln Gly Ile	
335 340 345 350	
gtg gac ata gcc att tcc agt gtc ttc cca ccc cca gat gtg gag caa	1103
Val Asp Ile Ala Ile Ser Ser Val Phe Pro Pro Pro Asp Val Glu Gln	
351 356 361 366	
cct cag acc cag cca gct gcc ttc atc aag ctg tga caga gggcactccc	1153
Pro Gln Thr Gln Pro Ala Ala Phe Ile Lys Leu *	
367 372 377	
tgctgccttg gaaaaagcac ggtgtactgc tc	1185

<210> 400
 <211> 1986
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (251)..(916)

<400> 400	
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cgcgtcggag cctcggcggc ggcggcggtg cttacagcct gagaagagcg tctcgcccgg	120
gagcggcggc ggccatcgag acccacccaa ggcgcggtccc cctcggcctc ccagcgctcc	180
caagccgtag cggccgcgcc cttcagcta gctcgctcgc tcgctctgct tccctgctgc	240
cggctgcgcc atg gcg ttg gcg ttg gcg gcg ctg gcg gcg gtc gag ccg	289
Met Ala Leu Ala Leu Ala Ala Leu Ala Ala Val Glu Pro	
1 5 10	
gcc tgc ggc agc cgg tac cag cag ttg cag aat gaa gaa gag tct gga	337
Ala Cys Gly Ser Arg Tyr Gln Gln Leu Gln Asn Glu Glu Glu Ser Gly	
14 19 24 29	
gaa cct gaa cag gct gca ggt gat gct cct cca cct tac agc agc att	385
Glu Pro Glu Gln Ala Ala Gly Asp Ala Pro Pro Pro Tyr Ser Ser Ile	
30 35 40 45	
tct gca gag agc gca gca tat ttt gac tac aag gat gag tct ggg ttt	433

Ser	Ala	Glu	Ser	Ala	Ala	Tyr	Phe	Asp	Tyr	Lys	Asp	Glu	Ser	Gly	Phe	
46					51					56					61	
cca	aag	ccc	cca	tct	tac	aat	gta	gct	aca	aca	ctg	ccc	agt	tat	gat	481
Pro	Lys	Pro	Pro	Ser	Tyr	Asn	Val	Ala	Thr	Thr	Leu	Pro	Ser	Tyr	Asp	
62					67					72					77	
gaa	gcg	gag	agg	acc	aag	gct	gaa	gct	act	atc	cct	ttg	gtt	cct	ggg	529
Glu	Ala	Glu	Arg	Thr	Lys	Ala	Glu	Ala	Thr	Ile	Pro	Leu	Val	Pro	Gly	
78					83					88					93	
aga	gat	gag	gat	ttt	gtg	ggg	cgg	gat	gat	ttt	gat	gat	gct	gac	cag	577
Arg	Asp	Glu	Asp	Phe	Val	Gly	Arg	Asp	Asp	Phe	Asp	Asp	Ala	Asp	Gln	
94					99					104					109	
ctg	agg	ata	gga	aat	gat	ggg	att	ttc	atg	tta	act	ttt	ttc	atg	gca	625
Leu	Arg	Ile	Gly	Asn	Asp	Gly	Ile	Phe	Met	Leu	Thr	Phe	Phe	Met	Ala	
110					115					120					125	
ttc	ctc	ttt	aac	tgg	att	ggg	ttt	ttc	ctg	tct	ttt	tgc	ctg	acc	act	673
Phe	Leu	Phe	Asn	Trp	Ile	Gly	Phe	Phe	Leu	Ser	Phe	Cys	Leu	Thr	Thr	
126					131					136					141	
tca	gct	gca	gga	agg	tat	ggg	gcc	att	tca	gga	ttt	ggg	ctc	tct	cta	721
Ser	Ala	Ala	Gly	Arg	Tyr	Gly	Ala	Ile	Ser	Gly	Phe	Gly	Leu	Ser	Leu	
142					147					152					157	
att	aaa	tgg	atc	ctg	att	gtc	agg	ttt	tcc	acc	tat	ttc	cct	gga	tat	769
Ile	Lys	Trp	Ile	Leu	Ile	Val	Arg	Phe	Ser	Thr	Tyr	Phe	Pro	Gly	Tyr	
158					163					168					173	
ttt	gat	ggg	cag	tac	tgg	ctc	tgg	tgg	gtg	ttc	ctt	ggt	tta	ggc	ttt	817
Phe	Asp	Gly	Gln	Tyr	Trp	Leu	Trp	Trp	Val	Phe	Leu	Val	Leu	Gly	Phe	
174					179					184					189	
ctc	ctg	ttt	ctc	aga	gga	ttt	atc	aat	tat	gca	aaa	ggt	cgg	aag	atg	865
Leu	Leu	Phe	Leu	Arg	Gly	Phe	Ile	Asn	Tyr	Ala	Lys	Val	Arg	Lys	Met	
190					195					200					205	
cca	gaa	act	ttc	tca	aat	ctc	ccc	agg	acc	aga	ggt	ctc	ttt	att	tat	913
Pro	Glu	Thr	Phe	Ser	Asn	Leu	Pro	Arg	Thr	Arg	Val	Leu	Phe	Ile	Tyr	
206					211					216					221	
taa	agat	gttttctggc	aaaggccttc	ctgcatttat	gaattctctc	tcaagaagca										970
*																
222																
agagaacacc	tgaggaagt	gaatcaagat	gcagaacaca	gaggaataat	cacctgcttt											1030
aaaaaaataa	agtactgttg	aaaagatcat	ttctctctat	ttgttcctag	gtgtaaaatt											1090
ttaatagtta	atgcagaatt	ctgtaatcat	tgaatcatta	gtggttaatg	tttgaaaaag											1150
ctcttgcaat	caagtctgtg	atgtattaat	aatgccttat	atattgtttg	tagtcatttt											1210
aagtagcatg	agccatgtcc	ctgtagtcgg	tagggggcag	tcttgcttta	ttcatcctcc											1270

atctcaaaat gaacttgga ttaaatttg taagatatgt ataatgctgg ccatttttaa 1330
 ggggttttct caaaagttaa acttttggtg tgactgtgtt tttgcacata atccatattt 1390
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 catataattt ttatagcctg tattcacaat tctgcggtac cttattgtac ctaagggatt 1570
 ctaaagggtg tgctactgta taaaacagaa agcactagga tacaaatgaa gcttaattac 1630
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 cccccccctt attttccttt tgtctcctgg tgattaggcc aaagtctggg agtaaggaga 1750
 ggattaggtg cttaggagca aagaaagaag tagcttgga cttttgagat gatccctaac 1810
 atactgtact acttgctttt acaatgtggt agcagaaacc agtgggttat aatgtagaat 1870
 gatgtgcttt ctgccaagt ggtaattcat cttggtttgc tatgttaaaa ctgtaaatac 1930
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 Met Ala Leu Ala
 1
 tcc ggg ccc gca agg cgg gcg cta gct ggc tcc ggg cag ctg ggc ctt 162
 Ser Gly Pro Ala Arg Arg Ala Leu Ala Gly Ser Gly Gln Leu Gly Leu
 5 10 15 20
 ggg ggc ttc ggg gcc ccg aga cgc ggg gcg tat gag tgg ggc gtg cgc 210
 Gly Gly Phe Gly Ala Pro Arg Arg Gly Ala Tyr Glu Trp Gly Val Arg
 21 26 31 36
 tcc acg cgg aag tcg gag cct cct ccc ctg gat agg gtg tac gag atc 258
 Ser Thr Arg Lys Ser Glu Pro Pro Pro Leu Asp Arg Val Tyr Glu Ile
 37 42 47 52
 cct gga ctg gag ccc atc acc ttt gcg ggg aag atg cac ttc gtg ccc 306
 Pro Gly Leu Glu Pro Ile Thr Phe Ala Gly Lys Met His Phe Val Pro

53	58	63	68	
tgg ctg gcg cgg ccg atc ttt ccg ccc tgg gac cgc ggc tac aag gac				354
Trp Leu Ala Arg Pro Ile Phe Pro Pro Trp Asp Arg Gly Tyr Lys Asp				
69	74	79	84	
cca agg ttc tac cgc tgc ccc cct ctt cac gag cat ccg ctg tac aaa				402
Pro Arg Phe Tyr Arg Ser Pro Pro Leu His Glu His Pro Leu Tyr Lys				
85	90	95	100	
gac cag gcc tgc tat atc ttt cac cac cgt tgc cgc ctt ctc gag ggt				450
Asp Gln Ala Cys Tyr Ile Phe His His Arg Cys Arg Leu Leu Glu Gly				
101	106	111	116	
gta aag cag gcc ctc tgg ctc acc aag acc aag tta ata gaa ggc ctt				498
Val Lys Gln Ala Leu Trp Leu Thr Lys Thr Lys Leu Ile Glu Gly Leu				
117	122	127	132	
ccc gag aaa gtg ctt agc ctt gtt gat gat cca agg aac cac ata gag				546
Pro Glu Lys Val Leu Ser Leu Val Asp Asp Pro Arg Asn His Ile Glu				
133	138	143	148	
aac caa gac gag tgc gtt ctg aat gtg atc tct cac gcc cgt ctc tgg				594
Asn Gln Asp Glu Cys Val Leu Asn Val Ile Ser His Ala Arg Leu Trp				
149	154	159	164	
cag acc act gag gaa atc ccc aag aga gag acc tac tgc ccg gtc atc				642
Gln Thr Thr Glu Glu Ile Pro Lys Arg Glu Thr Tyr Cys Pro Val Ile				
165	170	175	180	
gtg gac aac cta ata cag ctg tgt aaa tct cag att ctc aag cat cct				690
Val Asp Asn Leu Ile Gln Leu Cys Lys Ser Gln Ile Leu Lys His Pro				
181	186	191	196	
tct ctg gcc agg agg atc tgt gtc caa aac tcc acg ttt tct gct acc				738
Ser Leu Ala Arg Arg Ile Cys Val Gln Asn Ser Thr Phe Ser Ala Thr				
197	202	207	212	
tgg aac cga gag tct ctt ctc ctt caa gtc cgt ggt tct ggt gga gcc				786
Trp Asn Arg Glu Ser Leu Leu Leu Gln Val Arg Gly Ser Gly Gly Ala				
213	218	223	228	
cga ctg agc act aag gat cct ctg ccc acc atc gcc tcc aga gag gag				834
Arg Leu Ser Thr Lys Asp Pro Leu Pro Thr Ile Ala Ser Arg Glu Glu				
229	234	239	244	
att gaa gct act aag aat cat gtt cta gag acc ttc tac ccc ata tca				882
Ile Glu Ala Thr Lys Asn His Val Leu Glu Thr Phe Tyr Pro Ile Ser				
245	250	255	260	
ccc atc atc gat ctt cat gaa tgc aat att tat gat gtg aaa aat gac				930
Pro Ile Ile Asp Leu His Glu Cys Asn Ile Tyr Asp Val Lys Asn Asp				
261	266	271	276	
aca gga ttc cag gaa ggc tat cct tac ccc tat ccc cat acc ctg tac				978
Thr Gly Phe Gln Glu Gly Tyr Pro Tyr Pro Tyr Pro His Thr Leu Tyr				
277	282	287	292	

tta ctg gac aaa gcc aat tta cga cca cac cgc ctt caa cca gat cag	1026
Leu Leu Asp Lys Ala Asn Leu Arg Pro His Arg Leu Gln Pro Asp Gln	
293 298 303 308	
ctg cgg gcc aag atg atc ctg ttt gct ttt ggc agt gcc ctg gct cag	1074
Leu Arg Ala Lys Met Ile Leu Phe Ala Phe Gly Ser Ala Leu Ala Gln	
309 314 319 324	
gcc cgg ctc ctc tat ggg aat gat gcc aag gtc ttg gag cag ccc gtg	1122
Ala Arg Leu Leu Tyr Gly Asn Asp Ala Lys Val Leu Glu Gln Pro Val	
325 330 335 340	
gtg gtg cag agc gtg ggc acg gat gga cgt gtc ttc cat ttc cta gtg	1170
Val Val Gln Ser Val Gly Thr Asp Gly Arg Val Phe His Phe Leu Val	
341 346 351 356	
ttt caa ctg aat acc aca gac ctg gac tgt aac gag ggt gtc aag aat	1218
Phe Gln Leu Asn Thr Thr Asp Leu Asp Cys Asn Glu Gly Val Lys Asn	
357 362 367 372	
ttg gcc tgg gtg gac tca gac cag ctc ctc tat cag cat ttt tgg tgt	1266
Leu Ala Trp Val Asp Ser Asp Gln Leu Leu Tyr Gln His Phe Trp Cys	
373 378 383 388	
ctc cca gtg atc aaa aag aga gtg gtt gtg gaa cct gtt ggg cca gtt	1314
Leu Pro Val Ile Lys Lys Arg Val Val Val Glu Pro Val Gly Pro Val	
389 394 399 404	
ggg ttc aag cca gag aca ttc aga aag ttt tta gct cta tat ttg cat	1362
Gly Phe Lys Pro Glu Thr Phe Arg Lys Phe Leu Ala Leu Tyr Leu His	
405 410 415 420	
ggg gct gcg tga gca gaggaccct ctgaatcctg aaaccctct tgcctctctt	1417
Gly Ala Ala *	
421	
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tgacaataaa gagcccttgc gttgcaaaaa aaaaaaa	1514

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ggacattgtg tgggccagag gcaggg atg gtt ggc tat gac ccc aaa cca gat	173
Met Val Gly Tyr Asp Pro Lys Pro Asp	
1 5	
ggc agg aat aac acc aag ttc cag gtg gca gtg gct ggg tct gtg tct	221
Gly Arg Asn Asn Thr Lys Phe Gln Val Ala Val Ala Gly Ser Val Ser	
10 15 20 25	
gga ctt gtt act cgg gcg ctg atc agt ccc ttc gac gtc atc aag atc	269
Gly Leu Val Thr Arg Ala Leu Ile Ser Pro Phe Asp Val Ile Lys Ile	
26 31 36 41	
cgt ttc cag ctt cag cat gag cgc ctg tct cgc agt gac ccc agc gca	317
Arg Phe Gln Leu Gln His Glu Arg Leu Ser Arg Ser Asp Pro Ser Ala	
42 47 52 57	
aag tac cat ggc atc ctc cag gcc tct agg cag att ctg cag gag gag	365
Lys Tyr His Gly Ile Leu Gln Ala Ser Arg Gln Ile Leu Gln Glu Glu	
58 63 68 73	
ggg ccg aca gct ttc tgg aaa gga cac gtc cca gct cag att ctc tcc	413
Gly Pro Thr Ala Phe Trp Lys Gly His Val Pro Ala Gln Ile Leu Ser	
74 79 84 89	
ata ggc tat gga gct gtc caa ttc ttg tca ttt gaa atg ctg acg gag	461
Ile Gly Tyr Gly Ala Val Gln Phe Leu Ser Phe Glu Met Leu Thr Glu	
90 95 100 105	
ctg gtc cac aga ggc agc gtg tac gac gcc cgg gaa ttc tca gtg cac	509
Leu Val His Arg Gly Ser Val Tyr Asp Ala Arg Glu Phe Ser Val His	
106 111 116 121	
ttt gta tgt ggt ggc ctg gct gcc tgt atg gcc acc ctc act gtg cac	557
Phe Val Cys Gly Gly Leu Ala Ala Cys Met Ala Thr Leu Thr Val His	
122 127 132 137	
ccc gtg gat gtt ctg cgc acc cgc ttt gca gct cag ggt gag ccc aag	605
Pro Val Asp Val Leu Arg Thr Arg Phe Ala Ala Gln Gly Glu Pro Lys	
138 143 148 153	
gtc tat aat acg ctg cgc cac gcc gtg ggg acc atg tat agg agc gaa	653
Val Tyr Asn Thr Leu Arg His Ala Val Gly Thr Met Tyr Arg Ser Glu	
154 159 164 169	
ggc ccc cag gtt ttc tac aaa ggc ttg gct ccc acc ttg atc gcc atc	701
Gly Pro Gln Val Phe Tyr Lys Gly Leu Ala Pro Thr Leu Ile Ala Ile	
170 175 180 185	
ttc ccc tac gcc ggg ctg cag ttc tct tgc tac agc tcc ttg aag cac	749
Phe Pro Tyr Ala Gly Leu Gln Phe Ser Cys Tyr Ser Ser Leu Lys His	
186 191 196 201	
ctg tac aag tgg gcc ata cca gcc gaa gga aag aaa aat gag aac ctc	797
Leu Tyr Lys Trp Ala Ile Pro Ala Glu Gly Lys Lys Asn Glu Asn Leu	
202 207 212 217	

caa aac ctg ctt tgt ggc agt gga gct ggt gtc atc agc aag acc ctg	845
Gln Asn Leu Leu Cys Gly Ser Gly Ala Gly Val Ile Ser Lys Thr Leu	
218 223 228 233	
aca tat ccg ctg gac ctc ttc aag aag cgg cta cag gtt gga ggg ttt	893
Thr Tyr Pro Leu Asp Leu Phe Lys Lys Arg Leu Gln Val Gly Gly Phe	
234 239 244 249	
gag cat gcc aga gct gcc ttt ggc cag gta cgg aga tac aag ggc ctc	941
Glu His Ala Arg Ala Ala Phe Gly Gln Val Arg Arg Tyr Lys Gly Leu	
250 255 260 265	
atg gac tgt gcc aag cag gtg cta caa aag gaa ggc gcc ctg ggc ttc	989
Met Asp Cys Ala Lys Gln Val Leu Gln Lys Glu Gly Ala Leu Gly Phe	
266 271 276 281	
ttc aag ggc ctg tcc ccc agc ttg ctg aag gct gcc ctc tcc aca ggc	1037
Phe Lys Gly Leu Ser Pro Ser Leu Leu Lys Ala Ala Leu Ser Thr Gly	
282 287 292 297	
ttc atg ttc ttc tcg tat gaa ttc ttc tgt aat gtc ttc cac tgc atg	1085
Phe Met Phe Phe Ser Tyr Glu Phe Phe Cys Asn Val Phe His Cys Met	
298 303 308 313	
aac agg aca gcc agc cag cgc tga gcgcaggaag gacccaggt cttccctgga	1139
Asn Arg Thr Ala Ser Gln Arg *	
314 319	
ggcagcctcc tgaaggaagg aagattcagt ctccactgag aggtgccgtc tggcccttcc	1199
ctgcaggcca gctgccccaa gcggggtagc agccttgaac ccacccagct gggacaccac	1259
cagaaggtcc agggctctcc ccatgagaga atcagaggga atgcaggacg tggctctatgg	1319
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actgcaaagg aaacagacgc catcctacac ctatcagccc tgccctgccag gagaacagaa	1439
cacactcctg gtctggatgg ggctgctgct tgagtgcaga gggctgcggt aggccctttg	1499
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<220>
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 <222> (266)..(1759)

<400> 403

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cggagatgtc gctcggccgc cttctaccag gagcctgac cgtgccgccc gccgcccgga	180
tgggaccacc agagtgtct aaagtctcca gtgaatattg aattgctgag gattttggga	240
aaagacaaat caaagttccc attcc atg gat ccc tta ggt gca cct tcc cag	292
Met Asp Pro Leu Gly Ala Pro Ser Gln	
1 5	
ttt gtg gat gtg gat aca cta cca agc tgg ggt gac tca tgc caa gat	340
Phe Val Asp Val Asp Thr Leu Pro Ser Trp Gly Asp Ser Cys Gln Asp	
10 15 20 25	
gaa tta aat tcc tct gat act aca gct gaa ata ttt cag gaa gac act	388
Glu Leu Asn Ser Ser Asp Thr Thr Ala Glu Ile Phe Gln Glu Asp Thr	
26 31 36 41	
gtt cga tca cct ttt ctt tat aat aag gac gtc aat gga aaa gtg gtt	436
Val Arg Ser Pro Phe Leu Tyr Asn Lys Asp Val Asn Gly Lys Val Val	
42 47 52 57	
ctt tgg aaa gga gat gtg gca tta ctg aac tgt aca gcc att gtg aat	484
Leu Trp Lys Gly Asp Val Ala Leu Leu Asn Cys Thr Ala Ile Val Asn	
58 63 68 73	
acc agc aat gaa agt ctc aca gat aag aat cct gtg tca gaa agt atc	532
Thr Ser Asn Glu Ser Leu Thr Asp Lys Asn Pro Val Ser Glu Ser Ile	
74 79 84 89	
ttc atg ctt gca ggg cct gat ttg aag gaa gat ctc cag aaa ctt aaa	580
Phe Met Leu Ala Gly Pro Asp Leu Lys Glu Asp Leu Gln Lys Leu Lys	
90 95 100 105	
ggg tgc cga aca ggt gaa gca aaa ttg aca aaa gga ttc aat cta gct	628
Gly Cys Arg Thr Gly Glu Ala Lys Leu Thr Lys Gly Phe Asn Leu Ala	
106 111 116 121	
gcc cgg ttc atc att cac aca gtg gga cct aaa tat aaa agc cgc tat	676
Ala Arg Phe Ile Ile His Thr Val Gly Pro Lys Tyr Lys Ser Arg Tyr	
122 127 132 137	
cgc aca gca gct gag agt tcc ctt tat agc tgc tac aga aac gta ctt	724
Arg Thr Ala Ala Glu Ser Ser Leu Tyr Ser Cys Tyr Arg Asn Val Leu	
138 143 148 153	
caa cta gca aaa gag cag tca atg tct tct gtt ggc ttc tgt gtc atc	772
Gln Leu Ala Lys Glu Gln Ser Met Ser Ser Val Gly Phe Cys Val Ile	
154 159 164 169	
aat tct gca aaa cgt ggt tat cct tta gag gat gca aca cac ata gca	820
Asn Ser Ala Lys Arg Gly Tyr Pro Leu Glu Asp Ala Thr His Ile Ala	
170 175 180 185	
ctt cgc act gta aga aga ttc cta gag att cat ggg gaa acc att gaa	868

Leu	Arg	Thr	Val	Arg	Arg	Phe	Leu	Glu	Ile	His	Gly	Glu	Thr	Ile	Glu	
186					191					196					201	
aaa	gta	gta	ttt	gct	gtc	tct	gat	ctt	gaa	gag	ggg	act	tac	caa	aag	916
Lys	Val	Val	Phe	Ala	Val	Ser	Asp	Leu	Glu	Glu	Gly	Thr	Tyr	Gln	Lys	
202					207					212					217	
ctg	cta	cct	ctc	tac	ttc	cca	agg	tca	tta	aaa	gag	gag	aat	cga	tca	964
Leu	Leu	Pro	Leu	Tyr	Phe	Pro	Arg	Ser	Leu	Lys	Glu	Glu	Asn	Arg	Ser	
218					223					228					233	
ttg	ccc	tac	cta	cct	gca	gat	att	gga	aat	gca	gaa	ggg	gag	cct	gtg	1012
Leu	Pro	Tyr	Leu	Pro	Ala	Asp	Ile	Gly	Asn	Ala	Glu	Gly	Glu	Pro	Val	
234					239					244					249	
gta	cct	gaa	cga	cag	att	aga	ata	agt	gag	aaa	cct	ggg	gct	cca	gaa	1060
Val	Pro	Glu	Arg	Gln	Ile	Arg	Ile	Ser	Glu	Lys	Pro	Gly	Ala	Pro	Glu	
250					255					260					265	
gat	aac	caa	gaa	gag	gag	gat	gaa	ggc	ttg	gga	gtt	gat	ctc	tct	ttc	1108
Asp	Asn	Gln	Glu	Glu	Glu	Asp	Glu	Gly	Leu	Gly	Val	Asp	Leu	Ser	Phe	
266					271					276					281	
att	ggc	tct	cat	gct	ttt	gct	cga	atg	gaa	gga	gat	att	gac	aag	caa	1156
Ile	Gly	Ser	His	Ala	Phe	Ala	Arg	Met	Glu	Gly	Asp	Ile	Asp	Lys	Gln	
282					287					292					297	
aga	aaa	ctg	atc	ctt	cag	gga	caa	tta	tca	gag	gca	gct	ctg	cag	aag	1204
Arg	Lys	Leu	Ile	Leu	Gln	Gly	Gln	Leu	Ser	Glu	Ala	Ala	Leu	Gln	Lys	
298					303					308					313	
cag	cat	caa	aga	aat	tat	aat	cgc	tgg	tta	tgt	caa	gca	cga	gct	gag	1252
Gln	His	Gln	Arg	Asn	Tyr	Asn	Arg	Trp	Leu	Cys	Gln	Ala	Arg	Ala	Glu	
314					319					324					329	
gat	ctg	tct	gat	att	gct	tct	cta	aaa	gcc	tta	tac	caa	aca	ggg	gtt	1300
Asp	Leu	Ser	Asp	Ile	Ala	Ser	Leu	Lys	Ala	Leu	Tyr	Gln	Thr	Gly	Val	
330					335					340					345	
gat	aac	tgt	ggg	cga	aca	gtg	atg	gtg	gta	gtt	gga	aga	aac	att	cct	1348
Asp	Asn	Cys	Gly	Arg	Thr	Val	Met	Val	Val	Val	Gly	Arg	Asn	Ile	Pro	
346					351					356					361	
gta	aca	tta	ata	gat	atg	gac	aag	gct	ctc	tta	tat	ttc	att	cat	gta	1396
Val	Thr	Leu	Ile	Asp	Met	Asp	Lys	Ala	Leu	Leu	Tyr	Phe	Ile	His	Val	
362					367					372					377	
atg	gat	cac	att	gct	gtg	aag	gag	tat	gta	tta	gtg	tat	ttt	cac	acc	1444
Met	Asp	His	Ile	Ala	Val	Lys	Glu	Tyr	Val	Leu	Val	Tyr	Phe	His	Thr	
378					383					388					393	
ctg	acc	agc	gaa	tac	aat	cac	ctg	gac	tcc	gac	ttc	ctg	aag	aaa	ctc	1492
Leu	Thr	Ser	Glu	Tyr	Asn	His	Leu	Asp	Ser	Asp	Phe	Leu	Lys	Lys	Leu	
394					399					404					409	
tac	gat	gtt	gtt	gat	gtc	aag	tac	aag	agg	aat	ttg	aag	gct	gtt	tat	1540
Tyr	Asp	Val	Val	Asp	Val	Lys	Tyr	Lys	Arg	Asn	Leu	Lys	Ala	Val	Tyr	

410	415	420	425	
ttt gta cat ccc aca ttt cgt tca aag gtg tca aca tgg ttt ttt acc				1588
Phe Val His Pro Thr Phe Arg Ser Lys Val Ser Thr Trp Phe Phe Thr				
426	431	436	441	
acc ttt tct gtc tca gga ctg aag gac aaa atc cac cat gtg gac agc				1636
Thr Phe Ser Val Ser Gly Leu Lys Asp Lys Ile His His Val Asp Ser				
442	447	452	457	
ctc cac cag ctg ttt tct gcc ata tca cca gaa cag att gac ttt cct				1684
Leu His Gln Leu Phe Ser Ala Ile Ser Pro Glu Gln Ile Asp Phe Pro				
458	463	468	473	
cct ttt gtc ctt gaa tat gat gcc agg gaa aac ggg cct tac tat aca				1732
Pro Phe Val Leu Glu Tyr Asp Ala Arg Glu Asn Gly Pro Tyr Tyr Thr				
474	479	484	489	
tca tat ccc cca tca cca gat ttg tga cctgc catctttcag tgcttcttg				1784
Ser Tyr Pro Pro Ser Pro Asp Leu *				
490	495			
ttcccaggat gccacttcct ccacgaatag ctacctgttg aagtgatatt cattgttgct				1844
gtacagatcc agagagcctt ttgtccccac ctctctggta tttttttatt gactgtatat				1904
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aacttttgag tatcttttagt ttcttgaagg acaccgaatt ctccattaga taaaccacca				2084
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ccttcaggcc tcaggcagag tcacggtggc agcattgaga gttggacacc cgggtccttg	180
aagtgatctc taggccccag ccccaaatec gccaccattc cgtgctgcgg ggacacc	237
atg gct cca gaa gag gac gct gga ggg gag gcc tta ggg ggc agt ttc	285

Met	Ala	Pro	Glu	Glu	Asp	Ala	Gly	Gly	Glu	Ala	Leu	Gly	Gly	Ser	Phe	
1				5					10					15		
tgg	gag	gct	ggc	aac	tac	agg	cgc	acg	gta	cag	cgg	gtg	gag	gac	ggg	333
Trp	Glu	Ala	Gly	Asn	Tyr	Arg	Arg	Thr	Val	Gln	Arg	Val	Glu	Asp	Gly	
17					22				27						32	
cac	cgg	ctg	tgc	ggg	gac	ctg	gtc	agc	tgc	ttc	cag	gag	cgc	gcc	cgc	381
His	Arg	Leu	Cys	Gly	Asp	Leu	Val	Ser	Cys	Phe	Gln	Glu	Arg	Ala	Arg	
33					38					43					48	
atc	gag	aag	gct	tat	gcc	cag	cag	ttg	gct	gac	tgg	gcc	cga	aag	tgg	429
Ile	Glu	Lys	Ala	Tyr	Ala	Gln	Gln	Leu	Ala	Asp	Trp	Ala	Arg	Lys	Trp	
49					54					59					64	
agg	ggg	acc	gtg	gag	aag	ggc	ccc	cag	tat	ggc	aca	ctg	gag	aag	gcc	477
Arg	Gly	Thr	Val	Glu	Lys	Gly	Pro	Gln	Tyr	Gly	Thr	Leu	Glu	Lys	Ala	
65					70					75					80	
tgg	cat	gcc	ttt	ttc	acg	gcg	gct	gag	cgg	ctg	agc	gcg	ctg	cac	ctg	525
Trp	His	Ala	Phe	Phe	Thr	Ala	Ala	Glu	Arg	Leu	Ser	Ala	Leu	His	Leu	
81					86					91					96	
gag	gtg	cgg	gag	aag	ctg	caa	ggg	cag	gac	agt	gag	cgg	gtg	cgc	gcc	573
Glu	Val	Arg	Glu	Lys	Leu	Gln	Gly	Gln	Asp	Ser	Glu	Arg	Val	Arg	Ala	
97					102					107					112	
tgg	cag	cgg	ggg	gct	ttc	cac	cgg	cct	gtg	ctg	ggc	ggc	ttc	cgc	gag	621
Trp	Gln	Arg	Gly	Ala	Phe	His	Arg	Pro	Val	Leu	Gly	Gly	Phe	Arg	Glu	
113					118					123					128	
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Ser	Arg	Ala	Ala	Glu	Asp	Gly	Phe	Arg	Lys	Ala	Gln	Lys	Pro	Trp	Leu	
129					134					139					144	
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Lys	Arg	Leu	Lys	Glu	Val	Glu	Ala	Ser	Lys	Lys	Ser	Tyr	His	Ala	Ala	
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Asp	Ser	Ala	Val	Ser	Gln	Glu	Gln	Leu	Arg	Lys	Leu	Gln	Glu	Arg	Val	
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Glu	Arg	Cys	Ala	Lys	Glu	Ala	Glu	Lys	Thr	Lys	Ala	Gln	Tyr	Glu	Gln	
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Thr	Leu	Ala	Glu	Leu	His	Arg	Tyr	Thr	Pro	Arg	Tyr	Met	Glu	Asp	Met	
209					214					219					224	
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Glu	Gln	Ala	Phe	Glu	Thr	Cys	Gln	Ala	Ala	Glu	Arg	Gln	Arg	Leu	Leu	

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Ser Ser Glu Lys Phe His Glu Leu His Arg	Asp Leu His Gln Gly Ile			
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Glu Ala Ala Ser Asp Glu Glu Asp Leu Arg	Trp Trp Arg Ser Thr His			
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Asp Thr Gln Arg Thr Ile Ser Arg Lys Glu	Lys Gly Gly Arg Ser Pro			
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Asp Glu Val Thr Leu Thr Ser Ile Val Pro	Thr Arg Asp Gly Thr Ala			
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Pro Pro Pro Gln Ser Pro Gly Ser Pro Gly	Thr Gly Gln Asp Glu Glu			
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Trp Ser Asp Glu Glu Ser Pro Arg Lys Ala	Ala Thr Gly Val Arg Val			
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Arg Ala Leu Tyr Asp Tyr Ala Gly Gln Glu	Ala Asp Glu Leu Ser Phe			
369	374 379 384			
cga gca ggg gag gag ctg ctg aag atg agt	gag gag gac gag cag ggc	1437		
Arg Ala Gly Glu Glu Leu Leu Lys Met Ser	Glu Glu Asp Glu Gln Gly			
385	390 395 400			
tgg tgc caa ggc cag ttg cag agt ggc cgc	att ggc ctg tac cct gcc	1485		
Trp Cys Gln Gly Gln Leu Gln Ser Gly Arg	Ile Gly Leu Tyr Pro Ala			
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aac tac gtg gag tgt gtg ggc gcc tga	gtgtc ctgacagccc ttctgcaacg	1537		
Asn Tyr Val Glu Cys Val Gly Ala *				
417	422			
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 ggggaaggagc ctggacacag tgacacattc tcaaaggccc tgcaggacca cc atg 175
 Met
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 gct tat gat gac tcc gtg aag aaa gaa gat tgt ttt gat ggt gat cat 223
 Ala Tyr Asp Asp Ser Val Lys Lys Glu Asp Cys Phe Asp Gly Asp His
 2 7 12 17
 acc ttt gag gac ata gga ctt gca gct ggc cga agc caa cga gag aaa 271
 Thr Phe Glu Asp Ile Gly Leu Ala Ala Gly Arg Ser Gln Arg Glu Lys
 18 23 28 33
 aaa cgt tct tac aaa gat ttt tta agg gaa gag gaa gaa att gct gct 319
 Lys Arg Ser Tyr Lys Asp Phe Leu Arg Glu Glu Glu Glu Ile Ala Ala
 34 39 44 49
 cag gtc agg aat tct tcc aag aag aag ttg aag gat agt gaa ctt tac 367
 Gln Val Arg Asn Ser Ser Lys Lys Lys Leu Lys Asp Ser Glu Leu Tyr
 50 55 60 65
 ttc ttg ggg acg gac aca cac aag aag aag agg aag cac tcc tct gat 415
 Phe Leu Gly Thr Asp Thr His Lys Lys Lys Arg Lys His Ser Ser Asp
 66 71 76 81
 gat tac tac tat gga gac att tcg tct ttg gaa tcg tca cag aag aaa 463
 Asp Tyr Tyr Tyr Gly Asp Ile Ser Ser Leu Glu Ser Ser Gln Lys Lys
 82 87 92 97
 aag aaa aag tcc agc cca cag tct act gat aca gct atg gac ctg ttg 511
 Lys Lys Lys Ser Ser Pro Gln Ser Thr Asp Thr Ala Met Asp Leu Leu
 98 103 108 113
 aaa gct atc act tcc cca ctg gca gca ggc tcc aag ccc tcc aaa aag 559

Lys	Ala	Ile	Thr	Ser	Pro	Leu	Ala	Ala	Gly	Ser	Lys	Pro	Ser	Lys	Lys	
114					119					124					129	
act	ggg	gag	aaa	tcc	tct	ggc	tct	tca	agc	cat	tcg	gag	agt	aaa	aag	607
Thr	Gly	Glu	Lys	Ser	Ser	Gly	Ser	Ser	Ser	His	Ser	Glu	Ser	Lys	Lys	
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gag	cac	cac	agg	aag	aaa	gtc	agt	gga	agc	agt	ggg	gaa	cta	ccc	cta	655
Glu	His	His	Arg	Lys	Lys	Val	Ser	Gly	Ser	Ser	Gly	Glu	Leu	Pro	Leu	
146					151					156					161	
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Glu	Asp	Gly	Gly	Ser	His	Lys	Ser	Lys	Lys	Met	Lys	Pro	Leu	Tyr	Val	
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Asn	Thr	Glu	Thr	Leu	Thr	Leu	Arg	Glu	Pro	Asp	Gly	Leu	Lys	Met	Lys	
178					183					188					193	
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Leu	Ile	Leu	Ser	Pro	Lys	Glu	Lys	Gly	Ser	Ser	Ser	Val	Asp	Glu	Glu	
194					199					204					209	
tct	ttt	caa	tat	ccc	tcc	caa	caa	gcg	act	gtg	aaa	aaa	tcc	tca	aag	847
Ser	Phe	Gln	Tyr	Pro	Ser	Gln	Gln	Ala	Thr	Val	Lys	Lys	Ser	Ser	Lys	
210					215					220					225	
aaa	tca	gct	cgg	gat	gag	cag	ggg	gct	tta	ctc	cta	gga	cat	gag	tta	895
Lys	Ser	Ala	Arg	Asp	Glu	Gln	Gly	Ala	Leu	Leu	Leu	Gly	His	Glu	Leu	
226					231					236					241	
cag	agc	ttt	ctg	aaa	aca	gcc	cgg	aaa	aag	cac	aag	tca	tcc	tca	gac	943
Gln	Ser	Phe	Leu	Lys	Thr	Ala	Arg	Lys	Lys	His	Lys	Ser	Ser	Ser	Asp	
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Ala	His	Ser	Ser	Pro	Gly	Pro	Glu	Gly	Cys	Gly	Ser	Asp	Ala	Ser	Gln	
258					263					268					273	
ttc	gca	gag	tcc	cac	agt	gct	aac	ctt	gat	ctt	tca	ggg	ctt	gaa	cct	1039
Phe	Ala	Glu	Ser	His	Ser	Ala	Asn	Leu	Asp	Leu	Ser	Gly	Leu	Glu	Pro	
274					279					284					289	
att	ctg	gta	gaa	tca	gac	tca	tcc	tct	ggg	ggg	gaa	cta	gag	gct	ggg	1087
Ile	Leu	Val	Glu	Ser	Asp	Ser	Ser	Ser	Gly	Gly	Glu	Leu	Glu	Ala	Gly	
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gag	tta	gtg	ata	gat	gat	tct	tac	cga	gaa	atc	aag	aag	aaa	aag	aag	1135
Glu	Leu	Val	Ile	Asp	Asp	Ser	Tyr	Arg	Glu	Ile	Lys	Lys	Lys	Lys	Lys	
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Ser	Lys	Lys	Ser	Lys	Lys	Lys	Lys	Asp	Lys	Glu	Lys	His	Lys	Glu	Lys	
322					327					332					337	
cga	cac	tcc	aag	tcc	aag	aga	agt	tta	gga	ctt	tct	gcc	gtg	cca	gtg	1231
Arg	His	Ser	Lys	Ser	Lys	Arg	Ser	Leu	Gly	Leu	Ser	Ala	Val	Pro	Val	

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gga gag gtc aca gtg	aca tct ggc cct cct	ccc agc atc cca tac gct	1279				
Gly Glu Val Thr Val	Thr Ser Gly Pro Pro	Pro Ser Ile Pro Tyr Ala					
354	359	364	369				
gga gca gca gca cct	ccc ctg cca ctt cct	ggc ctc cac aca gat ggg	1327				
Gly Ala Ala Ala Pro	Pro Leu Pro Leu Pro	Gly Leu His Thr Asp Gly					
370	375	380	385				
cat agt gaa aaa aaa	aaa aaa aaa gag aag	gac aaa gag aga gag	1375				
His Ser Glu Lys Lys	Lys Lys Lys Lys Glu	Lys Asp Lys Glu Arg Glu					
386	391	396	401				
aga gga gaa aag cca	aaa aag aag aac atg	tcg gcc tac cag gtg ttc	1423				
Arg Gly Glu Lys Pro	Lys Lys Lys Asn Met	Ser Ala Tyr Gln Val Phe					
402	407	412	417				
tgt aaa gag tat cgc	gtg acc att gtg gct	gac cat cca ggt ata gat	1471				
Cys Lys Glu Tyr Arg	Val Thr Ile Val Ala	Asp His Pro Gly Ile Asp					
418	423	428	433				
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Phe Gly Glu Leu Ser	Lys Lys Leu Ala Glu	Val Trp Lys Gln Leu Pro					
434	439	444	449				
gaa aaa gac aaa ctg	att tgg aag caa aaa	gct cag tat ctg cag cac	1567				
Glu Lys Asp Lys Leu	Ile Trp Lys Gln Lys	Ala Gln Tyr Leu Gln His					
450	455	460	465				
aaa cag aac aaa gca	gaa gcc aca act gtg	aaa agg aaa gca tcc agc	1615				
Lys Gln Asn Lys Ala	Glu Ala Thr Thr Val	Lys Arg Lys Ala Ser Ser					
466	471	476	481				
tca gaa ggt tcc atg	aaa gtc aaa gcc tct	tct gta gga gta ctg tca	1663				
Ser Glu Gly Ser Met	Lys Val Lys Ala Ser	Ser Val Gly Val Leu Ser					
482	487	492	497				
ccc cag aag aag tcc	cca ccc acc acc atg	ctg tta cca gcc tca cca	1711				
Pro Gln Lys Lys Ser	Pro Pro Thr Thr Met	Leu Leu Pro Ala Ser Pro					
498	503	508	513				
gcc aaa gcc cct gag	aca gag ccc att gat	gtt gct gct cat ctt cag	1759				
Ala Lys Ala Pro Glu	Thr Glu Pro Ile Asp	Val Ala Ala His Leu Gln					
514	519	524	529				
ctg ttg gga gag tcc	cta agc ctc att gga	cac cgt ctg cag gaa act	1807				
Leu Leu Gly Glu Ser	Leu Ser Leu Ile Gly	His Arg Leu Gln Glu Thr					
530	535	540	545				
gag ggt atg gtg gct	gtg tct ggc agt ttg	tca gtg ctt ctg gat tcc	1855				
Glu Gly Met Val Ala	Val Ser Gly Ser Leu	Ser Val Leu Leu Asp Ser					
546	551	556	561				
att atc tgt gcc ctt	ggc ccc ttg gca tgt	ctc acc aca caa cta cct	1903				
Ile Ile Cys Ala Leu	Gly Pro Leu Ala Cys	Leu Thr Thr Gln Leu Pro					
562	567	572	577				

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Val Ala Asp His Pro Lys Arg Phe Ser Ala Asp Cys Cys Val Leu Gly				
42	47	52	57	
gcc cag ggc ttc cgc tcc ggc cgg cac tac tgg gag gta gag gtg ggc				425
Ala Gln Gly Phe Arg Ser Gly Arg His Tyr Trp Glu Val Glu Val Gly				
58	63	68	73	
ggg cgg cgg ggc tgg gcg gtg ggt gct gcc cgt gaa tca acc cat cat				473
Gly Arg Arg Gly Trp Ala Val Gly Ala Ala Arg Glu Ser Thr His His				
74	79	84	89	
aag gaa aag gtg ggc cct ggg ggt tcc tcc gtg ggc agc ggg gat gcc				521
Lys Glu Lys Val Gly Pro Gly Gly Ser Ser Val Gly Ser Gly Asp Ala				
90	95	100	105	
agc tcc tgc cgc cat cac cat cgc cgc cgc cgg ctc cac ctg ccc cag				569
Ser Ser Ser Arg His His His Arg Arg Arg Arg Leu His Leu Pro Gln				
106	111	116	121	
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Gln Pro Leu Leu Gln Arg Glu Val Trp Cys Val Gly Thr Asn Gly Lys				
122	127	132	137	
cgc tat cag gcc cag agc tcc aca gaa cag acg ctg ctg agc ccc agt				665
Arg Tyr Gln Ala Gln Ser Ser Thr Glu Gln Thr Leu Leu Ser Pro Ser				
138	143	148	153	
gag aaa cca agg cgc ttt ggt gtg tac ctg gac tat gaa gct ggg cgc				713
Glu Lys Pro Arg Arg Phe Gly Val Tyr Leu Asp Tyr Glu Ala Gly Arg				
154	159	164	169	
ctg ggc ttc tac aac gca gag act cta gcc cac gtg cac acc ttc tgc				761
Leu Gly Phe Tyr Asn Ala Glu Thr Leu Ala His Val His Thr Phe Ser				
170	175	180	185	
gct gcc ttc ctg ggc gag cgt gtc ttt cct ttc ttc cgg gtg ctc tcc				809
Ala Ala Phe Leu Gly Glu Arg Val Phe Pro Phe Phe Arg Val Leu Ser				
186	191	196	201	
aag ggc acc cgc atc aag ctc tgc cct tga t taccctgccca cccgcagggg				860
Lys Gly Thr Arg Ile Lys Leu Cys Pro *				
202	207			
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Gly Leu Pro Glu Thr Arg Thr Asp Ala Ala Met Ser Glu Leu Val Pro	
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Glu Pro Arg Pro Lys Pro Ala Val Pro Met Lys Pro Met Ser Ile Asn	
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Ser Asn Leu Leu Gly Tyr Ile Gly Ile Asp Thr Ile Ile Glu Gln Met	
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Gly	Gln	Ser	Gly	Leu	Gly	Lys	Ser	Thr	Leu	Val	Asn	Thr	Leu	Phe	Lys	
68					73					78					83	
tcc	caa	gtg	agc	cgc	aag	gcc	tcc	agc	tgg	aac	cgg	gag	gag	aag	atc	464
Ser	Gln	Val	Ser	Arg	Lys	Ala	Ser	Ser	Trp	Asn	Arg	Glu	Glu	Lys	Ile	
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ccc	aag	aca	gtg	gag	atc	aaa	gct	atc	ggg	cat	gtg	ata	gag	gaa	ggc	512
Pro	Lys	Thr	Val	Glu	Ile	Lys	Ala	Ile	Gly	His	Val	Ile	Glu	Glu	Gly	
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ggt	gtc	aaa	atg	aag	ctg	acc	gtc	atc	gac	acc	cca	ggc	ttt	gga	gac	560
Gly	Val	Lys	Met	Lys	Leu	Thr	Val	Ile	Asp	Thr	Pro	Gly	Phe	Gly	Asp	
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caa	atc	aac	aat	gaa	aac	tgc	tgg	gag	ccc	att	gag	aag	tac	atc	aat	608
Gln	Ile	Asn	Asn	Glu	Asn	Cys	Trp	Glu	Pro	Ile	Glu	Lys	Tyr	Ile	Asn	
132					137					142					147	
gag	cag	tac	gag	aag	ttc	ctg	aag	gag	gag	gtc	aac	atc	gcc	agg	aag	656
Glu	Gln	Tyr	Glu	Lys	Phe	Leu	Lys	Glu	Glu	Val	Asn	Ile	Ala	Arg	Lys	
148					153					158					163	
aaa	cgc	atc	cct	gac	act	cgt	gtc	cac	tgc	tgc	ctt	tac	ttc	atc	tct	704
Lys	Arg	Ile	Pro	Asp	Thr	Arg	Val	His	Cys	Cys	Leu	Tyr	Phe	Ile	Ser	
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ccc	aca	gga	cac	tcc	ttg	cga	cct	ctg	gat	ctt	gag	ttc	atg	aaa	cac	752
Pro	Thr	Gly	His	Ser	Leu	Arg	Pro	Leu	Asp	Leu	Glu	Phe	Met	Lys	His	
180					185					190					195	
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Leu	Ser	Lys	Val	Val	Asn	Ile	Ile	Pro	Val	Ile	Ala	Lys	Ala	Asp	Thr	
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atg	acc	ctg	gag	gag	aag	tct	gaa	ttc	aag	caa	agg	gtt	cgc	aag	gag	848
Met	Thr	Leu	Glu	Glu	Lys	Ser	Glu	Phe	Lys	Gln	Arg	Val	Arg	Lys	Glu	
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Leu	Glu	Val	Asn	Gly	Ile	Glu	Phe	Tyr	Pro	Gln	Lys	Glu	Phe	Asp	Glu	
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Pro	Phe	Ala	Val	Val	Gly	Ser	Asp	Lys	Glu	Tyr	Gln	Val	Asn	Gly	Lys	
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agg	gtc	ctc	ggc	cga	aaa	act	cca	tgg	ggg	atc	atc	gaa	gtg	gaa	aac	1040
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Leu Asn His Cys Glu Phe Ala Leu Leu Arg Asp Phe Val Ile Arg Thr				
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His Leu Gln Asp Leu Lys Glu Val Thr His Asn Ile His Tyr Glu Thr				
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Tyr Arg Ala Lys Arg Leu Asn Asp Asn Gly Gly Leu Pro Pro Val Ser				
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Val Asp Thr Glu Glu Ser His Asp Ser Asn Pro *				
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Ala Glu Gln Pro Met Arg Tyr Glu Thr Leu Phe Gln Ala Leu Asp Arg				

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Asn Gly Asp Gly Val Val Asp Ile Gly Glu Leu Gln Glu Gly Leu Arg				
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Asn Leu Gly Ile Pro Leu Gly Gln Asp Ala Glu Glu Lys Ile Phe Thr				
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act gga gat gtc aac aaa gat ggg aag ctg gat ttt gaa gaa ttt atg				355
Thr Gly Asp Val Asn Lys Asp Gly Lys Leu Asp Phe Glu Glu Phe Met				
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Lys Tyr Leu Lys Asp His Glu Lys Lys Met Lys Leu Ala Phe Lys Ser				
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Leu Asp Lys Asn Asn Asp Gly Lys Ile Glu Ala Ser Glu Ile Val Gln				
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Ser Leu Gln Thr Leu Gly Leu Thr Ile Ser Glu Gln Gln Ala Glu Leu				
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Ile Leu Gln Ser Ile Asp Val Asp Gly Thr Met Thr Val Asp Trp Asn				
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Ile Ser Leu Val Lys Arg Asn Ala Val Leu Pro Ser Lys Pro Leu Gln	
232 237 242 247	
gac aga gaa gct atg gat gat aaa cca ggt gtg agt ggt cag ctt cca	941
Asp Arg Glu Ala Met Asp Asp Lys Pro Gly Val Ser Gly Gln Leu Pro	
248 253 258 263	
aaa gga aaa gct cta gag ctg gct ttg aag aga cca cgg cca cct gtt	989
Lys Gly Lys Ala Leu Glu Leu Ala Leu Lys Arg Pro Arg Pro Pro Val	
264 269 274 279	
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Leu Ser Val Cys Ser Ser Ser Glu Thr Pro Tyr Leu Leu Lys Glu Thr	
280 285 290 295	
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Asn Lys Gly Asn Gly Gln Gly Glu Asp Arg Asn Leu Leu Tyr Tyr Ser	
296 301 306 311	
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Lys Leu Gly Leu Val Ile Pro Ser Ser Gly Ser Gly Ser Gly Asn Gln	
312 317 322 327	
agc att gac agg agt ggc cca ctt gtt aag agt ctc ctc aga cgg tca	1181
Ser Ile Asp Arg Ser Gly Pro Leu Val Lys Ser Leu Leu Arg Arg Ser	
328 333 338 343	
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Leu	Ser	Met	Asp	Ser	Gln	Val	Pro	Val	Tyr	Ser	Pro	Ser	Ile	Asp	Leu
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Lys	Ser	Ser	Gln	Gly	Ile	Ile	Phe	Gly	Val	Gln	*				
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ctaattcggc atg tta aaa aat aag ggt cac tca tct aag aaa gat aac 289
Met Leu Lys Asn Lys Gly His Ser Ser Lys Lys Asp Asn
1 5 10
ttg gca gtc aat gca gtt gct tta caa gat cac att tta cat gat ctt 337
Leu Ala Val Asn Ala Val Ala Leu Gln Asp His Ile Leu His Asp Leu
14 19 24 29
caa ctt cga aat ctt tca gtt gca gat cat tct aag aca caa gta caa 385
Gln Leu Arg Asn Leu Ser Val Ala Asp His Ser Lys Thr Gln Val Gln
30 35 40 45

aag aaa gag aac aaa tct cta aaa aga gat aca aag gca ata ata gat	433
Lys Lys Glu Asn Lys Ser Leu Lys Arg Asp Thr Lys Ala Ile Ile Asp	
46 51 56 61	
act gga ctt aaa aaa act aca cag tgc ccc aaa cta gaa gac tca gaa	481
Thr Gly Leu Lys Lys Thr Thr Gln Cys Pro Lys Leu Glu Asp Ser Glu	
62 67 72 77	
aaa gaa tat gtt ctt gat ccc aaa ccg ccg ccg ttg act ttg gca cag	529
Lys Glu Tyr Val Leu Asp Pro Lys Pro Pro Pro Leu Thr Leu Ala Gln	
78 83 88 93	
aag ttg ggc ctc att ggg cct cca cca cct cca ctg tca tca gat gaa	577
Lys Leu Gly Leu Ile Gly Pro Pro Pro Pro Pro Leu Ser Ser Asp Glu	
94 99 104 109	
tgg gag aag gtg aaa cag cgc tct ctc ctg caa ggg gac tcc gtg caa	625
Trp Glu Lys Val Lys Gln Arg Ser Leu Leu Gln Gly Asp Ser Val Gln	
110 115 120 125	
cca tgc ccc atc tgt aaa gaa gaa ttc gag ctt cgt cct cag gtg ttt	673
Pro Cys Pro Ile Cys Lys Glu Glu Phe Glu Leu Arg Pro Gln Val Phe	
126 131 136 141	
agc ata cga ggg tgc tgc ttt cat gct ccc atg tgt tcc aca aag cat	721
Ser Ile Arg Gly Cys Cys Phe His Ala Pro Met Cys Ser Thr Lys His	
142 147 152 157	
gtc ttc agg ctt ttg aaa agt tca caa ata aga aaa cct gtc ctc tct	769
Val Phe Arg Leu Leu Lys Ser Ser Gln Ile Arg Lys Pro Val Leu Ser	
158 163 168 173	
gta gaa aga acc agt atc aaa ccc gag tga t acacgatggg gcccgccgtg	820
Val Glu Arg Thr Ser Ile Lys Pro Glu *	
174 179	
tcagaatcaa gtgtgtgacc agaatccaag cctactggag aggatgtgtt gttagaaagt	880
ggtacagaaa cctgaggaaa acagtacctc ccacagatgc caagttaaga aaaaaattct	940
ttgaaaaaaaa gttcacagaa atcagccacc gcatcctgtg ctcatacaac accaacattg	1000
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tcatagtcaa gtagagcgag gtcagtctga ggtataaagt tcgccaatcg ttcggtagt	1420
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<400> 412

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gag gac agc ata agc agt act ata atg gat gta gac agc aca att tcc	98
Glu Asp Ser Ile Ser Ser Thr Ile Met Asp Val Asp Ser Thr Ile Ser	
14 19 24 29	
agt ggg cgt tca act cca gca atg atg aat gga caa gga agc act act	146
Ser Gly Arg Ser Thr Pro Ala Met Met Asn Gly Gln Gly Ser Thr Thr	
30 35 40 45	
tct tca agc aaa aat att gcc tat aat tgt tgt tgg gac cag tgc cag	194
Ser Ser Ser Lys Asn Ile Ala Tyr Asn Cys Cys Trp Asp Gln Cys Gln	
46 51 56 61	
gct tgc ttc aac tct agc cca gat ctg gca gat cac atc cgt tcc ata	242
Ala Cys Phe Asn Ser Ser Pro Asp Leu Ala Asp His Ile Arg Ser Ile	
62 67 72 77	
cat gta gat ggt cag cga gga ggg gta ttt gtt tgc tta tgg aaa ggt	290
His Val Asp Gly Gln Arg Gly Gly Val Phe Val Cys Leu Trp Lys Gly	
78 83 88 93	
tgt aaa gta tat aac act cca tct acc agt caa agt tgg tta caa agg	338
Cys Lys Val Tyr Asn Thr Pro Ser Thr Ser Gln Ser Trp Leu Gln Arg	
94 99 104 109	
cat atg ctg aca cac agt gga gac aaa cct ttc aag tgt gtt gtt ggt	386
His Met Leu Thr His Ser Gly Asp Lys Pro Phe Lys Cys Val Val Gly	
110 115 120 125	
ggc tgc aat gcc agc ttt gct tct cag gga ggg cta gct cgt cat gta	434
Gly Cys Asn Ala Ser Phe Ala Ser Gln Gly Gly Leu Ala Arg His Val	
126 131 136 141	
ccc aca cac ttc agt cag cag aac tcc tca aaa gtt tct agc cag cca	482
Pro Thr His Phe Ser Gln Gln Asn Ser Ser Lys Val Ser Ser Gln Pro	
142 147 152 157	
aag gcc aaa gaa gaa tct cct tct aaa gct gga atg aac aaa agg agg	530
Lys Ala Lys Glu Glu Ser Pro Ser Lys Ala Gly Met Asn Lys Arg Arg	
158 163 168 173	

aaa tta aag aac aaa aga cga cgc tca tta cca cgg cca cat gat ttc	578
Lys Leu Lys Asn Lys Arg Arg Arg Ser Leu Pro Arg Pro His Asp Phe	
174 179 184 189	
ttc gat gca caa aca ctg gat gcg ata aga cat cga gcc ata tgc ttt	626
Phe Asp Ala Gln Thr Leu Asp Ala Ile Arg His Arg Ala Ile Cys Phe	
190 195 200 205	
aac ctc tca gct cat ata gaa agt tta ggg aag gga cac agt gtt gtt	674
Asn Leu Ser Ala His Ile Glu Ser Leu Gly Lys Gly His Ser Val Val	
206 211 216 221	
ttt cat agt cct gta ata gct aag aga aaa gaa gat tct ggg aag atc	722
Phe His Ser Pro Val Ile Ala Lys Arg Lys Glu Asp Ser Gly Lys Ile	
222 227 232 237	
aaa ctt ttg ctt cat tgg atg cct gaa gac att ctg cat gat gtg tgg	770
Lys Leu Leu Leu His Trp Met Pro Glu Asp Ile Leu His Asp Val Trp	
238 243 248 253	
gtg aat gaa agt gaa cga cat cag tta aaa act aaa gta gtt cat tta	818
Val Asn Glu Ser Glu Arg His Gln Leu Lys Thr Lys Val Val His Leu	
254 259 264 269	
tca aag cta ccc aaa gat act gcc ttg ctt ttg gac cca aac ata tac	866
Ser Lys Leu Pro Lys Asp Thr Ala Leu Leu Leu Asp Pro Asn Ile Tyr	
270 275 280 285	
aga aca atg ccg cag aag agg ttg aag agg taa aaaaaaaaaa aaaaa	914
Arg Thr Met Pro Gln Lys Arg Leu Lys Arg *	
286 291 296	

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<211> 913

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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<400> 413

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	1 5	
cag ctg atg gcg gag gcc gag aag cga gtc aag gcc tcc cac tcc ttc	98	
Gln Leu Met Ala Glu Ala Glu Lys Arg Val Lys Ala Ser His Ser Phe		
12 17 22 27		
ctc cga ggg ctg ttt gga gga aac aca aga ata gaa gag gct tgt gaa	146	
Leu Arg Gly Leu Phe Gly Gly Asn Thr Arg Ile Glu Glu Ala Cys Glu		

28	33	38	43	
atg tat acc aga gct gca aat atg ttc aag atg gct aaa aat tgg agt				194
Met Tyr Thr Arg Ala Ala Asn Met Phe Lys Met Ala Lys Asn Trp Ser				
44	49	54	59	
gct gca gga aac gca ttt tgt cag gca gcc aag ctc cac atg cag ctt				242
Ala Ala Gly Asn Ala Phe Cys Gln Ala Ala Lys Leu His Met Gln Leu				
60	65	70	75	
cag agc aaa cat gac tct gct acc agc ttt gtg gat gct gga aat gct				290
Gln Ser Lys His Asp Ser Ala Thr Ser Phe Val Asp Ala Gly Asn Ala				
76	81	86	91	
tac aaa aag gca gat ccc caa gag gct atc aac tgc tta aat gca gcc				338
Tyr Lys Lys Ala Asp Pro Gln Glu Ala Ile Asn Cys Leu Asn Ala Ala				
92	97	102	107	
atc gac att tac aca gac atg gga agg ttt aca att gca gcc aag cac				386
Ile Asp Ile Tyr Thr Asp Met Gly Arg Phe Thr Ile Ala Ala Lys His				
108	113	118	123	
cac att act att gca gag atc tat gag act gaa ctt gta gac att gag				434
His Ile Thr Ile Ala Glu Ile Tyr Glu Thr Glu Leu Val Asp Ile Glu				
124	129	134	139	
aag gct att gca cat tat gaa caa tct gct gat tat tac aaa gga gaa				482
Lys Ala Ile Ala His Tyr Glu Gln Ser Ala Asp Tyr Tyr Lys Gly Glu				
140	145	150	155	
gaa tcc aac agc tca gca aac aag tgt ctg ctg aag gtg gca gca tat				530
Glu Ser Asn Ser Ser Ala Asn Lys Cys Leu Leu Lys Val Ala Ala Tyr				
156	161	166	171	
gct gcc cag ctt gag cag tac cag aaa gcc att gag atc tat gag cag				578
Ala Ala Gln Leu Glu Gln Tyr Gln Lys Ala Ile Glu Ile Tyr Glu Gln				
172	177	182	187	
gtt ggg gcc aac aca atg gaa tat ccc ttt gtg gaa tac agg cca aag				626
Val Gly Ala Asn Thr Met Glu Tyr Pro Phe Val Glu Tyr Arg Pro Lys				
188	193	198	203	
gat act tct tca aag ctg cct ttt gcc act cta tag agac gagttgaagg				676
Asp Thr Ser Ser Lys Leu Pro Phe Ala Thr Leu *				
204	209	214		
ccagcttgct cttgagaata tgaggaatgt tccagcatta ctgattcaga gatgtaaatt				736
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gctcatatct gcttgacaga gttgacacat gtggtcgatc aaagccttcc agggatgaga				856
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<400> 414

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acccggaacg gccgtcctct tcccccgccc tccgcgcgct cctccttctc ctctcctctc      240
tctcctcctt ccttctcggc ttctcctca gccccgggccc ggagcggggg gtcggcgggc      300
gccggttcgg gcggcgactc gcgcttcttt gggcgggcggc gcttggccat gtcgtgtcgg      360
ggaaggta atg agc cgc aga gcc ccg ggg tct cgg ctg agc agc ggc ggc      410
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              1              5              10

ggc ggc ggc ggc acc aag tat ccg cgg agc tgg aat gac tgg caa ccc      458
Gly Gly Gly Gly Thr Lys Tyr Pro Arg Ser Trp Asn Asp Trp Gln Pro
      15              20              25              30

aga act gat agt gca tca gcc gac cca gat aat tta aaa tat tct tca      506
Arg Thr Asp Ser Ala Ser Ala Asp Pro Asp Asn Leu Lys Tyr Ser Ser
      31              36              41              46

tcc aga gat aga ggt ggt tct tcc tct tat gga ctg caa cct tca aat      554
Ser Arg Asp Arg Gly Gly Ser Ser Ser Tyr Gly Leu Gln Pro Ser Asn
      47              52              57              62

tca gct gtg gtg tct cgg caa agg cac gat gat acc aga gtc cac gct      602
Ser Ala Val Val Ser Arg Gln Arg His Asp Asp Thr Arg Val His Ala
      63              68              73              78

gac ata cag aat gac gaa aag ggt ggc tac agt gtc aat gga gga tct      650
Asp Ile Gln Asn Asp Glu Lys Gly Gly Tyr Ser Val Asn Gly Gly Ser
      79              84              89              94

ggg gaa aat act tat ggt cgg aag tcg ttg ggg caa gag ctg agg gtt      698
Gly Glu Asn Thr Tyr Gly Arg Lys Ser Leu Gly Gln Glu Leu Arg Val
      95              100              105              110

aac aat gtg acc agc cct gag ttc aca agt gtt cag cat ggc agt cgt      746
Asn Asn Val Thr Ser Pro Glu Phe Thr Ser Val Gln His Gly Ser Arg
      111              116              121              126

gct tta gcc acc aaa gac atg agg aaa tca cag gag aga tcg atg tct      794
Ala Leu Ala Thr Lys Asp Met Arg Lys Ser Gln Glu Arg Ser Met Ser
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tttgctttga agtcaccttc ttatcttttg ccttggttga ctctgaagg caaa atg	297
Met	
1	
gat cac aag cag ctc tgc tgg agc cac cca caa aaa tct ggc cag agt	345
Asp His Lys Gln Leu Cys Trp Ser His Pro Gln Lys Ser Gly Gln Ser	
2 7 12 17	
tct cgc tct tgt tgc atc tgc tca aac cag cat ggt ctg atc tgg aaa	393
Ser Arg Ser Cys Cys Ile Cys Ser Asn Gln His Gly Leu Ile Trp Lys	
18 23 28 33	
tat agc ctc aat atg tgc ctc cag tgt tgc cat cag tac gtg aag gat	441
Tyr Ser Leu Asn Met Cys Leu Gln Cys Cys His Gln Tyr Val Lys Asp	
34 39 44 49	
ata ggt ttc att aaa ttg gac taa gtgatcttcc ttgaatggat tatccaaggc	495
Ile Gly Phe Ile Lys Leu Asp *	
50 55	
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 <222> (589) .. (858)

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gcagagagaa gggactgaac caggagcccc aaggcagggg tctggccctc cagaagatgg	180
gtcaagagga agagagccct ccaagagagg agaggcccca gcagagtcca aaggtacagt	240

gtggagccgc ctgacaagga ctgccatcca cc	atg gtg aag ctg ggc tgc agc	173
	Met Val Lys Leu Gly Cys Ser	
	1 5	
ttc tct ggg aag cca ggt aaa gac cct ggg gac cag gat ggg gct gcc	221	
Phe Ser Gly Lys Pro Gly Lys Asp Pro Gly Asp Gln Asp Gly Ala Ala		
8 13 18 23		
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Met Asp Ser Val Pro Leu Ile Ser Pro Leu Asp Ile Ser Gln Leu Gln		
24 29 34 39		
ccg cca ctc cct gac cag gtg gtc atc aag aca cag aca gaa tac cag	317	
Pro Pro Leu Pro Asp Gln Val Val Ile Lys Thr Gln Thr Glu Tyr Gln		
40 45 50 55		
ctg tcc tcc cca gac cag cag aat ttc cct gac ctg gag ggc cag agg	365	
Leu Ser Ser Pro Asp Gln Gln Asn Phe Pro Asp Leu Glu Gly Gln Arg		
56 61 66 71		
ctg aac tgc agc cac cca gag gaa ggg cgc agg ctg ccc acc gca cgg	413	
Leu Asn Cys Ser His Pro Glu Glu Gly Arg Arg Leu Pro Thr Ala Arg		
72 77 82 87		
atg atc gcc ttc gcc atg gcg cta ctg ggc tgc gtg ctg atc atg tac	461	
Met Ile Ala Phe Ala Met Ala Leu Leu Gly Cys Val Leu Ile Met Tyr		
88 93 98 103		
aag gcc atc tgg tac gac cag ttc acc tgc ccc gac ggc ttc ctg ctg	509	
Lys Ala Ile Trp Tyr Asp Gln Phe Thr Cys Pro Asp Gly Phe Leu Leu		
104 109 114 119		
cgg cac aag atc tgc acg ccg ctg acc ctg gag atg tac tac acg gag	557	
Arg His Lys Ile Cys Thr Pro Leu Thr Leu Glu Met Tyr Tyr Thr Glu		
120 125 130 135		
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Met Asp Pro Glu Arg His Arg Ser Ile Leu Ala Ala Ile Gly Ala Tyr		
136 141 146 151		
ccg ctg agc cgc aag cac ggc acg gag acg ccg gcg gcc tgg ggg gac	653	
Pro Leu Ser Arg Lys His Gly Thr Glu Thr Pro Ala Ala Trp Gly Asp		
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Ile Gly Lys Leu Leu Phe Asp Tyr Asp Lys Val Glu Leu Ala Asn
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